



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 117363

To: **Phuong Bui**
Location: **rem 2a15& 2c18**
Art Unit: **1638**
Tuesday, March 23, 2004

Case Serial Number: **10/059909**

From: **Beverly Shears**
Location: **Remsen Bldg.**
RM 1A54
Phone: **571-272-2528**

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Search Notes

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: March 22, 2004, 21:56:37 ; Search time 11831 Seconds
(without alignments)
11481.453 Million cell updates/sec

Title: US-10-059-909-15
Perfect score: 3134
Sequence: 1 ccacgcgtccggccgagcg.....aaaaaaaaaaaaaaaaag 3134

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1780.2	56.8	3167	8	AK072689	AK072689 Oryza sat
2	1698	54.2	2851	8	AK072869	AK072869 Oryza sat
3	1582.4	50.5	3003	8	BLYLOXB	L37359 Hordeum vul
4	1523.4	48.6	2516	6	AX660218	AX660218 Sequence
5	1424.6	45.5	2115	6	AX653247	AX653247 Sequence
6	1326	42.3	3007	6	AR404677	AR404677 Sequence
7	1324	42.2	2595	6	AR404678	AR404678 Sequence
8	1324	42.2	2595	8	AF329371	AF329371 Zea mays
9	1275.2	40.7	2845	8	AF271894	AF271894 Zea mays
10	1222.2	39.0	2818	6	AR438184	AR438184 Sequence
11	1222.2	39.0	2818	6	AX469803	AX469803 Sequence
12	1222.2	39.0	2818	6	AX469867	AX469867 Sequence
13	1222.2	39.0	2818	8	BLYLOXA	L35931 Barley lipo
14	1210.2	38.6	2928	8	AK073529	AK073529 Oryza sat
15	1209	38.6	2613	6	AX653181	AX653181 Sequence
16	1198.2	38.2	2910	8	BLYLOXC	L37358 Hordeum vul
17	1148.2	36.6	2830	6	E03480	E03480 cDNA encodi
18	1148.2	36.6	2830	8	OSLRNA	X64396 O.sativa mR
19	1130.2	36.1	2830	8	AK103565	AK103565 Oryza sat
20	1119	35.7	2988	8	AB099850	AB099850 Oryza sat
21	1119	35.7	3033	6	BD180907	BD180907 Novel ric
22	1111.6	35.5	1726	8	AK071121	AK071121 Oryza sat
23	1066.8	34.0	2559	6	AX653886	AX653886 Sequence
24	1053.4	33.6	2267	8	AF149803	AF149803 Zea mays
25	1017.8	32.5	1560	8	AK105792	AK105792 Oryza sat
26	906.4	28.9	155106	8	AC117988	AC117988 Oryza sat
27	850.6	27.1	3010	8	AK073570	AK073570 Oryza sat
28	830.6	26.5	124138	8	AC093017	AC093017 Oryza sat
29	796.6	25.4	2835	8	AF361893	AF361893 Gossypium
30	777.6	24.8	2562	8	ATH302043	ATH302043 Arabidops
31	774	24.7	2930	8	AK102084	AK102084 Oryza sat
32	772.6	24.7	2589	8	PD0418043	AJ418043 Prunus du
33	768.8	24.5	2655	8	FRX578035	AJ578035 Fragaria
34	767.6	24.5	2854	8	AD001673	AD001673 Persea am
35	762.4	24.3	1814	8	TAU32428	U32428 Triticum ae
36	760	24.3	5013	8	AF465643	AF465643 Zea mays
37	751.4	24.0	2574	8	AY162142	AY162142 Brassica
38	749.6	23.9	200626	8	AC109929	AC109929 Oryza sat
39	748.2	23.9	2888	8	NTRNALOX1	X84040 N.tabacum m
40	748.2	23.9	3390	6	AX644612	AX644612 Sequence
41	729.6	23.3	2580	6	AX506809	AX506809 Sequence
42	729.6	23.3	2580	6	AX651411	AX651411 Sequence
43	729.6	23.3	2580	8	BT010358	BT010358 Arabidops
44	729.6	23.3	2797	8	AY093104	AY093104 Arabidops
45	729.6	23.3	2801	8	ATHLIPOXY	L04637 Arabidopsis

ALIGNMENTS

RESULT 1
AK072689
LOCUS
DEFINITION
AK072689
Oryza sativa (japonica cultivar-group) cDNA clone:J023143H13, full
insert sequence.
ACCESSION
AK072689
VERSION
AK072689.1 GI:32982712
KEYWORDS
FLI_CDNA; CAP trapper.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1
AUTHORS
The Rice Full-Length cDNA Consortium, National Institute of

AK072689 3167 bp mRNA linear PLN 24-JUL-2003
Oryza sativa (japonica cultivar-group) cDNA clone:J023143H13, full
insert sequence.

Agrobiological Sciences Rice Full-Length cDNA Project Team:
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
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Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J.,
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Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y.,
Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Yoshino, M. and Hayashizaki, Y.

FEATURES

ORIGIN

Query Match 56.8%; Score 1780.2; DB 8; Length 3167;
Best Local Similarity 79.9%; Pred. No. 1.1e-250;
Matches 2159; Conservative 0; Mismatches 513; Indels 31; Gaps 4

QY	203	GAAGCGAGGAGCGAGAAAGCGCAAGAGCGGCCATGTTCTGGCACGGGGTTCGCGACCGGC	267
DB	261	GAGGAGGGGATTGTGACTTGTGATCTGCGAGGATGCGAGGTGCAGGGGTCTTTGACAGGT	320
QY	263	TGACGGGAAAGAAACAAGAGGCGTGGAGCGAGGGCAAGATCCGCGGCACGGTGAGGCTGG	322
DB	321	TGACGGGAGGAAACAAGAGGCGTGGAAAGGAGGAGGATCCGTGGGACGGCGGTGCTGG	380
QY	323	TCAAGAAAGGAGGTGCTGGACGTGCGCGACTTCAACGCCTCGCTCCTCGACGGCGTCCACA	382
DB	381	TGAAGAAAGGACGTGCTCGGCTCGGCGACTTCCACGCCCTCCCTCGACGGCGTCCACA	440
QY	383	GGATCCTCGGCTGGGACGACGGCGTGCCTTCCAGTCTGTCAGCGCCACCGCGGCCGACC	442
DB	441	ACATCCTCGGCCACAAGAGGGCGTGCCTTCCGCCTCGTCAGCGCCACCGCCCGCGACC	500
QY	443	CCAGCAACGGGGCCGTGGCAAGGTGGGAAGCGCGGCACCTGGAGGAGCGGTGGTGT	502
DB	501	CAAGCAATGGAGGGAGGGGAAGCTGGGAAGCCGGCGCACCTGGAGGAGTGGTGGTGA	560
QY	503	CGCTCAAGTCCACGGCGGACGGGAGACCGGTGTACCGSGTGAGCTTCGAGTGGGACGAGT	562
DB	561	CGATGAAGTCGACGGCGCGGGGAGTCGGTGTTCGGGTGGCGTTCGAGTGGGACGAGT	620
QY	563	CGCAGGGCATCCCGGCGCCGTCTGCTGAGCAAGCTGCAGCACGCCGAGTCTCTTCCTCA	622
DB	621	CGCAGGGGATCCCGGCGCCGTGCTGCTACCAACTCCAACCGGTCCGAGTCTCTTCCTCA	680
QY	623	AGACGCTCACCTCGAGGGCGTCCCAGGCAAGGGCACCGTCTTCTCGTCGCCAACTCGT	682
DB	681	AGACGCTCACCTCGACGGCGTCCCCGGCAAGGGCACCGTCTTCTCGTCGCCAACTCGT	740
QY	683	GGGTCTACCCGCAAAAGCTCTACTCCCAGGAACGCATCTTCTTCGCCAACGACACCTATC	742
DB	741	GGATCTACCCCGCGACAACCTACAGTACGAGCGCGTCTTCTTCGCCAACGATACATATC	800
QY	743	TGCCGAGCAAAATGCCGGCGGCGTTGGTGCCTTATCGGCAAGATGAGCTCAAGATTCTCC	802
DB	801	TGCCTAGCAAAATGCCTGCACCTTTGATCCCTTACCGGCAAGAACTCAACATTCTAC	860
QY	803	GTGGCGACGATAATCCTGGACCATAACGAGGACATGATCGCGTCTACCGTTACGACTACT	862
DB	861	GAGGGGACGGTAAAAATTGGACCATACAAGGACATGACCGTATCTACCGTTATGATTACT	920
QY	863	ACAATGACCTTGGTGATCCCGACAAGGGCGAAGAGCACGCTCGGCCGATCTCTCGGTGGCA	922
DB	921	ATAACGACCTTGGCCAAACAGACAAGGCGAGTAAGTAAGTAACTAGTACGACCGTCCCCGGTGGCA	980
QY	923	GCCAAAGAACCCCGTATCCCGTCGCTGCAAGAACTGGCCGGCACCCCAACAAAGAAAGACC	982
DB	981	GCCAAAGAACTCCCTATCCCGTCGAGGCGAGAACTGGCCGGGCCCCCAACAAAGACTGACC	1040
QY	983	CAAAATTCGGAGACGAGGCTTTTCTGCTGAACCTGAACATCTACGTCCCGCGTGACGAAC	1042
DB	1041	CAAAATACAGAAAGCAGGCTTCCCTCTGCTGGACTTGAACATTTATGTCCACGCGACGAAC	1100

QY 1043 GCTTTGGGCATCTCAAGATGTTCGGACTTCCCTTGGGTAATCGCTGAAGACGATCATCGAGG 1102
Db 1101 GGTTCGGGCACCTCAAGATGTTCAGACTTCCCTTGGGTAATCTCTTAAGGCTATGTGTGAGG 1160
QY 1103 CTGTTCTTCCAAACACTGGGACTTTCGTGATGACACGCCCAAGGAGTTCGATTGTTG 1162
Db 1161 GTGTTCTCCCAATAATAAGACCTATGTGATACGACACCAAGGAGTTGATTCTTTTC 1220
QY 1163 AGGATATCCTCGGGCTTCAGAGCTGGGCCAGAGGACCCCAACAACCCACTGATAGCAG 1222
Db 1221 AAGACATCATGGAACCTCTATGAAGGTGGATTGAAGTGGCCAAATGCCTCTGCAC TAGCAG 1280
QY 1223 AGATCAGGAAGAAGATCCCGACGAGTTCCTTCGAAGCATCTTCGCCGAACGGTAGCCATG 1282
Db 1281 AGATCAAGAAGAGAGTTCCCTTTGAACCTTATTAAGAGTCTTTTGGCCAGTTGCTGGC--G 1337
QY 1283 ACCACCCGCTAAAGATGCCCTTCCAAATGTCAATAATCAGATGTGTGAAAAAGGCTC 1342
Db 1338 ATCAAGTCTTGAAGTTACCCCTACCACATGTTATCAAA----- 1375
QY 1343 CGGAGTTTAAGTTTGGCTGGAGGACTGACGAAGAGTTCCGGAGAGAGACACTTGCAGGCG 1402
Db 1376 --GAGGACAAATTTGCTTGAGGACTGATGAGGAGTTTGACGAGAAATGCTCGCAGGAG 1433
QY 1403 TGAACCCAGTAATCATCAAAACGCTGACCGGAGTTTCCCGCTAAAAGCACCTTGGACCCAA 1462
Db 1434 TTAACCCAGTGATGATCAAGCGTCTGACGAATTTCCCGCAAAAAGTACTCTGGATCCAA 1493
QY 1463 GGCAGTACGGAGACCACACAGCAAGATCACTGAAGCTCACATCCGGCATAAACATGGGAG 1522
Db 1494 ATGTGTACGGTGACCATACCAGCAAGATCACCGAAGTCCACATTAAGCAACAATGGAGG 1553
QY 1523 GCCTGTCCGTGCAGAACGCACTGAGGAACAAGAGGCTCTTCATCCTAGACCAACCATGACC 1582
Db 1554 GCCTCACGGTGCAAAATGCACTGAAGGGCAACAGGCTTTTCATCCTAGACCAACCATGTC 1613
QY 1583 ATTTTCATGCCGTACCTGACGAGATCAACGAGGTGGAGGGGAATTTTCATCTACGCCAGCA 1642
Db 1614 ACTTCATGCCGTTCTTGACAAGATCAACAAGTTGACGGTAACCTTCATATATATGCGAGCA 1673
QY 1643 GGACCCCTACTGTTCTGAAGGACGATGGCACGCTGAAGCCCTTGCCATCGAGCTGAGCC 1702
Db 1674 GGACCATCTGCTCCTGAAGGACGATGGCACCTGAAGCCCTTGGCGATCGAGCTGAGCC 1733
QY 1703 TGCCCCACCTTGACGGCCAGCAGCGCGCGGTGAGCAAGGTGTAACCCCGGCTCACA 1762
Db 1734 TGCCGCACCCCGATGGCCAGCAGCACCGCGCCCTCAGCAAGGTGTACACTCCAGCCAAACA 1793
QY 1763 CCGGCGTTCGAGGGCCAGCTTGGCAGCTCGCCAAGGCTTATGCTGCGTAAACGACTCTG 1822
Db 1794 CCGGCGTTCGAGAGCCAAATCTGGCAGCTCGCCAAAGGCTTACGCTCCGTCAACGACTCTG 1853
QY 1823 CCTGGCATCAGCTGATCAGCCACTGGCTGAACACGACGCGGTGATGAGCCGTTTCGTAA 1882
Db 1854 CTTGGCACCACTGATCAGCCACTGGCTGAACACTCACGCCGTGATCAGCCGTTTCGTGA 1913
QY 1883 TCGCGACAAACCGGCAGCTCAGCGTGGTGCTATCCCGTGCAAGCTGCTGAGCCCGCACT 1942
Db 1914 TCGCGACGAACCGGCAGCTCAGCGTGGTGCCACCCCGTGCAAGCTGCTGAGCCCGCACT 1973
QY 1943 ACCGTGACACGCTGAACATCAACGCCCTGGCACGCCAGACACTCATCAACCGCGGGCGG 2002
Db 1974 ACCGCGACACGATGAACATCAACGCTCTGGCACGGCAGACACTCATCAACCGCGATGGCA 2033
QY 2003 TCTTCGAGCGCACCGGTCTCCCTGCAAAAGTACCGCTGGGGATGTCCGCAGACGTTGTACA 2062
Db 2034 TCTTCGAGAAGACCGGTCTCCAGGCAAGTACCGCTCGAGATGTCTCTCCGTCTGTGTACA 2093
QY 2063 AGAGCTGGAATTTCAACGAGCAGGCTCTCCACAGCAGATCTCGTCAAGAGAGGTGTGGCTG 2122
Db 2094 AGAAGTGAAGTTTCCAGGACGAGGCTCTCCCGCTCGATCTCGTCAAGAGAGGGGTGGCCG 2153
QY 2123 TGCCGGACCACTCAAGCCCCATATGGTGTCCGACTGCTGATCAAGGACTACCCCTATGCCG 2182

Db 2154 TGCCGACCCGACGAGCCCGTACAACGTCCGGCTGCTGATCAAGGACTACCCGTACGCCG 2213
QY 2183 TTGACGGGCTCGTCACTCTGTTGGGCGGATCGAGCGGTTGGGTCAAGGAGTACCTGGACATCT 2242
Db 2214 TGAACGGGCTGGTATCTGTTGGGCGATCGAGCGGTTGGGTGGGCGAGTACCTGGCCATCT 2273
QY 2243 ACTACCTTAACGACGGCGAGCTCCAGCGTGAAGCTGAGGCTGCAGGCGTGGTGAAGGAGG 2302
Db 2274 ACTACCCCAACGACGGCGTCTCCGGCGGACGAGGAGCTGCAGGCGTGGTGAAGGAGG 2333
QY 2303 TGCGTGAGG-AGGCGCACGGCGACCTCAAGGACCGAGACTGGTGGGCCAGGATGGACACC 2361
Db 2334 TGCGGAGGTGGGCCATGGCGACCTCAAGGACCGACTGGTGGGCCAAGATGGACACC 2393
QY 2362 GTCCAGCAGCTGGCTAGGGCGTGACGACCATCATCTGGGTGGCATCCGCGCTGCACGCG 2421
Db 2394 GTCCAGGAGCTCACCCGGCGTGACCATCATCATCTGGATCGCGTCCGCGCTGCACGCG 2453
QY 2422 GCTGTCAACTTTGGGCACTACCCATACGCCGGGTACCTCCGAACCGGCCGACGCCCAGC 2481
Db 2454 GCGGTCAACTTCGGCCAGTACCCGTACCGGGGTTCTCTCCGAACCGGCCGACGGTGAGC 2513
QY 2482 CGGCGCCGATGCCGGAGCGGAGCGCACGACTACAAAGAAAGCTGGAGCGGGGCGAGAAG 2541
Db 2514 CGGCGCCGATGCCGGAGCGGGCACCGAGGAGTACGCGAAAGCTGGAGCGCGCGGTGAC 2573
QY 2542 GAGCGCGACATGGTGTTCATCCGACCCATCACCAAGCAGTTCAGACCATCTCTGGGSCATC 2601
Db 2574 GAGCGCGACCTGGTGTTCATCCACACAATCACCAAGCAGTTCAGACCATCTCTCGGCATC 2633
QY 2602 TCGTTCATCGAGATCCTCTCCAAGCACTCCTCCGACGAGGTGTACCTCGGCCAGCGTGAC 2661
Db 2634 TCGTTCATCGAGATCCTCTCCAAGCACTCCTCCGACGAGGTCTACCTCGGCCAAGCGGAC 2693
QY 2662 GAGCTGATCGCTGGACGTCAGACGCCAAGCGCTGGATCGTTCAAAGAGATTCCGGGAGC 2721
Db 2694 ACGCCGGA--GTGGACGTCGGACGCCAAGCGCTGGACGCGTTCAAGAGGTTCCGGCAGC 2750
QY 2722 CGGCTGGTGCAGATTGGAATGCCGTACATGCTGTGTACCCCAACACAGCTCGGACGTTAAC 2781
Db 2751 CGGCTGGTGGATATCGAGAACCAGGATCAAGGACATGAACGGCACTCGGCGCTCAAGAAC 2810
QY 2782 CGGAAGGGCCCTGTGGAATGCCGTACATGCTGTGTACCCCAACACAGCTCGGACGTTACC 2841
Db 2811 CGGAACGGCCCGTGAAGATGCCGTACATGCTGTGTACCCCAACACAGCTCGGATGTCACC 2870
QY 2842 GCGAGAAGGGCCGAGGGGCTTACTGCCATGGGCAATCCCAACAGCATCTCCATATGAGCC 2901
Db 2871 AAGGAGAAGGGCCAAAGGCTCACCGCCATGGGCAATCCCAACAGCATCTCCATCTGAGTC 2930
QY 2902 TGG 2904
Db 2931 TCG 2933

RESULT 2
AK072869

LOCUS Oryza sativa (japonica cultivar-group) cDNA clone.J023143017, full insert sequence.
DEFINITION

AK072869

VERSION AK072869.1 GI:32982892

KEYWORDS FLI.CDNA; CAP trapper.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE 1

AUTHORS The Rice Full-length cDNA Consortium, National Institute of

Agrobiological Sciences Rice Full-length cDNA Project Team,

Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,

2851 bp mRNA linear
Oryza sativa (japonica cultivar-group) cDNA clone.J023143017, full insert sequence.

AK072869
AK072869.1 GI:32982892

FLI.CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1

AUTHORS The Rice Full-length cDNA Consortium, National Institute of

Agrobiological Sciences Rice Full-length cDNA Project Team,

Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,

Db 886 CTTTTCAGACATCATGGAACCTCTATGAAGGTGGATGAAAGTGGCCAAATGCCTCTGCAC 945
Qy 1217 TAGCAGAGATCAGGAAGAAGATCCCCACGCGAGTTCCTTCGAAGCATTCCTGCCGAACGGTA 1276
Db 946 TAGCAGAGATCAAGAAGAGAGTTCCTTTGAACTATTAAAGAGTCTTTTGCCAGTTGCTG 1005
Qy 1277 GCCATGACCAACCCGCTAAAGATGCCCTTCCAAATGTTCATCAATCAGATGTGTTGAAAA 1336
Db 1006 GC---GATCAAGTCTTGAAGTTACCCCTACCAATGTTATCAAA----- 1046
Qy 1337 AGGCTCCGGAGTTTAAGTTTGGCTGGAGGACTGACGAAGAGTTTCGCGAGAGAGACACTTG 1396
Db 1047 -----GAGGACAAATTTGCTTGGAGGACTGATGAGGAGTTTGCACGAGAAATGCTAG 1098
Qy 1397 CAGGCGTGAACCCAGTAATCATCAAAACGCTGACGGAGTTCCCGCTAAAAGCACCCCTGG 1456
Db 1099 CAGGAGTTAACCCAGTGATGATCAAGCGCTGACGAATTTCCCGGCAAAAAGTACTCTGG 1158
Qy 1457 ACCCAAGGCAGTACGGAGACCAACACGAGCAAGATCACTGAAGCTCACATCCGGCATAACA 1516
Db 1159 ATCCAAATGTGTACGGTGACCATACCCAGCAAGATCACCGAAGCTCACATTAAGCACAA 1218
Qy 1517 TGGGAGGCCTGTTCGGTGAGAACGCACTGAGGAACAAGAGGCTCTTCATCCTAGACCACC 1576
Db 1219 TGGAGGGCCTCACGGTGCAAAATGCACCTGAAGGCAACAGGCTTTTCATCCTAGACCACC 1278
Qy 1577 ATGACCAATTTATGCGGTACCTCGACGAGATCAACGAGCTGGAGGGAACCTTCATCTACG 1636
Db 1279 ACGATCACTTCATGCGGTTCTTGACAAGATCAACAAGTTGGACGTAACCTTCATATATG 1338
Qy 1637 CCAGCAGGACCTACTGTTCTCTGAAGGACGATGGCACGCTGAAGCCCTGGCCATCGAGC 1696
Db 1339 CGAGCAGGACCATTCCTGCTCTGAAGGACGATGGCACCCCTGAAGCCCTGGCGATCGAGC 1398
Qy 1697 TGAGCCTGCCCCACCTGACGGCCAGCAGCGCGCGCGGTGAGCAAGGTGTACACCCCGG 1756
Db 1399 TGAGCCTGCCGACCCCGATGGCCAGCAGCAGCGCGCGCGGTGAGCAAGGTGTACACTCCAG 1458
Qy 1757 CTCACACCGCGCTCGAGGGCCACGCTCTGGCAGCTCGCCAAGGCTTATGCCTGCGTAAACG 1816
Db 1459 CCAACACCGCGCTCGAGAGCCAAATCTGGCAGCTCGCCAAGGCTTACGCTCCGTCACG 1518
Qy 1817 ACTCTGCTGGCATCAGCTGATCAGCCACTGGCTGAACACGCGCGGCTGATCGAGCCGT 1876
Db 1519 ACTCTGCTGGCACCAGCTGATCAGCCACTGGCTGAACACTCAGCGCTGATCGAGCCGT 1578
Qy 1877 TCGTAATCGCGCAAAACCGGACGCTCAGCGTGGTGATCCCGTGACAAAGCTGCTGAGCC 1936
Db 1579 TCGTGATCGCGAGCAACCGGACGCTCAGCGTGGTGACACCCCGTGCAAGGCTGCTGAGCC 1638
Qy 1937 CGCACTACCGTGACAGCTGAACATCAACGCGCTGGCACGCGCAGACACTCATCAACGCGG 1996
Db 1639 CGCACTACCGCGACACGATGAACATCAACGCTCTGGCACGCGCAGACACTCATCAACGCGG 1698
Qy 1997 GCGGCGTCTTCGAGCGCACCGTGTTCCTTGCAAAAGTACGCGCTGGGATGTCGGCAGAG 2056
Db 1699 ATGGCATCTTCGAGAAGACCGTCTTCCAGCAAGTACGCGCTCGAGATGTCCTCCGTCG 1758
Qy 2057 TGTACAAGAGCTGGAATTTCAACGAGCAGGCTCTCCAGCAGATCTCGTCAAGAGAGGTG 2116
Db 1759 TGTACAAGAACTGGAAAGTTCAACGAGCAGGCTCTCCCGTCTGATCTCGTCAAGAGAGGGG 1818
Qy 2117 TGGCTGTGCCGACAGTCAAGCCCATATGTTGTCGACTGCTGATCAAGGACTACCCCT 2176
Db 1819 TGGCCGTGCCGAGCCCGACGAGCCCGTACAACGCTCCGGCTGCTGATCAAGGACTACCCGT 1878
Qy 2177 ATGCCGTTGACGGGCTCGTTCATCTGTTGGGCGATCGAGCGGTGGTCAAGGAGTACCTGG 2236
Db 1879 ACGCCGTGGACGGGCTGGTGTATCTGTTGGCGGATCGAGCGGTGGTGGCGAGTACCTGG 1938
Qy 2237 ACATCTACTACCTAAACGACGGCGAGCTCCAGCGTGACGTGGAGTGCAGGCGTGGTGA 2296
Db 1939 CCATCTACTACCCCAACGACGCGGCTGCTCCGCGGCGACGAGGAGTGCAGGCGTGGTGA 1998

Qy 2297 AGGAGTGCCTGAGGAGGCGCACGGCGACCTCAAGGACCGAGACTGGTGGCCCAAGATGG 2356
Db 1999 GGGAGGTGCGCGAGGTGCGCCATGGCGACCTCAAGGACCGAGACTGGTGGCCCAAGATGG 2058
Qy 2357 ACACCGTCCAGCAGCTGGCTAGGGCGTGACAGCAGCAGCATCTGGGTGGCATCCGCGCTGC 2416
Db 2059 ACACCGTCCAGGAGCTCACCGGGCGTGACCCATCATCTGGATCGCGTGGCGCTGC 2118
Qy 2417 ACGGCGCTGTCAACTTTGGGAGTACCCCATACGCGGGGTACCTCCCGAACCGGCGCAGCG 2476
Db 2119 ACGGCGCGGTCAACTTCGCGCAGTACCCGTACGCGGGGTTCCTCCCGAACCGGCGCAGCG 2178
Qy 2477 CCAGCGCGCGCCGATGCGGAGCCAGGAGCCACGACTACAAGAGCTGGAGCGGGGC 2536
Db 2179 TGAGCGCGCGCGGATGCGGAGCCGGGACCCGAGGAGTACGCGAAGCTGGAGCGCGCG 2238
Qy 2537 AGAAGGAGGCGGACATGTTGTTTCATCCGACCATCACAGCCAGTTCAGACCATCTCTGG 2596
Db 2239 GTGACGAGGCGGACCTGTTTCATCCACAAATCACAGCCAGTTCAGACCATCTCTCG 2298
Qy 2597 GCATCTCGCTCATCGAGATCCTCTCCAAGCACTCTCCGACGAGGTCTACCTCGGCGAAC 2656
Db 2299 GCATCTCGCTCATCGAGATCCTGTCCAAGCACTCTCCGACGAGGTCTACCTCGGCGAAC 2358
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RESULT 3
BLYLOXB
LOCUS 3003 bp mRNA linear PLN 06-JUL-1999
DEFINITION Hordeum vulgare lipoxigenase (LoxB) mRNA, complete cds.
ACCESSION L37359
VERSION L37359.1 GI:2182266
KEYWORDS
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 3003)
AUTHORS van Mechelen,J.R., Schuurink,R.C., Smits,M., Graner,A., Douma,A.C., Sedee,N.J., Schmitt,N.F. and Valk,B.E.
TITLE Molecular characterization of two lipoxigenases from barley
JOURNAL Plant Mol. Biol. 39 (6), 1283-1298 (1999)
MEDLINE 99308521
PUBMED 10380814
REFERENCE 2 (bases 1 to 3003)
AUTHORS Van Mechelen,J.R.
TITLE Direct Submission
JOURNAL Submitted (08-NOV-1994) Plantbiotechnology, Center for Phytotechnology, Wassenaarseweg 64, Leiden 2333AL, Netherlands
REFERENCE 3 (bases 1 to 3003)
AUTHORS Van Mechelen,J.R.
TITLE Direct Submission

Db 1242 CACGGAGATGCTCGCAGCGGTTGACCCGGTTTGCATCAGACGTCCTGACGAAGTTCCTG 1301
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RESULT 4
AX660218
LOCUS AX660218 2516 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 575 from Patent WO03000906.
ACCESSION AX660218
VERSION AX660218.1 GI:29162108
KEYWORDS
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1
AUTHORS Glazebrook,J., Briggs,S., Cooper,B., Goff,S.A., Moughamer,T.,
Katagiri,F., Kreps,J., Provart,N., Ricke,D. and Zhu,T.
TITLE Plant disease resistance genes
JOURNAL Patent: WO 03000906-A 575 03-JAN-2003;
Syngenta Participations AG (CH)
FEATURES
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:4530"

ORIGIN
Query Match 48.6%; Score 1523.4; DB 6; Length 2516;
Best Local Similarity 77.5%; Pred. No. 4e-213;
Matches 2004; Conservative 0; Mismatches 456; Indels 127; Gaps 8;
QY 243 GCACGGGGTTCGGGACCGGGTACGGGAAGAAAGAGGCGGTGGAGCGGCAAGAT 302
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QY 303 CCGCGGCACGGTGAGGCTGGTCAAGAAGGAGGTGCTGGACGTGGCGACTTCAACGCCTC 362
Db 69 CCGTGGGACGGCGGTGCTGGTGAAGAAGGAGTGTCTGGCCTCGGCGACTTCCACGCCTC 128
QY 363 GCTCCTCGACGGCTCCACAGGATCCTCGGCTGGGACGACGGCGTTCGCTTCCAGTCTGT 422
Db 129 CTTCTCGACGGCGTCCAC----- 147
QY 423 CAGGCCCAACCGCGCGCACCCAGCAACCGGGGCGGTGGCAAGGTGGGAAGGCGGCGCA 482

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Db 184 CTTGAGGAGCTGGTGGTGAACATGAAGTCGACGGCGGCGGGGAGTCGGTGTTCGGGT 243
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Db 2580 CAGCATCTCCATCTGA 2595
|||||

RESULT 8
AF329371
LOCUS AF329371 2595 bp mRNA linear PLN 31-JAN-2001
DEFINITION Zea mays lipoxxygenase mRNA, complete cds.
ACCESSION AF329371
VERSION AF329371.1 GI:12620876
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 2595)
Wilson, R.A., Gardner, H.W. and Keller, N.P.
Cultivar-dependent expression of a maize lipoxxygenase responsive to
seed-infesting fungi
Unpublished
2 (bases 1 to 2595)
Wilson, R.A., Maddox, J., Duveck, J. and Keller, N.P.
Direct Submission
Submitted (14-DEC-2000) Plant Pathology and Microbiology, Texas A&M
University, TAMUS 2132, College Station, TX 77843, USA
Location/Qualifiers
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1..2595
/codon_start=1
/product="lipoxxygenase"
/protein_id="AAG61118.1"
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LGGADHPYPRRCRTGRKPTKTDPSDSRLSLVEQIYVPRDERFHLKMSDFLGSIK
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KEYEELRDPERGFHTITSQIOTIIGISLIEILSHSDEVYLGQRTDPEWTSDARA
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ORIGIN
Query Match 42.2%; Score 1324; DB 8; Length 2595;
Best Local Similarity 71.7%; Pred. No. 5.6e-184;
Matches 1904; Conservative 0; Mismatches 680; Indels 72; Gaps 10;
QY 246 CGGGGTCCGGACCGCTGACGGGAAAGAACAGGAGGCGTGGAGCGGCAAGATCCG 305

Db 9 CGGATCATCGACGGGCTGACGGGGCGAACAAGCATGCGCGCTCAAG----- 57
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QY 306 CGGCACGGTGAGGCTGGTCAAGAAAGAGGTGCTGGAGCTGGCGACTTCAACGCTCGCT 365
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Db 58 -GGCACGGTGGTCTCATGCGCAAGAACGTGCTGGACCTCAACGACTTCGGCGCACCGT 116
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QY 366 CCTCGACGGCGTCCACAGGATCCTCGGCTGGGACGACGGCGTGCCTTCCAGTCTGTCA 425
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Db 117 CGTTGACAGCATCAGCGAGTTCCTCGGCA-----AGGGGTACCTGCCAGTCTATCAG 170
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QY 426 CGGCACCGCGCGACCCACAGCAACGGGGCCGCTGSCAAGTGGGAAGGCGCGCACCT 485
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Db 171 CTCACCTCTGTCGACGCCCAACACGGCAACCGCGGGCGGTTCGGGCGGAGCGAACCT 230
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QY 486 GGAGGAGCGGTGGTGTGCTCAAGTCCACGGCGGACGGGAGACCGTGTACCGGTGAG 545
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Db 231 GGAGCAGTGGCTGACGAGCTGCCGTGCTGACGACGCGGAGTCCAAATTTCGGCGTCA 290
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QY 546 CTTGAGTGGGA---CGAGTCGACGGGCATCCCGGGCGCGCTCCTGGTCAGGAACCTGCA 602
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Db 291 GTTCGACTGGAGGTGGAGAGCTGGGAGTCCCGGGGCGCTCGTCGTCAGGAACAACCA 350
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QY 603 GCACGCGAGTTCCTTCTCAAGACGCTCACCTTCAGGGCGTCCCAGGCAAGGACACCT 662
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Db 351 CGCGCGGAGTTCCTTCTCAAGACAATCACCTTCAGACGCTGCCCGCGCGCGCT 410
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QY 663 CGTCTTCGTCGCCAACTCGTGGGTCTACCCGCAACAGCTCTACTCCAGGAACGATCTT 722
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Db 411 CACCTTCGTCGCCAACTCTGGGTCTACCCCGGGGCAAGTACCGCTACAAACCGGTCTT 470
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QY 723 CTTGCGCAACGACACCTATCTGCCGAGCAAAATGCGGGCGGTGGTGCCTTATCGGCA 782
|||||
Db 471 CTTCTCCAACGATACGTAACCTGCCAAGCCAGATGCGGGCGGTGAAGCCGTACCGCG 530
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QY 783 AGATGAGCTCAAGATTCTCGTGGCGACGATATCTCTGGACCATACCAGGAGCATGATCG 842
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Db 531 CGACGAGCTCCGCAACCTCCGCGCGACGACCCAGAGGGCCCCCTACCAGGAGCACGACCG 590
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QY 843 CGTCTACGTTACGACTACTACAATGACCTTGGTGATCCCGACAAGGGCGAAGAGCACGC 902
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Db 591 CGTGACCGCTACGACGCTTACAACGACCTCGGCGAGCCCGACGGCGGC-----AACCC 644
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QY 903 TCGGCGCATCCTCGTGGCAGCCAAGAACACCCGCTATCCCGTCGCTGCAGAACTGGCCG 962
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QY 963 GCACCCAACAAAGAAAGACCAAATTCGGAGACAGGCTTTTCTGCTGAACCTGAACAT 1022
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QY 1023 CTACGTCCCGCTGACGAACGCTTTGGGCACTCAAGATGTGGACTTCCTTGGGTACTC 1082
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Db 762 CTACGTCCCGCGGAGAGCGCTTCGGCCACCTCAAGATGTCCGACTTCTTGGGTACTC 821
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QY 1083 GCTGAAGACGATCATCGAGGCTGTCTTCCAACACATGGGGACTTTCGTCGATGACACGCC 1142
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Db 822 CATCAAGGCCATCAGCAGGGCATCATCCCGCGGTGCGCACGTACGTGACACACACCCC 881
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QY 1143 CAAGGAGTTCGATTCTGAGGATATCCTCGGGCTCTACGAGCTGGGCGCCAGAGGCACC 1202
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Db 882 GGGGAGTTCGACTCCTCCAGGACATCATCAACCTGTACGAGGGGGGATCAAGCTGCC 941
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QY 1203 CAACAACCCACTGATAGCAGAGATCAGGAAGAAGATCCCAGCGAGTTCCTTCGAAGCAT 1262
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Db 942 CAAGATCCAGGCGCTCGAGGACATGCGCAAGCTTCTCCGCTCCAGCTCGTCAAGGACCT 1001
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QY 1263 TCTGCCGAACGGTAGCCATGACCAACCCGCTAAAGATGCCCTTCCAAATGTCAATAATC 1322
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Db 1002 CTTCCC---CGCGCGGGGACTACCTGTCTCAAGCTCCCATCCCACAGATCATCCAA-- 1056
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QY 1323 AGATGTGTTGAAAAAGGCTCCGGAGTTTAACTTTGGCTGGAGGACTGACGAAGAGTTCGC 1382
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ORIGIN

Query Match 40.7%; Score 1275.2; DB 8; Length 2845;

Best Local Similarity 68.9%; Pred. No. 7.6e-177;

Matches 1921; Conservative 0; Mismatches 808; Indels 61; Gaps 10;

Qy	338	TGGACGTCGGCGACTTCAACGCCTCGCTCCTCGACGGCGTCCACAGGATCCTCGGCTGGG	397
Db	110	TGGACGTCACCGATCGCGGCTCCTCCTCGACGGCATCGGCGAGTTCCTCGGCCG--	167
Qy	398	ACGACGGCGTCGCCCTTCAGCTCGTCAGCGCCACCGCGGCCGACCCACGAAACGGGGCC	457
Db	168	----CGGCGTCACCTGCGAGCTTATCAGCTCCACCGTCGTCGACCCCTAACACGGCAACC	223
Qy	458	GTGGCAAGTGGGGAAGCGCGCGCACCTGGAGGAGCGGTGGTGTGCTCAAGTCCACGG	517
Db	224	GCGGGAAGTTGGCGCGGAGGCGAGCCTGGAGAGTGGTGTGTAACCCGCGCGCTTC	283
Qy	518	CGGACGGGGAGACCGGTGTACCGGGGTGAGCTTCGAGTGGGA--CGAGTCGACGGGCATCC	574
Db	284	TGTCCAGCGAGAACCAAGTTCGCGGTCACTTCGACTGGGAGGTGGAGAGCAGGGGCATCC	343
Qy	575	CGGGCGCGCTCCTGGTCAGGAACCTGCAGCACCGCGGAGTTCCTCCTCAAGACGCTCACCC	634
Db	344	CGGGCGCCATCATCGTCAAGAAACAACCAACGCTTCGAGTTCCTCCTCAAGACCATCACCC	403
Qy	635	TCGAGGGCGTCCAGGGAAGGGCACCGTGTCTGTGCGCCAACTCGTGGGTCTACCCGC	694
Db	404	TCAACGACGTCCCGCGCACGGCACCATCGTCTCGTCGCCAACTCATGGATCTACCCGC	463
Qy	695	ACAAGCTCTACTCCAGGAACGCATCTTCTTCGCCAAACGACACCTATCTGCCGAGCAAAA	754
Db	464	AGTCCAAAGTACCGTTACAACCGCGTCTTCTTCTTCCAAACGACACGTACTCCCCAGCCAGA	523
Qy	755	TGCCGGCGCGTGTGGTGTATCGGCAAGATGAGCTCAAGATTCCTCGTGGCGGACGATA	814
Db	524	TGCCGGCGCGCTGAAGCCCTACCGCGACGAGCTCCGGAAACCTGAGGGGCGACGACC	583
Qy	815	ATCCTGGACCATACAGGAGCATGATCGCGTCTACCGTTACGACTACTACAATGACCTTG	874
Db	584	AGCAGGGCCCGTACCAGGAGCAGCACCGCGTCTACCGCTACGACGTCTACAACGACCTGG	643
Qy	875	GTGATCCCGACAAGGGCGAAGAGCACGCTCGCGCGATCCTCGGTGGCAGCCAAAGAACACC	934
Db	644	GCCTGCCGTGACAGCGG-----GAACCCCGCGCCGCTCCTCGGCGGCACCAAGGAGCTCC	697
Qy	935	CGTATCCCCGTCGTCAGAACTGGCCGGCACCCAAACAAAGAAAGACCCAAATTCGGAGA	994
Db	698	CCTACCCGCGCGCTGCGCACCGGCGGAAGCCACCAAGAGCGACCCCAACAGCGAGA	757
Qy	995	GCAGGCTTTTCTGCTGAACCTGAACATCTACGTCCCGCGTGCAGCAACGCTTTGGGCATC	1054
Db	758	GCAGGCTCACGCTGTCAGCGGCGACGTCTACGTGCGCGCGACGAGCGCTTCGGCCACA	817
Qy	1055	TCAAGATGTCGGACTTCCTTGGGTACTCGCTGAAGACGATCATCGAGGCTGTCTTCCAA	1114
Db	818	TCAAGAAGTCGGACTTCTACGGCTACGCCATCAAGGCGCTGGTGAACGCGCTCATCCCGG	877

Qy	1115	CACTGGGGACTTTTCTGTCGATGACACGCCCAAGGAGTTCGATTTCGTTTGAGGATATCCTCG	1174
Db	878	CAATCCGCACCTACGTGCACTGTGCCCCGGGAGTTCGACTCCTTCAAGGACATCATGA	937
Qy	1175	GGCTCTACGAGCTGGGGCCAGAGGACCCCAACACCCACTGATAGCAGAGATCAGAAAGA	1234
Db	938	AGCTGTACGAGGGGGGATCCAGCTGCCCAAAATACAGCCCTCGAGGACCTCGGGAAGC	997
Qy	1235	AGATCCCCAGCGAGTTCCTTCGAAGCATTCCTGCCGAACGGTAGCCATGACCCACCGCTAA	1294
Db	998	AGTTCCTCACTCGAGCTCGTCAAGGATGTCTCTCCCGGTGCGGGC--GACTACTCTCTCA	1054
Qy	1295	AGATGCCCCCTTCCAAATGTTCATCAAAATCAGATGTGTGAAAAAGGCTCCGGAGTTAAGT	1354
Db	1055	AGCTCCCCATGCCGACGATCATCAAA-----GAGGACAAGA	1090
Qy	1355	TTGGCTGGAGGACTGACGAAGAGTTTCGGGAGAGAGACACATTCGAGGGCGTGAACCCAGTAA	1414
Db	1091	CAGGTTGGATGACAGATGAGGAGTTTGGACGGGAGATTCTGCCGGCGTGAACCCCATGC	1150
Qy	1415	TCATCAAAACGTCTGACGGAGTTCCTCCGTAAAGACACCTTGAGACCCCAAGGAGTACGGAG	1474
Db	1151	TCGTCAAGCGTCTCACGGAGTTCCTCCGAGGAGCAGTCTTGACCCGAGCAAGTACGGCG	1210
Qy	1475	ACCACACAGCAAGATCACTGAAGCTCACATCCGGCATAAACATGGAGGCGCTGTGCGGTGC	1534
Db	1211	ACCACACAGCACCATCAGGGAGGGCGGACCTCGAGAAACAAGCTCGAGGGCGCTGACGGTGC	1270
Qy	1535	AGAACGCACCTGAGGAACAAGAGGCTCTTTCATCTTAGACCAACCATGACCATTCATGCCGT	1594
Db	1271	AGCAGGCGCTGCACGGCAACCGGCTCTACATCTCTGACCAACACGACAACTTCATGCCGT	1330
Qy	1595	ACCTCGACGAGATCAACGAGCTGGAGGGGAACCTTCATCTAGACCAACCATGACCACTACTGT	1654
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Qy	1655	TCCTGAAGGACGATGGCACGCTGAAGCCCTTGCCATCGAGCTGAGCTGCCGACCCCTG	1714
Db	1391	TCCTCGCGGCGACGCGACGCTGGTCCCGTGGCCATCGAGCTGAGCTGCCGAGCTCC	1450
Qy	1715	ACGGCCAGCAGCGCGCGGTGAGCAAGGTGTACACACCC--GGCTCACACCGCGCGTGC	1771
Db	1451	GGACGCGCTGACCAACCGCAAGAGCACCGTGTACACGCCCAAGTCGACCAACCGCGCGG	1510
Qy	1772	AGGCCACGCTGTGCGAGCTCGCAAGGCTTATGCTGCTGTAACGACTCTGCTGGGCATC	1831
Db	1511	AGCGTGGGTGTGGCACCTGGCCAAAGGCTACGCCCAACGTAACGACTACTGTGGCACC	1570
Qy	1832	AGTGTATCAGCCACTGGCTGAACACGACGCGGTGATCGAGCCGTTCTGTAATCGCGACAA	1891
Db	1571	AGTCTATCAGCCACTGGCTCAACACCCACCGCGGTGATGGAGCCGTTCTGATCGCCACCA	1630
Qy	1892	ACGGCAGCTCAGCGTGGTGCATCCCGTGCACAAAGCTGCTGAGCCGCACTACCGTGACA	1951
Db	1631	ACGGCAGCTCAGCGTGCAGCACCCCGTGCACAAAGCTCCTCCTGCCGCACTACCGTGACA	1690
Qy	1952	CGCTGAACATCAACGCCCTGGCACGCCAGACACTCATCAACGCCGGCGGCTCTTCGAGC	2011
Db	1691	CCATGAACATCAACTCCAACGCGCGCAGATGTCTGTCACCGCCGCGCATCTTCGAGA	1750
Qy	2012	GCACCGTGTCCCTGCAAGTACGCGCTGGGGATGTGGCAGACGTTGTACAAGAGCTGGA	2071
Db	1751	CCACCGTCTTCCCGCGCAGTACGCGTTCGAGATGTCTCCGTCTATCAAGGACTGGA	1810
Qy	2072	ATTTCAACGAGCAGGCTCTCCAGCAGATCTCTGTCAGAGAGGTGTGGTGTGCGCGACC	2131
Db	1811	ACTTCAAGAGCAGGCTCTCCCTGACGACCACTAATCAAGAGAGGATGGCGTGCAGACC	1870
Qy	2132	AGTCAAGCCCATATGGTTCGACTGCTGTGATCAAGGACTACCCCTATGCCGTTGACGGGC	2191
Db	1871	CGTCGAGCCCGTACAGGTACGGTGTGTTGGAGGACTACCCGTAACGCTCGGACGGGC	1930
Qy	2192	TCGTCTCTGTGGGCGATCGAGCGGTGGGTCAAGGAGTACCTGGACATCTACTACCTA	2251

Db 1931 TGGCCATCTGGCAGCCATCGAGCAGTGGGTGACGGAGTACTCGCGTCTACTACCCCA 1990
Qy 2252 ACGACGGCAGCTCCAGCGTACGCTGAGCTGAGCGCTGCTGGAAGGAGTGCCTGAGG 2311
Db 1991 ACGACGGCAGCTGCGGCGGACGCTGAGCTGAGCGCTGCTGGAAGGAGGCGCGGAGG 2050
Qy 2312 AGCGCAGCGGACCTCAAGGACCGAGACTGGTGGCCCGAGATGGACACCGTCCAGCAGC 2371
Db 2051 TCGGGCAGCGGACCTCAAGGACCGGCGCTGGTGGCCCGAGATGCAGACGGTGGCGGAGC 2110
Qy 2372 TGGCTAGGCGTGCACGACCATCATCTGGGTGGCATCCGCGCTGCACGCGCTGTCAACT 2431
Db 2111 TGGTCAAGGCGTGCACACCATCATCTGGATCGCGTGGCGCTCCACGCGCGCTCAACT 2170
Qy 2432 TTGGCAGTACCCATACGCGGCTACCTCCGAACCGCGGACCGCCAGCGCGCCCGA 2491
Db 2171 TCGGGCAGTACCGGTACGCGGCTACCTCCGAACCGCGCTCGTCAAGCGGAGCGGA 2230
Qy 2492 TGCGGAGCGGACCGACCGACTACGAAGCTGGGAGCGGGGAGGAGGAGCGGACA 2551
Db 2231 TGCGGCGCGGACCGACCGAGTACGGGAGCTGG-----AGCGCAAGCGGAGA 2281
Qy 2552 TGGTGTTCATCCGACCATCACAGCCAGTTCAGACCATCTGGGCATCTCGTCAATCG 2611
Db 2282 AGTGTTCGTGCGCACCATCACAGCCAGTTCAGGCGCTCGTGGCATCTCGTGTCTGG 2341
Qy 2612 AGATCCTCTCAAGCACTCCTCCGACGAGGTGTACCTCGGCCAGCGTGACGACCTGATC 2671
Db 2342 AGATCCTGTCCAGCCACTCCTCCGACGAGGTGTACCTCGGCCAGCG---CGACACCAAG 2398
Qy 2672 GCTGGACGTCAGACGCCAAGGCGCTGGATGCGTTCAAAAGATTCCGGAGCGCGTGGTG 2731
Db 2399 AGTGGACGTCGACGCCAAGGCGCAGGAGCGTTCAACGCGTTCGGCGCGCGTGACCG 2458
Qy 2732 AGATTGAGAAATCGGATCAAGACGATGAACGACAGTCCGGAATTGAAGAACCGGAAGGGG 2791
Db 2459 AGATCAGAAACGCGTGTACCATGAACCGGACCTCGCCTCAAGAACCGCAACGGCC 2518
Qy 2792 CTGTGAAATGCGGTACATGCTGCTGTACCCCAACAGTCCGACGTTACCGCGGAGAGG 2851
Db 2519 CGGCGAGTTCCTCTACAGCTGTCTACCCCAACACTCCGACACGAAGGCG---ACG 2575
Qy 2852 CCGAGGGCTTACTGCCATGGGCATTCCTCAACAGCATCTCCATATGAGCCTGGGCAGATT 2911
Db 2576 CCGCGGCATCACCGCCAAGGCATTCCTCAACAGCATCTCCATTTGAGTTCTGTGTCT 2635
Qy 2912 GTGTCTCGTAGTAAATTTGTGTGCTGCGCGTGGCATGTGTTCTTCAATTGTTGTCA 2971
Db 2636 GAGTGAGGACGTACGGTGTGCGCACTAGATTGTTGGGTTTCCCGTTCCGTTCCGTGA 2695
Qy 2972 GTCTCAGGGTAGGGATGGAGATCATACCATGATCTTTGTAG-GGTTGAGAGAGGAGTCC 3030
Db 2696 AGTGTGTTCTCATTGCGCGGTATTGTGCAAAATATGCCAAGTACTCCTTACAGAAGTCG 2755
Qy 3031 ACGTTGAATATTGTTGTATGTATGTAATTCTTGGTTAATAATAAAGTTGTCAGTTCA 3090
Db 2756 CTACGTGAGGACTGTTGTATAAAGGCTCTATTCTGTCTCTCAATAATGAAGTTACCTTGT 2815
Qy 3091 TTTCTTAAAAAACAACAAAAA 3120
Db 2816 GTTCAAAAAA 2845

RESULT 10
AR438184
LOCUS AR438184 2818 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 10 from patent US 6660915.
ACCESSION AR438184
VERSION AR438184.1 GI:40204686
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
1 (bases 1 to 2818)
Duma,A.C., Doderer,A., Cameron-Mills,V., Skadhauge,B., Bech,L.M.,
Schmitt,N., Heistek,J.C. and van Mechelen,J.R.
Low lipoxigenase 1 barley
Patent: US 6660915-A 10 09-DEC-2003;
Location/Qualifiers
1..2818
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ORIGIN
Query Match 39.0%; Score 1222.2; DB 6; Length 2818;
Best Local Similarity 69.0%; Pred. No. 4.3e-169;
Matches 1868; Conservative 0; Mismatches 758; Indels 81; Gaps 11;

Qy 210 GGAGCGAGAAAAAGCGAGCGGCGCATGTTCTGGACGGGTCGCGGACCGGTCGACGGG 269
Db 32 GGAGCAGTGAAGCGAGGAGGAGGCGCAAGAACAAAGATGCTGCTGGAGGGCTGATCGA 91
Qy 270 AAAGAACAAAGAGGCGTGGAGCGAGGGCAAGATCCGCGGACCGGTGAGGTCGTCAGAA 329
Db 92 CACCTCACGGGGCGAACAGAGCGCCCGCTCAAGGCGACGGTGGTCTCATGCGCAA 151
Qy 330 GGAGGTGCTGGACGTCGGCGACTTCAACGCCCTCGTCTCTCGACGGCGTCCACAGATCCT 389
Db 152 GAACGTGCTGGACCTCAACGACTTCGGCGCCACCATCATCGACGGCATCGGCGAGTTCT 211
Qy 390 CGGCTGGGACGACGGCGTCCGCTTCCAGCTCGTCAAGCGCACCGCGCGGACCCAGCAA 449
Db 212 CGG-----CAAGGGCGTCACTGCCAGCTTATCAGTCCACCGCGTCCAGCAAGACAA 265
Qy 450 CGGGGCGCGTGGCAAGGTGGGAAAGGCGGCGCACCTCGAGGAGGCGGTGGTGTCTCAAG 509
Db 266 CGGCGTGGCGGAAGTGGGCGGAGGCGGAGCTGGAGCAGTGGGTGACGAGCCTGCC 325
Qy 510 GTCCACGGCGGACGGGGAGACCGTGTACCGGCTGAGTTCGAGTGGGA--CGAGTCGCA 566
Db 326 GTCGTGACGACGGGGAGTCCAAAGTTCGGCCTCAGTTCGACTGGGAGTGGAGAGCT 385
Qy 567 GGGCATCCCGGGCGCGTCTGTTGTCAGGAACCTGACGACCGCGGAGTCTTCTCTCAAGAC 626
Db 386 CGGGTGGCGGCGCCATCGTCTCAACAACTACACAGTCCGAGTCTCTGTTAAAC 445
Qy 627 GCTCACCTCGAGGGCGTCCCAG--GCAAGGGCAGCGTCTCTCGTCCGCACTCGTG 683
Db 446 CATCACCTCCACGACGTCGCCGGCGGCGAGCGGCACTCCTTCTCGTCCGCACTCATG 505
Qy 684 GGTCTACCGGCACAAGCTCTACTCCAGGAACGATCTTCTTCCGCAACGACACCTATCT 743
Db 506 GATCTACCGCGCGCCAACTACCGATACAGCGCGCTTCTTCCGCAACGACACGATACCT 565
Qy 744 GCCGAGCAAAATGCCGGCGCGTGGTGGCTTATCGGCAAGATGAGCTCAAGATTCTCCG 803
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Qy 804 TGCGACGATAATCTCTGACCATACCGAGGAGCATGATCGGCTCTACCGTTACGACTACTA 863
Db 626 TGCGACGACCAAGAGGGCGCGTACCGAGGACGACCGCATCTACCGCTACGACGCTCTA 685
Qy 864 CAATGACCTTGGTGTATCCGACAAAGGGCGAAGACGACGCTCGGCGGATCTCTGGTGGCAG 923
Db 686 CAACGACCTCGGCGAG-----GGCGCGCCCATCTCTCGGCGGCAA 724
Qy 924 CCAAGAACACCCGTATCCCGTGGTGGAGAACTGGCGCGGACCCCAACAAAGAAAGACCC 983
Db 725 CTCCGACCACTTACCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 784
Qy 984 AAATTCCGAGAGCAGGCTTTCTGCTGAACCTGAACATCTACGTCGCGGCTGACGAAACG 1043
Db 785 GAGCCTGGAGAGCGCGCTGTCTGCTGGA---GCAGATCTACGTCGCGCGGCGGAGAA 841
Qy 1044 CTTTGGGCATCTCAAGATGTGGACTTCTCTTGGGTACTCTGCTGAAGACGATCATCGAGGC 1103

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QY 1284 CCACCCGCTAAAGATGCCCTTCCAAATGTATCAATCAATCAGATGTGTTGAAAAAGGCTCC 1343
Db 1079 CTCCCTGCTTAAGCTCCCGCTGCCCAATCATC-----CA 1114
QY 1344 GGAGTTTAAGTTTGGCTGGAGGACTGACGAAGAGTTTCGGAGAGAGACACTTGCAGGCGT 1403
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RESULT 11
AX469803
LOCUS AX469803
DEFINITION Sequence 10 from Patent WO02053720..
ACCESSION AX469803
VERSION AX469803.1 GI:22205059
KEYWORDS
SOURCE Hordeum vulgare
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE 1
AUTHORS Bech,L.M., Douma,A.C., van Mechelen,J.R., Doderer,A., Schmitt,N.,
Cameron-Mills,V., Heistek,J.C. and Skadhauge,B.
TITLE Low-lipoxygenase 1 barley
JOURNAL Patent: WO 02053720-A 10 11-JUL-2002;
CARLSBERG RES LAB (DK); KRONENBOURG BRASSERIES (FR); HEINEKEN TECH

FEATURES		SERVICES (NL)			
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ORIGIN					
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	Best Local Similarity	69.0%;	Pred. No. 4.3e-169;		
	Matches 1868; Conservative	0; Mismatches 758; Indels 81; Gaps 11;			
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QY	270 AAAGAAACAAGAGGCGGTGGAGCGAGGGCAAGATCCGCGGCACCGGTGAGGCTGAGGAA	329	Db	962 GGACATCATCAACCTCTATGAGGGCGGCATCAAGCTGCCCAAGGTGGCGCCCTGGAGGA	1021
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RESULT 12
AX469867
LOCUS AX469867
DEFINITION Sequence 10 from Patent WO02053721.
ACCESSION AX469867
VERSION AX469867.1 GI:22205145
KEYWORDS
SOURCE Hordeum vulgare
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
REFERENCE 1
AUTHORS Bech, L.M., Cameron-Mills, V., Skadhauge, B., Douma, A.C., van
Mechelen, J.R., Doderer, A., Heister, J.C. and Schmitt, N.
TITLE Low-lipoxygenase 1 barley
JOURNAL Patent: WO 02053721-A 10 11-JUL-2002;
CARLSBERG RES LAB (DK); KRONENBOURG BRASSERIES (FR); HEINEKEN TECH
SERVICES (NL)
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Best Local Similarity 69.0%; Pred. No. 4.3e-169;
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QY 2841 CCGCGAGAAGCGCGGCGCTTACTGCCATGGCATTCCTCAACAGCATCTCCCATATGAGC 2900
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QY 2901 CTGGGCA 2907
Db 2660 TAAGCCA 2666

RESULT 13
BLYLOXA
LOCUS 2818 bp DNA linear PLN 07-APR-1995
DEFINITION Barley lipoxigenase 1 (Loxa) gene, complete cds.
ACCESSION L35931
VERSION L35931.1 GI:532571
KEYWORDS carotene oxidase; linoleate:oxygen oxioeductase; lipoxidase; lipoxigenase 1.
SOURCE
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 2818)
AUTHORS van Mechelen,J.R., Smits,M., Douma,A.C., Rouster,J., Cameron-Mills,V., Heidekamp,F. and Valk,B.E.
TITLE Primary structure of a lipoxigenase from barley grain as deduced from its cDNA sequence
JOURNAL Biochim. Biophys. Acta 1254 (2), 221-225 (1995)
MEDLINE 95127754
PUBMED 7827128
COMMENT Original source text: Hordeum vulgare DNA.
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/mol_type="genomic DNA"

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	69. .2657			
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	/protein_id="AAA64893.1"			
	/db_xref="GI:532572"			
	/translation="MLLGLLIDTLTGANKSARLKGTVVLMRKNVLDLNDFGATIIDGI GEFLKGVTICQLISSTAVDQDNGGRKVGAEAELEQWVTSPLTGTGESKFGLTFDWE VEKLGVGAIVNNYHSSEFLKTIILHDVPGRSNLTFFVANSWIYPAANYRYSRVFF ANDTYLPSQMEPAALKPYRDDENLRNGDDQOQPYQEHDRIVRYDVYNDLGEGRPIILGG NSDHPYPRRGTERKPNASDPSLESRLSLEQIYVPRDEKFGHLKTSDFLGYSIKAIT QGILPAVRTYVDTTPGEFDSFQDIINLYEGGIKLPKVALEELRKFQFLQLIKOLLPV GGDSLLKLPVPHIIOENKQAWRTDEEFAREVLAVGNPVMITRLTEFFPKSSLDPSKFG DHTSTITAEHIEKNLEGLTVQQALESNRLYLIDHHRFMPFLIDVNNLPGNFIYATRT LFLLRGDGLTPLAIELSEPIIQGGLTTAKSKVYTPVPSGVEGVWELAKAYVAVND SGWHLQVSHWLNTHAVMEPFVISTNRHLSVTHPVHKLLSPHYRDTMTINALARQTLIN AGGIFEMTVFPGKFALGMSAVVYKDWKFTQGLPDDLIKRGMAVEDPSSPYKVRLLVS DYPYAADGLAIWHAIEQYVSEYLAIYYPNDGVLOQDTEVQAWKETREVGHGDLKDAF WYPMQSVPELAKACTTIWIGSALHAANFVGQYPYAGFLPNRPTVSRRRMPEPSTEE YAELEDRPRAFIHTITISQIOTIIGVSLLEVLVSKHSSDELYLQORDTPEWTSDDPKALE VFKRFSRLVLEIESKVGMNHDPELKNRNGPAKFPFYMLLYPNTSDHKGAAGLTAKGI PNSISI"			
3'UTR	2658. .2818			
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	2818			
ORIGIN				
Query Match 39.0%; Score 1222.2; DB 8; Length 2818;				
Best Local Similarity 69.0%; Pred. No. 4.3e-169;				
Matches 1868; Conservative 0; Mismatches 758; Indels 81; Gaps 11;				
QY	210	GGAGCGAGAAAAGCGAAGAGCGGCCATGTTCTGGCACGGGTGCGCGACCGGCTGACGGG	269	
DB	32	GGAGCAGTGAAGCGAGGAGAGGAGGCCCAAGAAAGATGCTGCTGGAGGGCTGATCGA	91	
QY	270	AAAGAACAAAGGAGCGGTGGAGCGAGGGCAAGATCCGCGGACCGGTGAGGCTGGTCAAGAA	329	
DB	92	CACCCTCACGGGGCGAACAAGAGCGCCCGCTCAAGGGCACGGTGGTGTCTCATGCGCAA	151	
QY	330	GGAGGTGCTGGACGTGGCGGACTTCAACGGCTCGCTCCTCGACGGCGTCCACAGGATCCT	389	
DB	152	GAACGTGCTGGACTCAACGACTTCGGCGGCACCATCATCGACGGCATCGGCGAGTTCTT	211	
QY	390	CGGCTGGGACGACGGCGTGGCTTCCAGCTCGTCAGCGCCACCGCGGCGGACCCCGAGCAA	449	
DB	212	CGG-----CAAGGGCGTCACTGCCAGCTTATCAGCTCCACCGCGTGCACCAAGACAA	265	
QY	450	CGGGGGCGGTGGCAAGGTGGGAAGGCGGCGCACCTGGAGGAGCGCGTGGTGTGCTCAA	509	
DB	266	CGGCGGTGCGGGGAAGGTGGGCGGAGGCGGAGCTGGAGCAGTGGGTGACGAGCCTGCC	325	
QY	510	GTCCACGGCGGACGGGGAGACCGTGTACCGGGTGAGCTTCGAGTGGGA---CGAGTCGCA	566	
DB	326	GTCGCTGACGACGGGGGAGTCCAAAGTTCGGCTCACCTTCGACTGGGAGGTGGAGAAGCT	385	
QY	567	GGGCATCCCGGGCGCGTCTCTGGTCAAGGAACCTGCAGCACGCGGAGTTCTTCTCAAGAC	626	
DB	386	CGGGGTGCGGGGCGCCATCGTGTCAACAACTACCAAGCTCCGAGTTCCTGCTTAAAC	445	
QY	627	GCTCACCTTCAGGGCGTCCCAG---GCAAGGGCACCGTGTCTTCTGTGCGCCAACTCGTG	683	
DB	446	CATCACCTTCACGACGTCCCGCGGCGGCGGCAACCTCACCTTCGTGCGCCAACTCATG	505	
QY	684	GGTCTACCCGCAAGCTCTACTCTCCAGGAACGCATCTTCTTCGCCAACGACACCTATCT	743	

Db	506 GATCTACCCCGCGCCCACTACCGATACAGCCCGCTTCTTTCGCCAACGACACGTACCT 565		
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DB			
	566 GCGGAGCCAGATGCCGGCGGCTGAAGCCGTACCGGACGACGAGCTCCGGAACCTGCG 625		
QY	804 TGCGACGATAATCCTGGACCATACAGGAGCATGATCGGCTTACCGTTACGACTACTA 863		
DB			
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QY	864 CAATGACCTTGGTGATCCCGACAAGGGCGAAGAGACGCTCGGCCGATCCTCGTGGCAG 923		
DB			
	686 CAACGACCTCGGCGAG-----GGCCGCCCCATCTCTCGGCGGCAA 724		
QY	924 CCAAGAACACCCCGTATCCCGTTCGCTGCAGAACTGGCCGGCACCCCAACAAGAAAGACCC 983		
DB			
	725 CTCGACCAACCTTACCCGGCGCGCGCCGACGAGGCGCAAGCCCAACGCCACGACCC 784		
QY	984 AAATTGGAGAGCAGGCTTTCTGCTGAACTGAACTTACGTCCTCCCGCGTGACGAAAG 1043		
DB			
	785 GAGCCTGGAGAGCGCGCTGCTGCTGGA---GCAGATCTACGTGCGCGCGGACGAGAA 841		
QY	1044 CTTTGGGCATCTCAAGATGTGGGACTTCTCTGGGTACTCGCTGAAGACGATCATCGAGGC 1103		
DB			
	842 GTTCGGCCACCTCAAGACGTCGCACTTCTCTGGGTACTCCATCAAGGCCATCACGCAGGG 901		
QY	1104 TGTCTTCCAAACACTGGGACTTTCTGTCGATGACAGCCCAAGAGTTTCGATTCGTTTGA 1163		
DB			
	902 CATCTGCGGCGCGTGCACCTACGTGGACACCAACCCCGCGGAGTTTCGACTCCTTCCA 961		
QY	1164 GGATATCTCTGGGCTTACGAGCTGGGCGGACGAGGACCCCAACAACCCACTGATAGAGA 1223		
DB			
	962 GGACATCATCAACCTCTATGAGGGCGGCATCAAGCTGCCAAGGTGGCGCCCTGGAGGA 1021		
QY	1224 GATCAGGAAGAAGATCCCAGCGAGTTCTTTCGAAGCATTTCTGCCGAACGGTAGCCATGA 1283		
DB			
	1022 GCTCCGTAAGCAGTTCCCGCTCCAGCTCATCAAGGACCTCTCTCCCGTCCGCGGC---GA 1078		
QY	1284 CCACCCGCTAAAGATGCCCTTCCAAATGTATCAAAATCAGATGTGTGAAAGGCTCC 1343		
DB			
	1079 CTCCTGTCTTAAGTCCCGCTGCCCACTATC-----CA 1114		
QY	1344 GGAGTTTAAGTTTGGCTGGAGGACTGACGAAGAGTTTCGGAGAGAGACATTGCAGGCGT 1403		
DB			
	1115 GGAGAACAAAGCAGCGGTGGAGGACCGACGAGAGTTTCGCACGGGAGGTGCTCGCGGCGT 1174		
QY	1404 GAAACCCAGTAATCATCAAAACGTCTGACGGAGTTCCCGCTAAAGCACCTGGACCCAAAG 1463		
DB			
	1175 CAACCCGGTTCATGATCAGCGTCTCACGGAGTTCCCGCCAAAGTAGTCTGGACCCCTAG 1234		
QY	1464 GCAGTACGGAGACACACAGCAAGATCACTGAAGCTCACATCCGGCATAAACATGGGAGG 1523		
DB			
	1235 CAAGTTTGGTGACACACACAGCACCATCAACGGCGGAGCACATAGAGAAGAACCTCGAGGG 1294		
QY	1524 CCTGTGCGTGCAGAACGCACCTGAGGAACAAGAGGCTCTTTCATCTAGACCCACCATGACCA 1583		
DB			
	1295 CCTCACGGTGCAGCAGGCGCTGGAAAGCAACAGGCTGTACATCTTGTATCACCATGACCG 1354		
QY	1584 TTTTCATGCCGTACTCGACGAGATCAACGAGCTGGAGGGGAACCTTTCATCTACGCCAGCAG 1643		
DB			
	1355 GTTCATGCCGTTCCTGATCGACGTCAACAACTGCCCGGCAACTTTCATCTACGCCACGAG 1414		
QY	1644 GACCCCTACTGTTCCTGAAGGACGATGSCACGCTGAAGCCCTGGCCCATCGAGCTGAGCCT 1703		
DB			
	1415 GACCCCTCTTCTTCTGCGGCGACCGGAGGCTCAGCCGCTCGCCCATCGAGCTGAGCGA 1474		
QY	1704 GCCCCACCCCTGACGGCCAGCAGCGCGCGCGGTTCAGCAAGGTGTACACCCCGGCTCACAC 1763		
DB			
	1475 GCCCATCATCCAGGGCGGCTTACCACGGCCCAAGAGCAAGTTTACACGCCCGGTGCCAG 1534		
QY	1764 CGG---CGTCGAGGGCCACGCTCTGGCAGCTCGCCAAAGGCTTATGCTGCGGTAAACGACTC 1820		

Db	1535	CGGCTCCGTCGAAGGCTGGGTGTGGGAGCTCGCCAAAGGCGCTACGTGCGCCGTCAATGACTC	1599
QY	1821	TGCCTGGCATCAGCTGATCAGCCACTGGCTGAACACGCACGCGGTGATCGAGCCGTTGCT	1880
Dd	1595	CGGGTGGCACCCAGCTCGTCAGCCACTGGCTGAACACTCACGCGGTGATGGAGCCGTTGCT	1654
QY	1881	AATCGCGACAAACCGGAGCTCAGCGTGGTGTCATCCCGTGCAAAAGCTGCTGAGCCCGCA	1940
Dd	1655	GATCTCGACGAACCGGACCTTAGCGTGACGCACCCCGGTGCACAAGCTGCTGAGCCCGCA	1714
QY	1941	CTACCGTGACACGCTGAACATCAACGCCCTGGCACGCCAGACACTCATCAACGCCGCGG	2000
Dd	1715	CTACCGGACACCATGACCATCAACGCGCTGGCGCGGAGACGCTCATCAACGCCGCGG	1774
QY	2001	CGTCTTCGAGCGCACCGTGTTCCTTGCAAAAGTACGCGCTGGGGATGTCGGCAGACGTTGA	2060
Dd	1775	CATCTTCGAGATGACGCTGTTCGCGGGCAAGTTCGCGTTGGGGATGTGCGCCGTGGTGA	1834
QY	2061	CAAGAGCTGGAATTTCAACGAGCAGGCTCTCCCAGCAGATCTCGTCAAGAGAGGTGTGGC	2120
Dd	1835	CAAGGACTGGAAGTTACCGGACAGGGACTGCCGACGATCTCATCAAGAGGGGCAATGGC	1894
QY	2121	TGTGCGGACCAAGTCAAGCCCATATGGTGTCCGACTGCTGATCAAGGACTACCCCTATGC	2180
Dd	1895	GGTGGAGGACCCGTCGAGCCCGTACAAGGTGCGGTTGCTGTTGCTCGGACTACCCGTACGC	1954
QY	2181	CGTTGACGGGCTCGTTCATCTGTTGGGCGATCGAGCGGTGGGTCAAGGACTACCTGGACAT	2240
Dd	1955	GGCGGACGGGCTGGCGATCTGGCACGCCATTGAGCAGTACGTGAGCGAGTACCTGGCCAT	2014
QY	2241	CTACTACCTTAACGACGGCGAGCTCCAGCGTGACGTGGAGCTGCAGGCGTGTGGAAGGA	2300
Dd	2015	CTACTACCCGAACGACCGCGTGTGCAGGGCGATACGGAGGTGCAGGCGTGTGGAAGGA	2074
QY	2301	GGTGGGTGAGGAGGCCACCGGCACCTCAAGGACCCGAGACTGGTGGCCCGAGGATGGACAC	2360
Dd	2075	GACGCGCAGGTGCGGCACGGCGACCTCAAGGACGCCCCATGGTGGCCCAAGATGCAAG	2134
QY	2361	CGTCCAGCAGCTGGCTAGGGCGTGCACGACCATCATCTGGGTGGCATCCGCGTGCACGC	2420
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QY	2421	GGCTGTCAACTTTGGGCAGTACCCATACGCCGGTACCTCCGAAACCGGCCGACGCGCCAG	2480
Dd	2195	GGCAGTCAACTCGGCGAGTACCCCTACCGGGGTTCTCCGAAACCGGCCGACGCGTGAG	2254
QY	2481	CCGGCGCCGATCGGGAGCCAGGCAGCCACGACTACAAGAAGCTGGAGCGGGGCGAGAA	2540
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Dd	2306	CGACCCGGAGCGGSCCTTCATCCACACCATCAGAGCCAGATCCAGACCATCATCGGCGT	2365
QY	2601	CTCGCTCATCGAGATCCTCTCCAAGCACTCCTCCGACGAGGTGTACCTCGGCCAGCGTGA	2660
Dd	2366	GTGCTGTCTGGAGGTGCTGTGGAAGCACTCCTCCGACGAGTGTACCTCGGCAGCGGGA	2425
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Dd	2483	CCGGCTGGTGAGATCGAGAGCAAGGTGGTGGGCATGAACCATGACCCCGGAGCTCAAGAA	2542
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Dd	2543	CCGCAACGGCCCGGCTAAGTTTCCCTACATGCTGTCTACCCCAACACCTCCGACCAAA	2602
QY	2841	CGGCGAAGGCCGAGGGGCTTACTGCCATGGGCATTCCCAACAGCATCTCCCATATGAGC	2900
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RESULT 14		
LOCUS	AK073529	
DEFINITION	Oryza sativa (japonica cultivar-group) cDNA clone:J033046E17, full insert sequence.	linear mRNA 2928 bp PLN 24-JUL-2003
ACCESSION	AK073529	
VERSION	AK073529.1	GI:32983552
KEYWORDS	FLI_CDNA; CAP trapper.	
SOURCE	Oryza sativa (japonica cultivar-group)	
ORGANISM	Oryza sativa (japonica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartioideae; Oryzaceae; Oryza.	

RESULT 14
 AK073529
 LOCUS
 DEFINITION
 Oryza sativa (japonica cultivar-group) cDNA clone:J033046E17, full insert sequence.
 AK073529
 ACCESSION
 VERSION
 KEYWORDS
 FLI_CDNA; CAP trapper.
 SOURCE
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
 ORGANISM
 1
 REFERENCE
 The Rice Full-Length cDNA Consortium. National Institute of

1
REFERENCE
AUTHORS

The Rice Full-Length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-Length cDNA Project Team,
Kishichi.S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,
Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Ito,C.,
Ohtsuki,K., Shishiki,T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group:, Otomo,Y., Murakami,K.,
Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,
Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,
Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Ninkura,J.,
Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,
Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN:,
Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,
Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y.,
Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Yoshino,M. and Hayashizaki,Y.

TITLE
Collection, mapping, and annotation of over 28,000 cDNA clones from
oshimizu, and mayasuzuki, i.
japonica rice
Science 301 (5631), 376-379 (2003)
JOURNAL
MEDLINE
PUBMED
REFERENCE
2 (bases 1 to 2928)
AUTHORS
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,

AUCACI, J., Aizawa, K., Akimura, I., Arakawa, T., Carninci, F., Doi, K.,
 Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T.,
 Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K.,
 Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I.,
 Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M.,
 Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,
 Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
 Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M.,
 Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A.,
 Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M.,
 Namiki, T., Narikawa, R., Niikura, J., Nishi, K., Nomura, K.,
 Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H.,
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 Sakazume, N., Sano, H., Sasaki, D., Sato, K., Sato, K., Shibata, K.,
 Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S.,
 Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y.,
 Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A.,
 Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W.,
 Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
 Yoshimura, A.

TITLE	Direct Submission
JOURNAL	Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
COMMENT	This clone is one of the 28K full-length cDNA clones from japonica rice. URL : http://cdna01.dna.affrc.go.jp/cDNA/

QY 1898 AGCTCAGCGTGGTGCATCCCGTGCACAAGCTGCTGAGCCCGCACTACCGTGACACGCTGA 1957
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QY 1743 AGCTCAGCGTGGCGCACCCCGTGCACAAGCTGCTGCTGCCGCACTACCGGACACCATGA 1802
Dd |||||
QY 1958 ACATCAACGCCCTGGCACGCCAGACACTCATCAACGCCCGCGCGTCTTCGAGCGCACCG 2017
Dd |||||
QY 1803 CCATCAACGCCCTGGCGCGGAGACGCTCATCAACGCCCGCGGATCTTCGAGATGACCG 1862
QY 2018 TGTTCCTGCAAGTACCGCTGGGATGTCGGCAGACGCTGTACAAGAGCTGGAATTTCA 2077
Dd |||||
QY 1863 TGTTCGGCGGAAGCACCGCTGCCATGTCGTGCGGTTCTACAAGGACTGAGCTTCG 1922
QY 2078 ACGAGCAGGCTCTCCAGCAGATCTCGTCAAGAGAGGTGTGGCTGTGCGCGACCATCA 2137
Dd |||||
QY 1923 CCGACAGCGCTCCCGCAGACCTTGTCAAGCGCGGCTCGCGTGCAGACCCCGCGA 1982
QY 2138 GCCCATATGTTCCGACTGCTGATCAAGGACTACCCCTATGCCGTTGACGGGCTCGTCA 2197
Dd |||||
QY 1983 GCCCGTACAAGTGGCTGCTCATCGAGGACTACCGGTACGCCAACGACGGGCTGGCG 2042
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Dd |||||
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QY 2103 GCGTCTCCAGGCGACGCCGAGCTGCAGGCGTGGTGAAGAGGTCCGCGAGGTGCGGC 2162
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QY 2163 ATGGCGACATCAAGGACCGCAGCTGGTGGCCGGAGATGAAGACGCTGGCGAGCTGTCA 2222
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QY 2223 AGCGTGGCCACCATATCTGGATCGGTCCGCGCTGCACGCCCGCTCAACTTCGGGC 2282
QY 2438 AGTACCCATACGCCGGTACCTCCGAACCGGCCAGCGGCCAGCCCGGCTGATGCCGG 2497
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QY 2283 AGTACCCGTACGCCGGTACCTCCGAACCGTCCGTGGTGGTGGTGGTGGTGGTGGTGG 2342
QY 2498 AGCCAGGCGACCGACTACAAGAGCTGGGAGCGGGGCGAGAGGAGCGGACATGGTGT 2557
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QY 2394 TCGTCCGGACAATCACCAAGCAGATGCAGGCCATCGTGGGATCTCGTCTGGAGATCC 2453
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QY 2454 TGTCAAGCACTCCTCCGACGAGGTGTACCTCGGACAGCGGACAGCCCGA---GTGGA 2510
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QY 2511 CGTCGACGCCAAGCGCTGGAGCGTTCAAGCGGTTCCGGCGCGGCTGACGGAGATCG 2570
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QY 2571 AGAGCCGCTCGTCGCATGAACAAGGACCCCGACCGCAAGAACCGTGTGCGGCCGACCA 2630
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QY 2631 ATTTCCCTACAGCTGCTCTACCCAAACACTCCGACCTCAAGGGCG---ACGCTGCCG 2687
QY 2858 GGCTTACTGCCATGGCATTTCCCAACAGCATCTCCATATGAGC 2900
Dd |||||
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RESULT 15
AX653181
LOCUS
DEFINITION Sequence 3051 from Patent WO03000898.
2613 bp DNA linear PAT 22-MAR-2003

ACCESSION AX653181
VERSION AX653181.1 GI:29155995
KEYWORDS
SOURCE Oryza sativa
ORGANISM Oryza sativa
REFERENCE 1
AUTHORS Chang,H.S., Chen,W., Cooper,B., Glazebrook,J., Goff,S.A., Hou,Y.M.,
Katagiri,F., Quan,S., Tao,Y., Whitham,S., Xie,Z., Zhu,T. and Zou,G.
TITLE Plant genes involved in defense against pathogens
JOURNAL Patent: WO 03000898-A 3051 03-JAN-2003;
SYNGENTA Participations AG (CH)
FEATURES
Location/Qualifiers
1..2613
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/mol_type="unassigned DNA"
/db_xref="taxon:4530"
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Best Local Similarity 69.7%; Pred. No. 3.7e-167;
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Dd |||||
QY 50 TCAAGGGTCCCTCGTCTCATGCGCAAGAACGCCCTCGACATCAACGACTCGGCGCCA 109
Dd |||||
QY 362 CGCTCCTCGACGGCTCCACAGGATCTCTCGGCTGGGACGACGGCGTCCGCTTCCAGCTCG 421
Dd |||||
QY 110 CCGTATCGACGGCATCTCGAGTTCCTCGGCG-----CGGCTCATCTGCCAGCTCG 163
QY 422 TCAGCGCCACCGCGCGCCAGCCCGACCAACGGGGCGCTGGCAAGGTGGGGAAGCGCGCGC 481
Dd |||||
QY 164 TCAGCTCCTCCTCGTTCGACCCCAACAATGGGAAACAGGGGAGGDTGGGACGAGGCGA 223
QY 482 ACCTGGAGGAGCGGTGCTGCTCAAGTCCACGGCGGACGGGGAGACCGTGTACCGGG 541
Dd |||||
QY 224 GCCTGGAGCAGTGGCTGACGAGCCTGCCGTGACGACGGGAGAGTCAAGTTCGGGG 283
QY 542 TGAGCTTCGAGTGGGA---CGAGTCGAGGGCATCCCGGGCGCGTCTCTGGTCAGGAACC 598
Dd |||||
QY 284 TGACGTTGAGTGGGAGGTGGAGAGATGGGCATACCCGGCGCCATCATCGTCAAGAACA 343
QY 599 TGCAGCACGCGGAGTTCCTCAAGACGCTCACCTCGAGGGCGTCCAGGCAAGGGCA 658
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QY 344 ACCACGCCCGCGAGTTCCTCAAGACCATCACCTCGAACAACTCCCGCGGCGCAACGGCG 403
QY 659 CCGTCTGTCGTCGCAACTCTCGTGGGTCTACCCCGCACAAAGCTCTACTCCAGGAACGCA 718
Dd |||||
QY 404 CCGTCTGTCGTCGCAACTCTCGTGGATCTACCCCGCTCCAGTATCGCTACCAACCGCG 463
QY 719 TCTTCTTCGCCAACGACACCTATCTCGTGGGACGATAATCTTGACCATACAGGAGCATG 778
Dd |||||
QY 464 TCTTCTTCGCCAACGACACTTCACTGCGGAGCAAGATCCCGCGGCGCTGAAGCCGTACC 523
QY 779 GGCAAGATGAGTCAAGATTCTCGTGGGACGATAATCTTGACCATACAGGAGCATG 838
Dd |||||
QY 524 GCGACGACGAGTCCGCAACCTGCGCGGCGACGACGAGGCGCGTACAGGAGCACG 583
QY 839 ATCGGCTCTACCGTTACGACTACTACATGACCTTGGTGTATCCCGACAAGGCGGAGAGC 898
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QY 584 ACCGCTCTACCGTACGAGCTCTACAAGACCTCGGCGAGCGCCGACTCCGGC-----A 637
QY 899 ACGCTCGGCGGATCCTCGGTGGCAGCCCAAGAACACCCGATATCCCGCGCTGCGAAGCTG 958
Dd |||||
QY 638 ACCCTCGCCCTGCTCGGCGGCTCCCGCGACCGCCCTACCTACCTCGCGCGGCGCACCG 697
QY 959 GCCGGCACCCCAAGAAAGACCCCAATTCCGAGAGCAGGCTTTCTCTGCTGAACCTGA 1018
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QY 698 GCCGCAAAACCCCAAAACTGACCCCAACCGCGGAGAGCAGGCTGTCTTCTGCTGGA---GA 754

QY 1019 ACATCTACGTCCCGCGTGAACGACGCTTTGGGCATCTCAAGATGTCGGACTTCCTTGGGT 1078
Db 755 ACATCTACGTCCCGCACGCGACGAGCGGTTCGGGCACCTGAAGATGGCCGACTTCCTTGGGT 814
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QY 1439 CCGCTAAAGACACCCCTGGACCCCAAGCGAGTACGGAGACCAACAGCAAGATCACTGAAG 1498
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QY 1499 CTCACATCCGGCATAACATGGGAGGCTGTGCGTGCAGAACGCACTGAGGAACAAGAGGC 1558
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QY 1559 TCTTCATCCTAGACCACCATGACCAATTTTCATGCCGTACCTCGACGAGATCAACGAGCTGG 1618
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QY 1619 AGGGGAATTCATCTACGCCAGCAGGACCCCTACTGTTCTCTGAAGGACGATGGCAGCTGA 1678
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Db 1628 AGCTCAGGCTGGCGCACCCCGTGCAAGCTGCTGCTGCGCACTACCGCGACACCATGA 1687
QY 1958 ACATCAAGCCCTGGCACGCCAGACACTCATCAACGCGCGCGGCTTCTTCGAGCGCACCG 2017
Db 1688 CCATCAAGCGCTGGCGGCGGACGCTCATCAACGCGCGCGGCTTCTTCGAGATGACCG 1747
QY 2018 TGTTCCTGCAAGTACGCGCTGGGATGTGGCAGACTGTACAGAGCTGGAATTTCA 2077
Db 1748 TGTTCGCGGGAAGCACGCGCTCGCCATGTCTGTCGGCGTTCTACAAGGACTGGAGCTTCG 1807
QY 2078 ACGAGAGGCTCTCCCGACGAGATCTCGTCAAGAGAGGTGTGGCTGTGCCGACCAAGTCAA 2137

Db 1808 CCGACCAAGGCGCTCCCGACGACGACCTTGTCAAGCGCGCGTTCGCGTCCCGACCCGCGCA 1867
QY 2138 GCCCATATGTTGTCGACTGCTGATCAAGGACTACCCCTATGCGGTTGACGGGCTCGTCA 2197
Db 1868 GCCCGTACAAGGTGCGGCTGCTCATCGAGGACTACCCGTACGCCAAACGACGGGCTGGCG 1927
QY 2198 TCTGTGGCGCATCGAGCGGTGGTCAAGGAGTACCTGGACATCTACTACCTAACGACG 2257
Db 1928 TCTGGCACGCCATCGAGCAGTGGGCCACCGAGTACCTCGCCATCTACTACCCAAACGACG 1987
QY 2258 GCGAGCTCCAGCGTGAAGTGGAGCTGAGGCGCTGGTGAAGGAGGTGCGTGAGGAGGCG 2317
Db 1988 GCGTGTCCAGGGCGACGCGGAGCTGCAAGCGCTGGTGAAGGAGGTCCGCGAGGTCCGGC 2047
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Db 2279 TCGTCCGGACAATCACCAAGCAGATGCAGGCCCATCGTGGGATCTCGTGTGGAGATCC 2338
QY 2618 TCTCAAGCACTCTCCGACGAGGTGATCCTCGGCCAGCGTGACGAGCCTGATCGCTGGA 2677
Db 2339 TGTCCAAGCACTCTCCGACGAGGTGATCCTCGGACAGCGCGACACGCGGGA---GTGGA 2395
QY 2678 CGTCAGACGCGCAAGGCGCTGGATGCGTTCAAAAGATTTCGSGAGCGCGGCTGGTGCAGATTG 2737
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QY 2798 AAATGCCGTACATGCTGTGTACCCCAACACGTCGGACGTTACCGCGGAGAGGCGGAGG 2857
Db 2516 ATTTCCCTACACGCTGTCTTACCCAAACACCTCCGACCTCAAGGGCG---ACGCTGCCG 2572
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Db 2573 GCCTCTCGCCAGGGGCATCCCCAACAGCATCTCCATCTGA 2613

Search completed: March 23, 2004, 01:38:03
Job time : 11853 sec

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 21:56:06 ; Search time 1135 Seconds
(without alignments)
11730.267 Million cell updates/sec

Title: US-10-059-909-15
Perfect score: 3134
Sequence: 1 ccacgcgtccggccgagcg.....aaaaaaaaaaaaaaaaaag 3134

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04: *
1: Geneseqn1980s: *
2: Geneseqn1990s: *
3: Geneseqn2000s: *
4: Geneseqn2001as: *
5: Geneseqn2001bs: *
6: Geneseqn2002s: *
7: Geneseqn2003as: *
8: Geneseqn2003bs: *
9: Geneseqn2003cs: *
10: Geneseqn2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3134	100.0	3134	8	AAL57714 Corn (Zea
2	1523.4	48.6	2516	8	ADA48505
3	1424.6	45.5	2115	7	ADA69794 Rice gene
4	1222.2	39.0	2818	6	ABK88441 Barley li
5	1222.2	39.0	2818	6	ABK88515 DNA encod
6	1209	38.6	2613	7	ADA69728 Rice gene
7	1148.2	36.6	2830	2	AAQ24492 Rice lipo
8	1148.2	36.6	2830	2	AAQ24234 Lipoxigen
9	1119	35.7	3033	9	ADC53127 9'-specif
10	1066.8	34.0	2559	7	ADA70433 Rice gene
11	777.6	24.8	2562	7	ABX13452 A. thalia
12	748.2	23.9	3390	7	ABZ68210 Nucleotid
13	729.6	23.3	2580	6	ABZ13699 Arabidops
14	729.6	23.3	2580	7	ADA67958 Arabidops
15	664.2	21.2	2441	2	AAT60429 Tomato fr
16	662.6	21.1	2871	2	AAT60428 Tomato fr
17	657.6	21.0	2929	8	AAL57712 Balsam pe
18	601.2	19.2	2775	7	AAD57634 Rice dise
19	599.2	19.1	4663	6	ABK88442 Barley li
20	599.2	19.1	4663	6	ABK88516 DNA encod
21	599	19.1	4663	6	ABK88445 Barley li
22	599	19.1	4663	6	ABK88440 Barley li
23	599	19.1	4663	6	ABK88521 DNA encod

24	599	19.1	4663	6	ABK88514	Abk88514 Wild type
25	599	19.1	4663	6	ABK88522	Abk88522 DNA encod
26	584.4	18.6	1011	8	ADA49235	Ada49235 Maize gen
27	567.4	18.1	3007	2	AAQ68842	Aaq68842 Plant bli
28	551	17.6	2964	4	AAF88022	Aaf88022 Cucumber
29	551	17.6	2964	7	ABX13453	Abx13453 C. sativu
30	539.8	17.2	2763	7	ADA69752	Ada69752 Rice gene
31	521.2	16.6	2472	7	ADA70204	Ada70204 Rice gene
32	519.2	16.6	597	8	AAL57710	Aal57710 Corn (Zea
33	514	16.4	3018	6	ABK15653	Abk15653 Rice lipo
34	500.4	16.0	1196	8	ACD28871	Acd28871 Wine grap
35	466.4	14.9	1577	8	AAL57713	Aal57713 Garden ba
36	422	13.5	804	8	ADA49057	Ada49057 Wheat gen
37	398.6	12.7	2562	7	ADA70538	Ada70538 Rice gene
38	389.8	12.4	2760	6	ABZ13783	Abz13783 Arabidops
39	389.8	12.4	2760	7	ADA68392	Ada68392 Arabidops
40	335.4	10.7	4687	8	ACD28851	Acd28851 Wine grap
41	332.4	10.6	1622	3	AAC39940	Aac39940 Arabidops
42	330.6	10.5	4237	8	ACD28852	Acd28852 Wine grap
43	270.2	8.6	302	7	ABX85448	Abx85448 Corn ear-
44	261.4	8.3	319	6	ABL74378	Ab174378 Corn tass
45	259.4	8.3	1438	8	AAL57715	Aal57715 Corn (Zea

ALIGNMENTS

RESULT 1
AAL57714
ID AAL57714 standard; cDNA; 3134 BP.
XX
AC AAL57714;
XX
DT 06-NOV-2003 (first entry)
XX
DE Corn (Zea mays) lipoxigenase isozyme 4 cDNA.
XX
KW Lipoxigenase; hydroperoxidation; polyunsaturated fatty acid; plant;
KW fatty acid metabolite synthesis; signal molecule; growth regulation;
KW development regulation; plant development; wound response;
KW genetic mapping; hyperoxidation catalysis; Corn; gene; ss.
XX
OS Zea mays.
XX
FH Key
FT CDS
FT Location/Qualifiers
FT 235..2898
FT /*tag= a
FT /product= "Corn lipoxigenase 4"
XX
PN US2003074693-A1.
XX
PD 17-APR-2003.
XX
PF 29-JAN-2002; 2002US-00059909.
XX
PR 10-FEB-1999; 99US-0119597P.
PR 09-FEB-2000; 2000US-00501422.
XX
PA (CAHO/) CAHOON E B.
PA (KINN/) KINNEY A J.
PA (KLEI/) KLEIN T M.
PA (LEEJ/) LEE J.
PA (PEAR/) PEARLSTEIN R W.
PA (RAFA/) RAFALSKI J A.
PA (SHEN/) SHEN J B.
PA (THOR/) THORPE C J.
PA (TING/) TINGEY S V.
PA (WENG/) WENG Z.
XX
PI Cahoon EB, Kinney AJ, Klein TM, Lee J, Pearlstein RW;
PI Rafalski JA, Shen JB, Thorpe CJ, Tingey SV, Weng Z;
XX
DR WPI; 2003-567325/53.

QY 1654 TTCCTGAAGGACGATGGCAGCTGAAGCCCTGGCCATCGAGCTGAGCTTGCCCCACCCCT 1713
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QY 1714 GACGGCCAGCAGCGCGCGCGGTGACAAAGGTGACACCCCGGCTCACACCGGCGTGGAG 1773
Db 934 GATGGCCAGCAGCAGCGCGCGGTGACAAAGGTGACACCCCGGCTCACACCGGCGTGGAG 993
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QY 2074 TTCAACGAGCAGGCTCTCCAGCAGATCTCGTCAAGAGAGGTGTGGCTGTGCGGACCA 2133
Db 1294 TTCACCGAGCAGGCTCTCCCGTCTGATCTCGTCAAGAGAGGGTGGCGGTGCGGACCCG 1353
QY 2134 TCAAGCCCATATGGTGTCCGACTGCTGATCAAGGACTACCCCTATGCCGTTGACGGGCTC 2193
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Db 1834 ATCCTGTCCAAGCACTCTCCGACGAGGTGTACCTGGCCAAACCGGACACGCGCGA ---G 1890
QY 2674 TGGACGTCAGACGCGAAGCGCTGGATGCTTCAAAAGATTCCGGAGCCCGGCTGGTGCAG 2733
Db 1891 TGGACGTCGACGCGAAGCGCTGGACGCGTTCGAAGAGTTTCGGCAGCCCGGCTGGTGGAT 1950
QY 2734 ATTGAGAAATCGGATCAAGACGATGAACGACAGTCCGGAATTGAAGAACCGGAGGGCCT 2793

Db 1951 ATCGAGAACCGGATCAAGGACATGAACGGCAACTCGGCGCTCAAGAACCGGACGGCGC 2010
QY 2794 GTGGAATGCCGTACATGCTGCTGTACCCCAACACGTCGGACGTTACCGGCGGAGAGGCC 2853
Db 2011 GTGAAGATGCCGTACATGCTGCTGTACCCCAACACGTCGGATGTCAACCAAGGAGAGGCC 2070
QY 2854 GAGGGCTTACTGCCATGGCATTCCTCAACAGCATCTCCATATGA 2898
Db 2071 CAAGGCTCACCGCATGGCATCCCAACAGCATCTCCATCTGA 2115
RESULT 4
ABK8441
ID ABK8441 standard; cDNA; 2818 BP.
XX
AC ABK8441;
XX
DT 07-OCT-2002 (first entry)
XX
DE Barley lipoxigenase 1, LOX-1, cDNA.
XX
KW Barley; plant; ss; gene; lipoxigenase-1; LOX-1; transgenic; beer;
KW beverage; malt; organoleptic property; brewing; trans-2-nonenal; T2N;
KW elevated storage temperature; flavour stability; shelf-life.
XX
OS Hordeum vulgare.
XX
Key Location/Qualifiers
CDS 69..2657
FT /*tag= a
FT /product= "LOX-1"
XX
PN WO200253720-A1.
XX
PD 11-JUL-2002.
XX
PF 29-DEC-2000; 2000WO-IB002045.
XX
PR 29-DEC-2000; 2000WO-IB002045.
XX
PA (CARL-) CARLSBERG RES LAB.
PA (HETB) HEINEKEN TECH SERVICES BV.
PA (BRAS-) BRASSERIES KRONENBOURG SA.
XX
PI Douma AC, Doderer A, Cameron-Mills V, Skadhauge B, Bech LM;
PI Schmitt N, Heistek JC, Van Mechelen JR;
XX
WPI; 2002-557741/59.
DR P-PSDB; AAU99691.
XX
PT Novel barley cultivar having reduced lipoxigenase 1 activity and which
PT expresses mutant lipoxigenase protein, useful in brewing processes to
PT reduce formation of off-flavors in brewed products e.g. beer during
PT storage.
XX
PS Example 3; Page 89-91; 112pp; English.
XX
CC The invention relates to a barley plant or portion comprising a mutant
CC lipoxigenase-1 (LOX-1) protein, characterised by a reduction or absence
CC of LOX activity as compared to a non-mutated control, or comprising a
CC heterologous nucleic acid sequence expressing an antisense sequence to a
CC portion of a transcribed region of barley lox-1 gene, operably linked to
CC a promoter and a transcription terminator sequence. Also included are
CC grain or plant progeny produced from the barley plant or its portion, a
CC plant product produced from the barley plant or its portion or progeny,
CC and a beverage e.g. beer, manufactured using the plant product, plant or
CC its portion or progeny. The mutated barley plant, portions, progeny and
CC products are useful in the manufacture of a beverage, preferably malt or
CC beer, for stabilising organoleptic properties of a brewed product over a
CC measured period of time for the manufacture of a brewed product having
CC reduced levels of free trans-2-nonenal (T2N) over a measured period of
CC time or under conditions of elevated storage temperature and for the

Db 2426 CACGCCGGA---GTGGACCTCGGACCCAAAGGCCCTGGAGGTGTTCAAGCGGTTCAAGCGGA 2482
QY 2721 CCGGCTGGTGCAGATTGAGAAATCGGATCAAGACGATGAACGACAGTCCGGACTTGAAGAA 2780
Db 2483 CCGGCTGGTGGAGATCGAGAGCAAGGTGGTGGCATGAACCATGACCCGGAGTCAAGAA 2542
QY 2781 CCGGAAGGGCCTGTGGAAATGCCGTACATGCTGTGTACCCCAACACAGTCCGACGTTAC 2840
Db 2543 CCGCAACGGCCCGGCTAAGTTTCCCTACATGCTGTCTACCCCAACACCTCCGACCCAA 2602
QY 2841 CCGCGAGAAGCGAGGGGCTTACTGCCATGGGCATTCCCAACACAGCATCTCCATATGAGC 2900
Db 2603 GGGCG---CCGCTGCCGGGCTTACCGCAAGGGCATCCCCAACACAGCATCTCCATCTAATC 2659
QY 2901 CTGGGCA 2907
Db 2660 TAAGCCA 2666

RESULT 6

ADA69728
ID ADA69728 standard; DNA; 2613 BP.
XX
AC ADA69728;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice gene, SEQ ID 3051.
XX
KW Plant; bacterial infection; fungal infection; viral infection; rice;
KW gene; ds.
XX
OS Oryza sativa.
XX
PN WO2003000898-A1.
XX
PD 03-JAN-2003.
XX
PF 22-JUN-2001; 2001WO-IB001105.
XX
PR 22-JUN-2001; 2001WO-IB001105.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX WPI; 2003-175290/17.

DR
XX Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX Claim 6; SEQ ID NO 3051; 899pp; English.
PS
XX The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.

XX
SQ Sequence 2613 BP; 488 A; 947 C; 797 G; 380 T; 0 U; 1 Other;

Query Match 38.6%; Score 1209; DB 7; Length 2613;
Best Local Similarity 69.7%; Pred. No. 3.2e-205;
Matches 1827; Conservative 1; Mismatches 712; Indels 81; Gaps 11;

QY 302 TCCGGCGCACGGTGAGGCTGGTCAAGAGGAGGTGCTGGACGTGGCGACTTCAACGCCT 361
Db 50 TCAAGGGCTCCCTCGTCTCTCATGCGCAAGAACGCCCTCGACATCAACGACTTCGGCGCCA 109
QY 362 CGCTCCTCGACGGCGTCCACAGGATCCTCGGCTGGACGACGCGCTCGCCTTCCAGCTCG 421
Db 110 CCGTATCGACGGCATCTCCGAGTTCCTCGGCCG-----CGGCGTCACTGCCAGCTCG 163
QY 422 TCAGCGCCACCGCGGCCGACCCCGAGCAACCGGGGCCGTGGCAAGTGGGAAGCGCGCGC 481
Db 164 TCAGCTCCTCCTCGTCCGACCCCAACAATGGGAACAGGGGAGGTGGGACGGAGCGGA 223
QY 482 ACCTGGAGGAGGGGTGGTGTGCTCAAGTCCACGGCGGACGGGGAGACCGTGTACCGGG 541
Db 224 GCGTGGAGCAAGTGGCTGACGAGCCTGCGTGCCTGACGACGGGAGAGTCCAAGTTCGGGG 283
QY 542 TGAGCTTCGAGTGGGA---CGAGTCGAGGGGCATCCCGGGCGCGCTCCTGTCAGGAACC 598
Db 284 TGACGTTGAGTGGGAGGTGGAGAGATGGGCATACCCGGCGCCATCATCGTCAAGAACA 343
QY 599 TGCAGCACGCCGAGTTCCTTCTCAAGACGCTCACCTCGAGGGCGTCCCAGGCAAGGSCA 658
Db 344 ACCACGCCCGCGAGTTCCTTCTCAAGACCATCACCTCGACACGTCCTCCGCGCCACGCG 403
QY 659 CCGTCTCTTCGTCGCCAACTCGTGGTCTACCCCGCACAGCTCTACTCCCAGGAACGCA 718
Db 404 CCGTCTCTTCGTCGCCAACTCGTGGATCTACCCCGCTCCAGTATCGCTACAACCCGCG 463
QY 719 TCTTCTTCGCCAACGACACCTATCTGCCGAGCAAAATGCCGGCGGGTGGTGGCTTATC 778
Db 464 TCTTCTTCGCCAACGACACTTCACTGCCGAGCAAGATGCCGGCGGGCTGAAGCCGTACC 523
QY 779 GGCAAGATGAGCTCAAGATTCTCGTGGCGACGATAATCCTTGACCATACCAGGAGCATG 838
Db 524 GCGACGACGAGCTCCGCAACCTGCGGGCGGACGACGAGGGGCCGTACAGGAGCAGC 583
QY 839 ATCGGCTTACCGTTACGACTACTCAATGACCTTGGTGATCCGACAAAGGGCGAAGAGC 898
Db 584 ACCGCGTCTACCGCTACGAGCTCTACAACGACCTCGGGGAGCCCGACTCCGGC-----A 637
QY 899 ACGCTCGGCCGATCCTCGTGGCGAGCCAAAGAACACCCGTATCCCGTCTGCTGCAAACTG 958
Db 638 ACCCTCGCCCTGCTCTCGCGGGCTCCCGGACCGCCCTACCTCTGCGCGCGCGCACCG 697
QY 959 GCCGGCACCCCAAGAAAGACCCAAATTCGGAGAGCAGGCTTTCTCTGCTGAACCTGA 1018
Db 698 GCCGCAAAACCCAAACAACTGACCCCGCGGAGAGAGGCTGTCTATTGCTGA---GA 754
QY 1019 ACATCTACGTCGCGCGTGACGAAAGCTTTGGGCTCTCAAGATGTCGGACTTCTTGGGT 1078
Db 755 ACATCTACGTCGCGCGTGACGAGCGGTTGCGGCACTTGAAGATGCGCGACTTCTTGGGT 814
QY 1079 ACTCGCTGAAGACGATCATCGAGGCTGTTCTTCCAAACACTGGGAGCTTTCTGTCGATGACA 1138
Db 815 ACTCCATCAAGCGGCTCGTCCGACGGCATCGTCCCGCGATCCGCACTACGTCGACCTCA 874
QY 1139 CGCCCAAGGAGTTCGATTCTGTTGAGGATATCCTCGGGCTCTACGAGCTGGGCCAGAGG 1198
Db 875 CACCCGGCGAGTTCGACTCCTTCAAGGACATCCTCAAGCTCTACGAGGGCGGCTCAAGC 934
QY 1199 CACCCAAACACCCACTGATAGCAGAGATCAGGAAGAAGATCCCGACGAGTTCCTTCGAA 1258
Db 935 TGCCCAAGCATCCCGCGCTGGAGGAGCTCCGAAAGCGCTTCCCTCTCCAGCTCGTCAAGG 994
QY 1259 GCATTCTGCCGAACGGTAGCCATGACCAACCCCGTAAAGATGCCCTTCCAAATGTATCA 1318
Db 995 ACCTCATCCCGCGCGGGC---GACTACCTCTCAAGCTCCCGATCCCGACGCTCATC- 1050
QY 1319 AATCAGATGTTGAAAAGGCTCCGGAGTCTTAAGTTTGGCTGGAGGACTGACGAAGAGT 1378
Db 1051 -----CGGAGGACAAAGAGGCGGTGGATGACCGACGAGT 1087

QY	1379	TCGCGAGAGAGACAC	TTG	CAGCGGTGA	AAACCCAGTA	ATCATCAAAACGTCT	GACGGAGTTCC	1433
Db	1088	TCGCCCGGAGATCCT	CGCGGCGTCA	ACCCCAT	TGTTTCATCGCCCGCT	CACCGAGTTCC	1147	
QY	1439	CCGCTAAAAGCACC	CTG	GAACCAAGCAGT	ACGAGACACAC	CAGCAAGATCACT	GAAG	1498
Db	1148	CGCCGGAGCCGCTC	GAACCCGCGC	CAGGTAC	GGCGACAGACGAG	CACCATCACGCGG	1207	
QY	1499	CTCACATCCGGCATA	A	CATGGGAGGCCT	TGTCGGTGCAGAACG	CACCTGAGGAACA	AGAGGC	1558
Db	1208	CGCACGTCGAGCG	GGGCTCG	AGGGGCTCAC	CGTGCAGAGCGAT	CGACGCGCAACCTTC	1267	
QY	1559	TCTTCATCCTAGACC	ACCATG	ACCATTTTCAT	GCCGTACCTCGACGAG	ATCAACGAGCTGG	1618	
Db	1268	TCTACGTGGTGGA	CCACCA	CGATCATTTTCAT	GCCCTACTTGTGGAT	ATCAATAGCCTCG	1327	
QY	1619	AGGGGAACCTTCAT	CTACGCCAGCAGG	ACCTTACTGTCT	CTGAAGACGATG	CGCACGCTGA	1678	
Db	1328	ACGACAACTTCAT	CTACGCCACGCG	ACGCTGCTGTCT	GCGCGGACGCG	CACGCTGG	1387	
QY	1679	AGCCCTGGCCATCG	AGCTGAGCCT	TGCCCCAC	---CTGACGGCCAG	CAGCGCGGCGCGG	1735	
Db	1388	CGCCGCTCGCCAT	CGAGT	GAGCTTGCCG	CACCTGCAGACGAC	GGGCTGATCACG	CCA	1447
QY	1736	TCAGCAAGGTGTAC	ACCCCGC	-----TCAC	ACCGCGCTCGAGGGCC	1777		
Db	1448	GGAGCACCGTGTAC	CGCCGGCGCG	CGCGCGGCA	CCGGCGCGCGCGCTG	GAGTGGT	1507	
QY	1778	ACGTCTGGCAGCT	CGCCAAAGCTT	TATGCCCTGCGT	AAACGACTCTGCCT	GGCATCAGCTGA	1837	
Db	1508	GGGTGTGGCAGCT	CGCCAAAGCGT	ACGTCAACGT	GAACGACTACTGCT	GGCACAGCTGA	1567	
QY	1838	TCAGCCACTGGCT	GAACACGACG	CGCGTGATCG	AGCCGTTCTGTA	ATCGCGACAAAC	CCGGC	1897
Db	1568	TCAGCCACTGGCT	CAACACGACG	CGCGTGATGG	AGCCCTTCGTCA	TCGCGCACCAAC	CCGGC	1627
QY	1898	AGCTCAGCGTGGT	GCATCCCGTG	CACAAGCTG	CTGAGCCCGCACT	ACCGTGACAGCTGA	1957	
Db	1628	AGCTCAGCGTGGC	GAACCGGTG	CAACAAGCTG	CTGCTGCCGCACT	ACCGCGACACCATGA	1687	
QY	1958	ACATCAACGCCCT	TGGCAGCCAG	ACACTCATCAAC	CGCGCGCGGTCTT	TCGAGCGCACCG	2017	
Db	1688	CCATCAACGCGCT	TGGCGGCGAG	ACGCTCATCAAC	GGCGGGCATCTT	TCGAGATGACCG	1747	
QY	2018	TGTTCCCTGCAAG	PAACGCTGGG	GATGTGCGCAG	ACGTGTACAAGAG	CTTGAATTTCA	2077	
Db	1748	TGTTCCCGGGAAG	CACGCGCTCG	CCATGTCTCGCGGT	CTACAAGGACT	TGGAGCTTCG	1807	
QY	2078	ACGAGCAGGCTCT	CCAGCAGATCT	CGTCAAGAGAG	GTGGCTGTGCCG	ACCAGTCAA	2137	
Db	1808	CCGACCAGGCGCT	CCCCGACGAC	CTTGTCAAGCGCG	CGTCGCGGTGCCG	ACCAGTCCGCGA	1867	
QY	2138	GCCCATATGGTGT	CCGACTGCTGAT	CAAGGACTAC	CCCTATGCCGTTG	ACGSGCTCGTCA	2197	
Db	1868	GCCCGTACAAG	TGCGGCTGCTCAT	CGAGGACTAC	CCCGTACGCCAAC	CGACGCGGCTGGCCG	1927	
QY	2198	TCTGGTGGCGCAT	CGACCGGTGGG	TCAAGGAGTAC	CTTGGACATCTACT	ATCCCTAACGACG	2257	
Db	1928	TCTGGCACGCCAT	CGACGAGTGGG	CCAACGAGTAC	CTCGCCATCTACT	ATCCCCAACGACG	1987	
QY	2258	GCGAGCTCCAG	CGTGACGTGG	AGCTGCAGCG	GTGGTGAAGGAG	GTGCTGAGGAGCGC	2317	
Db	1988	GCGTGTCCAG	GGCGACCGG	AGCTGACGG	GTGGTGAAGGAG	GTCCGCGAGGTCCG	2047	
QY	2318	ACGGCGACCTCA	AGGACCGGAG	ACTGGTGGCC	CCAGGATGGAC	ACCGTCCAGCAGCTGG	2377	
Db	2048	ATGGCGACATCA	AGGACCGGAC	GTGGTGGCCG	GAGATGAAGAC	CGTGGCGGAGCTGGTCA	2107	
QY	2378	GGGCGTGACG	ACATCATCTGG	TGGTGCGATCCG	CGCTGCACGCGG	CTGTCAACTTTGGC	2437	
Db	2108	AGGCGTGGCC	ACCATCATCTG	GATCGGGTCCG	CGCTGCACGCGC	CGTCAACTTCGGG	2167	
QY	2438	AGTACCCATAC	GCGGGTACCT	TCCGAAACCGG	CCGACGGCCAG	CCCGGCGCCGATGCCG	2497	

Db	2168	AGTACCCGTAACCCCGGGTACCTCCCGAACCGTCCGTGGTGAGCCGGCGCCGATGCCGG	2227
QY	2498	AGCCAGGCAGCCACGACTACAAGAAGCTGGGAGCGGGGCAGAAAGGAGGCGGACATGGTGT	2557
Db	2228	AGCCGGGAACGAAGGAGTACGACGAGCTGG-----CGCGCGATCCGGAGAAGGTGT	2278
QY	2558	TCATCCGCACCATCACAGCCAGTTCAGACCATCTCTGGGCATCTCGCTCATCGAGATCC	2617
Db	2279	TCGTCCGGACAATCACCAAGCAGATCAGGCCATCGTGGGATCTCGTGTCTGGAGATCC	2338
QY	2618	TCTCCAAGCACTCCTCCGACGAGGTGTACCTCGGCCAGCGTGACGAGCCTGATCGCTGGA	2677
Db	2339	TGTCCAAGCACTCCTCCGACGAGGTGTACCTCGGACAGCGGCACACGCCGA---GTGGA	2395
QY	2678	CGTCAGACGCCAAGGCGCTGGATCGGTTCAAAAGATTCCGGAGCCGGCTGGTGCAGATTG	2737
Db	2396	CGTCGGACGCCAAGGCGCTGGAGGCGTTCAAGCGGTTCCGGCGCGGCTGACGGAGATCG	2455
QY	2738	AGAATCGGATCAAGACGATGAACGACAGTCCGGACTTGAAGAACCGGAAGGGGCCCTGTGG	2797
Db	2456	AGAGCCGCGTCGTGCGCATGAACAAGGACCCCCACCGCAAGAACCGTGTCCGGCCGACCA	2515
QY	2798	AAATGCCGTACATGCTGCTGTACCCCAACACGTCGGACGTTACCGGCGAGAAGCCGAGG	2857
Db	2516	ATTTCCCTTACACGCTGCTCTACCCCAACACCTCCGACCTCAAGGGCG---ACGCTGCCG	2572
QY	2858	GGCTTACTGCCATGGGCATTCCCAACAGCATCTCCATATGA	2898
Db	2573	GCCTCTCCGCCAGGGGCATCCCCAAGCAGCATCTCCATCTGA	2613

RESULT 7

AAQ24492
ID AAQ24492 standard; cDNA; 2830 BP.

AC AAQ24492;

24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 12-FEB-1993 (first entry)

DE Rice lipoxygenase gene.

KW Disease resistant; breeding; wheat flour bleaching; storage; ss.

OS *Oryza sativa*: (Nihon-bare).

Key	Location/Qualifiers
FH	

ET	98. .2695
CDS	

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FT
/*tag= a
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PN JP04094687-A.

PD 26-MAR-1992.

PF 13-AUG-1990; 90JP-00211469.

PR 13-AUG-1990: 90JP-00211469.

PA (MITS-) MITSUI GYOSAI SHOKU.

WPI: 1992-156057/19.

DR P-PSDB; AAR23797.

Rice lipoxigenase gene useful in breeding disease-resistant plant -
prepd. by introducing phage or plasmid into host microorganism pref.
escherichia coli.

PS Claim 1; Fig 1; 7pp; Japanese.

CC The rice variety Nihon-bare was allowed to germinate in a dark place and
CC the RNA isolated from it used to create a cDNA library which was screened
CC

Db 2016 CGCCAATCGAGCAAGTGAGCGCCACCGAGTACCTCGCCATCTACTACCCCAACGACGGCGTGC 2075
QY 2264 TCCAGCGTGACGTGGAGCTGCAGGCGTGGTGAAGAGGAGTCCGTGAGGAGCGCACGGCG 2323
Db 2076 TCCAGGGCGACGCCGAGCTGCAGGCGTGGTGAAGAGGAGTCCGCGAGGTCCGGCATGGCG 2135
QY 2324 ACCTCAAGGACCGGAGCTGGTGGCCAGGATGGACACCGTCCAGCAGCTGGTAGGCGT 2383
Db 2136 ACATCAAGGACCGGAGCTGGTGGCCGAGATGAAGACGGTGGCGGAGGTGGTCAAGGCGT 2195
QY 2384 GCAGGACCATCATCTGGGTGGCATCCGCGCTGCACGCGGTGTCAACTTTGGGCAGTACC 2443
Db 2196 GCGCCACCATCATCTGGATCGGTCCGCGCTGCACGCGCGCTCAACTTCGGGCAGTACC 2255
QY 2444 CATACGCGGGTACCTCCCGAACCAGCGCGCCAGCGCCAGCGCGCGCGATGCCGAGCCAG 2503
Db 2256 CGTACGCGGGTACCTCCCGAACCAGCTCCGTCGGTGAGCCGCGCGCGATGCCGAGCCCG 2315
QY 2504 GCAGCCACGACTACAAGAGCTGGGAGCGGGGCGAGAGGAGCGGACATGGTGTTCATCC 2563
Db 2316 GAACGAAGGAGTACGACGAGCTGG-----CGCGCATCCGAGAGAGGTGTTCTGTC 2366
QY 2564 GCACCATCACCAGCGAGTTCAGACCATCTCGGCGCATCTCGCTCATCGAGATCCTCTCCA 2623
Db 2367 GGACAATCACCAAGCAGATGCAGGCCATCTGCGGATCTCGCTGCTGGAGATCCTGTCCA 2426
QY 2624 AGCACTCCTCCGACGAGGTGTACCTCGGCCAGCGTGCAGAGCCGTGATCGCTGGACGTGAG 2683
Db 2427 AGCACTCCTCCGACGAGGTGTACCTCGGACAGCGCGACACGCGCGA---GTGGACGTGCG 2483
QY 2684 ACGCCAAGCGCTGGATCGTTCAAAAGATTCGGGAGCGCGCTGGTGCAGATTGAGATC 2743
Db 2484 ACGCCAAGCGCTGGAGCGTTCAAGCGGTTGCGCGCGCGGCTGACGGAGATCGAGAGCC 2543
QY 2744 GGATCAAGACGATGAACGACAGTCCGGAATTGAAGAACCGGAACGGGCGCTGTGGAATGC 2803
Db 2544 GCGTCGTCCGATGAACAAGGACCCCAACCGCAAGAACCGTGTGCGGCGCGACCAATTTC 2603
QY 2804 CGTACATGCTGTGTACCCCAACAGTCCGACGTTACCGGCGAGAGGCCGAGGGGCTTA 2863
Db 2604 CCTACACGCTGTCTACCCCAACACCTCCGACCTCAAGGGCG---ACGCTGCGGCGCTCT 2660
QY 2864 CTGCCATGGGATTCCTCCCAACAGCATCTCCATATGAGC 2900
Db 2661 CCGCCAGGGGATCCTCCCAACAGCATCTCCATCTGATC 2697

RESULT 8
AAQ24234
ID AAQ24234 standard; DNA; 2830 BP.
XX
AC AAQ24234;
XX
DT 24-OCT-2003 (revised)
DT 04-NOV-1992 (first entry)
XX
DE Lipoxigenase gene.
XX
KW Temperature; denaturation; rice; pRLC11; enzyme; ss.
XX
OS Oryza sativa; (Nihonbare).
XX
Key Location/Qualifiers
CDS 98..2695
FT /*tag= a
FT /label= lipoxigenase

XX JP04094681-A.
FN
XX
PD 26-MAR-1992.
XX
PF 13-AUG-1990; 90JP-00211470.
XX

PR 13-AUG-1990; 90JP-00211470.
XX
PA (MITS-) MITSUI GYOSAI SHOKU.
XX
DR WPI; 1992-156052/19.
DR P-PSDB; AAR20670.
XX
PT Prodn. of protein in E.coli without denaturation - by culturing
PT transformed E.coli at low temp.
PS
XX Disclosure; Fig 1 (1-4); 5pp; Japanese.
CC mRNA was extracted from a rice plant and used to prepare a cDNA library.
CC A clone contg. cDNA encoding the full length lipoxigenase gene was
CC isolated (pRLC11) and used to transform E.coli. The transformant was
CC deposited as FERM P-11635. pRLC11 was then ligated with an expression
CC vector to obtain clone ET3a/RL0X2, which was used to transform E.coli
CC BL21(DE3). The obtained clone was deposited as FERM P-11636. This clone
CC was inoculated to ampicillin contg. LB medium, and cultured at 37 degrees
CC C overnight. IPTG was then added, and the mixt. cultured below 20 degrees
CC C, e.g. 18 or 15 degrees C for 16 hrs. Cells were collected and disrupted
CC by ultrasonification to recover the enzyme solution. (Updated on 24-OCT-
CC 2003 to standardise OS field)
XX
SQ Sequence 2830 BP; 546 A; 992 C; 846 G; 446 T; 0 U; 0 Other;
Query Match 36.6%; Score 1148.2; DB 2; Length 2830;
Best Local Similarity 68.6%; Pred.No. 2e-194;
Matches 1795; Conservative 0; Mismatches 738; Indels 84; Gaps 12;
QY 302 TCCGCGGCACGGTGAGGCTGGTCAAGAGGAGGTGCTGGACGTGCGCGACTTCAACGCCT 361
Db 147 TCAAGGGCTCCCTCGTCTCATGGCAAGAACGCCCTCGACATCAACACTTCGGCGCCA 206
QY 362 CGTCTCTCGACGGCGTCCACAGGATCTCTGGCTGGGACGACGGCGTCCCTTCCAGCTCG 421
Db 207 CCGTCATCGAGCGCATCTCCGAGTTCCTCGGCGG-----CGGCGTCACTGCCAGCTCG 260
QY 422 TCAGCGCCACCGCGGCCGACCCCGAGCAACGGGGGCGGTGGCAAGTGGGGAGGCGCGC 481
Db 261 TCAGTCTCTCCCTCGTTCGACCCCAACAATGGGAACAGGGGAGGTGGGGACGGAGGCGA 320
QY 482 ACCTGGAGGAGCGGTGGTGTGCTCAAGTCCACGGCGGACGGGGAGACCGTGTACCGGG 541
Db 321 GCCTGGAGCAGTGGCTGACGAGCCTGCGTGCCTGACGACGGGAGAGTCCAAGTTCGGGG 380
QY 542 TGAGCTTCGAGTGGGA---CGAGTCGACGGGCGATCCCGGCGCGCTGCTGGTCAAGAAC 598
Db 381 TGACGTTTCGAGTGGGAGGTGGAGAGATGGGCATACCCCGCGCCATCATCGTCAAGAACA 440
QY 599 TGCAGCACGCGGAGTCTTCTCTCAAGACGCTCACCTTCGAGGGCGTCCAGGCAAGGGCA 658
Db 441 ACCACGCGCGCGAGTCTTCTCTCAAGACCATCACCTTCGACAACTCCCGCCCGCCACGGCG 500
QY 659 CCGTCGTCTTCGTCGCCAATCTCTGGTCTACCCGCAACAGCTCTACTCCAGGAACGCA 718
Db 501 CCGTCGTCTTCGTCGCCAATCTCTGGTCTACCCCGCTCCAGTATCGCTACAACCGCG 560
QY 719 TCTTCTTCGCCAACGACACCTATCTGCCGAGCAAAATGCCGCGCGCTTGGTGCCTTATC 778
Db 561 TCTTCTTCTCAACGACACTTCTACTGCCGAGCAAGATGGCGGCGCGCTGAAGCCGTACC 620
QY 779 GGCAAGATGAGCTCAAGATTCTCCGTGGCGACGATATCTCTGGACCATACCCAGGAGCATG 838
Db 621 GCGACGACGAGCTCCGCAACCTGCGGGCGACGACCCAGCAGGGCCCCGTACCAGGAGCAG 680
QY 839 ATCGCGTCTACCGTTACGACTACTACAATGACCTTGGTGTATCCCGACAAGGGCGAAGAGC 898
Db 681 ACCGCGTCTACCGTACGACGTCTACAACGACCTCGGCGAGCGCCGACTCCGGC-----A 734
QY 899 ACGTCTCGGCGCATCTCTCGGTGGAGCCCAAGAACACCCGTATCCCCGTCTCCGTCAGAACTG 958
Db 735 ACCCTCGCCCTGTCTCTCGGCGGCTCCCCCGACCGCCCTACCTCTGCCCGCGCGACCG 794

XX Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 112..2703
FT /*tag= a
FT /product= "9'-specific lipoxxygenase protein"
XX
PN JP2002325577-A.
XX
PD 12-NOV-2002.
XX
XX 27-APR-2001; 2001JP-00133611.
PF
XX 27-APR-2001; 2001JP-00133611.
PR
XX (SHIS) SHISEIDO CO LTD.
PA
XX WPI; 2003-460714/44.
DR P-PSDB; ADC53139.
XX
PT A new rice-derived 9-specific lipoxxygenase gene useful for production of
PT 9-specific lipoxxygenase.
XX
PS Claim 1; SEQ ID NO 1; 17pp; Japanese.
XX
CC The invention relates to a novel 9-specific lipoxxygenase comprising a
CC fully defined sequence of 863 amino acid residues, as given in the
CC specification and a derivative having 9'-specific lipoxxygenase activity.
CC The 9-specific lipoxxygenase gene is useful for production of the 9-
CC specific lipoxxygenase in microbes, animal or plant cells. This
CC polynucleotide sequence represents the 9'-specific lipoxxygenase gene of
CC the invention.
XX
SQ Sequence 3033 BP; 825 A; 801 C; 739 G; 668 T; 0 U; 0 Other;
Query Match 35.7%; Score 1119; DB 9; Length 3033;
Best Local Similarity 67.0%; Pred. No. 3.1e-189;
Matches 1749; Conservative 0; Mismatches 800; Indels 60; Gaps 9;
QY 298 AAGATCCGGCAGCGGTGAGGCTGTGCTCAAGAAGGAGGTGCTGGACGTGGCGACTTCAAC 357
DB 157 AAGATCAAAAGGCTTGCTGTGCTGATGAGCCGAAATTAAGTATCAAGGACTTCACT 216
QY 358 GCCTCGCTCCTCGACGGCGTCCACAGGATCCTCGGCTGGGACGACGGCGTCCGCTTCCAG 417
DB 217 GCCTCGCTCCTCGACAACTGCTCATGAGTCTTTGGAA-----ACAGCATCACCTGCCAG 270
QY 418 CTCGTACGCGCACCGCGCGCCGACCCAGCAACCGGGGCGGTGGCAAGGTGGGGAGGCG 477
DB 271 CTTGTCAGCGCACTGTTGCCGACCAAAACAATGAGGCGAGGGGATAGTTGGATCAGAG 330
QY 478 GCGCACCTGGAGGAGCGGTGGTGTGCTCAAGTCCACGGGCGGACGGGAGACCGGTGTAC 537
DB 331 GCGAATCTGGAGCAGGGGTTGACAGATTACCATCGGTATCACAAGGGGAGTCCAAGCTC 390
QY 538 CGGGTGAGCTTCGAGTGGGA---CGAGTCGAGGGGCATCCCGGGCGCGTCCCTGGTCAGG 594
DB 391 ACAGTGAGGTTCAACTGGGAGATGGACAAGCATGGTGTGCCAGGGGCCATCATCATCAAG 450
QY 595 AACCTGCAGCAGCGCGAGTTCTTCTCAAGACGCTCACCCCTCGAGGGCGTCCAGGCAAG 654
DB 451 AACCCACACAGTACCAAGTTCTTCTCAAGACCATCACCCCTCCATGATGTCCCTGGCTGT 510
QY 655 GGCACCGTCTGCTTCGTGCGCAACTGTTGGTGTCTACCCGCAACAAGCTCTACTCCAGGAA 714
DB 511 GACACTATGTGTTGTTGTCCTCACTCTGGATCTACCCCTGTTGAAAGTACCACATCAAT 570
QY 715 CGCATCTTCTTCGCCAACGACACCTATCTGCGGAGCAAAATGCCGGCGGTGGTGCCT 774
DB 571 CGTATCTTCTTTGCAAAACATTTCTTACCCCTCCAGCCAAATGCCAGAACACTGAGGCCA 630
QY 775 TATCGGCAAGATGAGCTCAAGATTCTCCGTGGCGACGATAATCTCTGGACCATACAGGAG 834

DB 631 TACCGTGAAGACGAGCTGAGGTACCTCAGAGGGGAGGACAGGCAAGSCCGTATCAAGAG 690
QY 835 CATGATCGCGTCTACCGTTACGACTACTACAATGACCTTGGTGATCCCGACAAGGGCGAA 894
DB 691 CATGACCGCATCTACCGGTACGATGTTTACAATGACCTCGGTGAACACAGACAGGACAA- 749
QY 895 GAGCACGCTCGGCGGATCCTCGGTGGCAGCAAGAACACCCGATATCCCGCTCGCTGCAGA 954
DB 750 -----CCACGCGCTGTCTAGGTGGCTCGAGAAGCACCCCTACCGCGCTCGTGGCGT 804
QY 955 ACTGGCCGGCACCCCAAAAGAAAGACCCAAATTCGGAGAGCAGGCTTTTCTCTGTGAAC 1014
DB 805 ACTGGCCGAATTCGACCAAAAGAACCCAAACTCGGAGAGCAGATTATCACTGCTGAA 864
QY 1015 CTGAACATCTACGTCGCCGCTGACGAACGCTTTGGGCATCTCAAGATGTGCGACTTCCTT 1074
DB 865 C---AAATTTACGTGCCAAGCGATGAGCGCTTCGCGCACCTCAAGATGTGAGACTTTGCT 921
QY 1075 GGGTACTCGCTGAAGACGATCATCGAGSGTGTCTTCCAAACACTGSGGACTTTTCGTGAT 1134
DB 922 GGGTACTCGATCAAGCAATTTGTTTCAGGCGCATCTTGCTGCCATTCCGACATATGTTGAT 981
QY 1135 GACACGCCCAAGGAGTTTCGATTTCGTTGAGGATATCCTCGGGCTCTACGAGCTGGGCCA 1194
DB 982 CTCACACCTGGTGAATTTGACTCGTTCGAGGACATCTTGAAGCTCTACAGGGGAGCCTG 1041
QY 1195 GAGGCACCCCAACCCACTGATAGCAGAGATCAGGAAGAAGATCCCCAGCGAGTTTCCTT 1254
DB 1042 AAGCTTCCAGCATCCAGCACTAGAGGAGTGGCAAGAGCTTCCCTGTCCAACTTATC 1101
QY 1255 CGAAGCATTTCTGCCGAACGGTAGCCATGACCAACCCGCTAAAGATGCCCCCTTCCAAATGTC 1314
DB 1102 AAGGACCTGCTCCGGTTGGAGGC---AGCTACCTGCTCAAGTTCCTCAACCTGATATC 1158
QY 1315 ATCAATCAGATGTGTTGAAAAGGCTCCGGAGTTTAAGTTTGGTGGAGGACTGACGAA 1374
DB 1159 ATCAA-----GGAGAACGAGGTTGCTGGAGGACAGATGAG 1194
QY 1375 GAGTTGGCAGAGAGACACTTGCAGGCGTGAACCCAGTAATCATCAAAACGTCTGACGGAG 1434
DB 1195 GAATTTGCACGAGAGATTCTTGTGCTGCTGAATCCCATGGTCAATCAGGCGTCTCACGGAA 1254
QY 1435 TTCCCGCTAAAAGCACCTTGGACCCCAAGGCGAGTACGGAGACACACCCAGCAAGATCACT 1494
DB 1255 TTCCCAACCAAAAAGTACTCTTGTATCTAGCAAGTACGGTACGAGACTAGCACAATCAC 1314
QY 1495 GAAGCTCACATCCGGCATAACTATGGAGGCGCTGTGCGTGCAGAACGCACTGAGGAACAAG 1554
DB 1315 CCAGCTCACATTGAGAAGAACCTCGAAGGCGCTCAGCGTGCACAGGCACTGGATAGCAAC 1374
QY 1555 AGGCTCTTCACTTAGACCAACCATGACCATTTTCATGCGGTACTCGACGAGATCAACGAG 1614
DB 1375 AGGCTCTACATCTGGATCATCATGATCATTTTCATGCCATTCTCTATTGACATTAACAGC 1434
QY 1615 CTGAGGGGAACTTTCATCTACGCCAGCAGGACCCCTACTGTTCTGTAAGGACGATGGCAG 1674
DB 1435 CTTGATGGTATCTTCACTATGCCCAAGGACCCCTGTTGTTCTTACGTGATGATATACC 1494
QY 1675 CTGAAGCCCTGGCCCATCGAGCTGAGCCTGCCCAACCCCTGACGCCCGCAGCGCGCGCG 1734
DB 1495 CTGAAGCCACTAGCAATTGAAGTGAAGTGGCTGCCACACATCGAGGGCAACCTAACATCTGCA 1554
QY 1735 GTCAGCAAGGTGTACACCCCGCTCACACCGGCGTTCGAGGGCCACGTCCTGGCAGCTCGCC 1794
DB 1555 AAGAGCAAGTCCATACACCTGCATCAAGTGGCATTTGAGTCTTGGGTGTGGCAGCTGGCC 1614
QY 1795 AAGGCTTATGCTCGTAAACGACTCTGCTTGGCATCAGCTGATCAGCCACTGGCTGAAC 1854
DB 1615 AAGGCTTATGCTGCTGTTAATGACTCCGGTTGGCGCCAGCTTATCAGCCACTGGCTCAAC 1674
QY 1855 ACGCACGCGGTGATCGAGCCGTTTCGTAATCGCGACAAACCCGAGACTCAGCGTGGTGCAT 1914

Db 1675 ACACATGCTGTGTAAGAGCCCTTCGTGATCGCTACAAACCGCCAGCTCAGTGTGACACAC 1734

QY 1915 CCCGTGCACAAGCTGCTGAGCCCGCACTACCGTGACACAGCTGAACATCAACGCCCTGGCA 1974

Db 1735 CCTGTGTACAAGCTCCTCCAGCCACACATATCGGACACAGATGACAATCAATGTCATTGGCA 1794

QY 1975 CGCCAGACACTCATCAACGCCCGCGGCTCTTCGAGCGCACCGTGTTCCTGTCAAAAGTAC 2034

Db 1795 CGCCAGACACTCATCAACGCCCGGTGGCATTTTCGAACAAACTGTCTTCTTGCAAAACAT 1854

QY 2035 GCGCTGGGATGTCGGCAGACGCTGTACAAAGAGCTGGAATTTCAACGAGCAGGCTCTCCCA 2094

Db 1855 GCTCTGGCAATGCTTCAGCAGTTTACAAAGAACTGGAATTCGCGAAACAGGGCCTTCCG 1914

QY 2095 GCAGATCTCGTCAAGAGAGGTGTGGCTGTGCGGACCAAGTCAAGCCCATATGTTGCCGA 2154

Db 1915 GATGATCTGATAAAGAGAGGCATTGCCATCAAGGACCCATCAAGCCCATCAAGGTGAAG 1974

QY 2155 CTGCTGATCAAGGACTACCCCTATGCCGTTGACGGGCTCGTATCTGGTGGCGATCGAG 2214

Db 1975 CTACTGATCAAGGACTACCCCTTATGCAACAGATGGCCTGGCGATCTGGCAAGCAATCGAG 2034

QY 2215 CGGTGGGTCAAGGAGTACCTGGACATCTACTACCTTAACGACGGGAGCTCCAGCGTGAC 2274

Db 2035 CAGTGGGTCACTGAGTACTGTGCCATCTACTACCCAAACGATGGTGTCTCCAGGAGAT 2094

QY 2275 GTGAGCTGCAGGCGTGTGGAAGGAGTGGCTGAGGAGGCGCACGCGGACCTCAAGGAC 2334

Db 2095 GTGGCGCTGCAAGCATGGTGAAGAGGTACGGGAAGTACGGGCAATGCTCAAGGAC 2154

QY 2335 CGAGACTGGTGGCCAGGATGGACACCGTCCAGCAGCTGGCTAGGCGGTGACGACCATC 2394

Db 2155 GCGGACTGGTGGCCAAAGATGCAGAGCTTGCTGAGCTCACCAAGGCGCTGCACCAATC 2214

QY 2395 ATCTGGGTGGCATCCGCGCTGCACGCGGCTGTCAACTTTGGSCAGTACCCATACGCCGG 2454

Db 2215 ATCTGATTGCTACGACATCCACGCGAGCGTCAATTTCCGGGCAATACCCATACGCCGG 2274

QY 2455 TACCTCCGAACCGCCGACGGCCAGCCGCGGCGGATGCGGAGCCAGGCGCACGAC 2514

Db 2275 TATCTTCCAAACCTCCGACCATAGCCGCGGCGGATGCCCCGAGCGGTTCCAAAGGAG 2334

QY 2515 TACAAGAAGCTGGAGCGGGGCGAGAGAGGCGGACATGGTGTTCATCCGACCATCAC 2574

Db 2335 TACACAGAGCTGG-----ACGAGRACCCAGAGAGTTCTTCATCCGACCATCAC 2385

QY 2575 AGCCAGTTCCAGACCATCTCTGGGCATCTCTGCTCATCGAGATCTCTTCCAGCACTCTCC 2634

Db 2386 AGCCAAATCCAAACCATTTCTCGGTGTCTGCTCATTTGAGATTCTATCAAGCACTCAG 2445

QY 2635 GACGAGGTGTACCTCGGCCAGCGTACGAGCCCTGATCGCTGGACGTGACAGCCCAAGCG 2694

Db 2446 GATGAGATCTATCTTGGGCGAGCGTGCACGCGCAGA---GTGGAATCATGACCCCAAG 2502

QY 2695 CTGGATGCGTTCAAAAGATTTCGGGAGCCGCTGGTGCAGATTGAGAAATCGGATCAAGAC 2754

Db 2503 CTGGAAGCATTCAGAGAGTTTCAGCAGGCGAGCTGGTGGAGATTGAGAGCAAGTGTGAAC 2562

QY 2755 ATGAACGACAGTCCGGAATTTGAAGAACCGGAAGGGGCTGTGGAATGCGGTACATGCTG 2814

Db 2563 ATGAACAAGGACCCCTCTGCTCAAGAACCGGGTCTGGTCCAGCCAAATTTCCCTACAC 2622

QY 2815 CTGTACCCCAACAGCTCGGACGTTTACCGGCGAGAGGCGGAGGGCTTACTGCCATGGGC 2874

Db 2623 ATGTTCCCAACAGCTCAGACAAATAGGG---GGCGGCTGAGGGGATCACTGCCAGGG 2679

QY 2875 ATTCCCAACAGCATCTCCATATGAGCCTG 2903

Db 2680 ATCCCAATAGCATCTCAATATGAGACTG 2708

RESULT 10
ADA70433

ID 1675 ACACATGCTGTGTAAGAGCCCTTCGTGATCGCTACAAACCGCCAGCTCAGTGTGACACAC 1734

XX 1915 CCCGTGCACAAGCTGCTGAGCCCGCACTACCGTGACACAGCTGAACATCAACGCCCTGGCA 1974

XX 1735 CCTGTGTACAAGCTCCTCCAGCCACACATATCGGACACAGATGACAATCAATGTCATTGGCA 1794

XX 1975 CGCCAGACACTCATCAACGCCCGCGGCTCTTCGAGCGCACCGTGTTCCTGTCAAAAGTAC 2034

XX 1795 CGCCAGACACTCATCAACGCCCGGTGGCATTTTCGAACAAACTGTCTTCTTGCAAAACAT 1854

XX 2035 GCGCTGGGATGTCGGCAGACGCTGTACAAAGAGCTGGAATTTCAACGAGCAGGCTCTCCCA 2094

XX 1855 GCTCTGGCAATGCTTCAGCAGTTTACAAAGAACTGGAATTCGCGAAACAGGGCCTTCCG 1914

XX 2095 GCAGATCTCGTCAAGAGAGGTGTGGCTGTGCGGACCAAGTCAAGCCCATATGTTGCCGA 2154

XX 1915 GATGATCTGATAAAGAGAGGCATTGCCATCAAGGACCCATCAAGCCCATCAAGGTGAAG 1974

XX 2155 CTGCTGATCAAGGACTACCCCTATGCCGTTGACGGGCTCGTATCTGGTGGCGATCGAG 2214

XX 1975 CTACTGATCAAGGACTACCCCTTATGCAACAGATGGCCTGGCGATCTGGCAAGCAATCGAG 2034

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y, Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G; WPI; 2003-175290/17.

XX Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection by determining or detecting plant gene expression.

XX Claim 6; SEQ ID NO 3756; 899pp; English.

XX The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to the expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.

XX Sequence 2559 BP; 686 A; 700 C; 641 G; 532 T; 0 U; 0 Other;

QY 298 AAGATCCGCGCACGGTGAGGCTGGTCAAGAGGAGGTGCTGGACGTCGGCGACTTCAAC 357

Db 46 AAGATCAAGGCTTGGCTGTGCTGATGAGCCGAAATTAAGGAGGACTTCACT 105

QY 358 GCCTCGCTCCTCGACGGCGTCCAGGATCCTCGGCTGGACGACGGCGTCCCTCCAG 417

Db 106 GCCTCGCTCCTCGACAAACGTCCTCATGAGTCTTTGGAA-----ACAGCATCACCTGCCAG 159

QY 418 CTCGTACGCGCCACCGCGCCGACCCAGCAACGGGGGCGCTGGCAAGGAGGCG 477

Db 160 CTTGTACGCGCCACTGTTGCCGACCAAAACAATGAGGCGAGGGGATAGTTGGATCAGAG 219

QY 478 GCGACCTGGAGGAGGCGGTGGTGTGCTCAAGTCCACGGCGGACGGGGAGACCGGTGAC 537

Db 220 GCGAATCTGGAGCAGGGGTTGACAGATTACCATCGGTATCACAGGGGAGTCCAAGCTC 279

QY 538 CGGGTGAGTTCAGTGGGA---CGAGTCGAGGGGCATCCCGGGCGCCGTCTCTGGTCAGG 594

Db 280 ACAGTGAGGTTCAACTGGGAGATGGACAAGCATGGTGTGCCAGGGGCCATCATCATCAAG 339

QY 595 AACCTGCAGCAGCCGAGTTCTTCTCTCAAGACGCTCACCTCGAGGGCGTCCAGGCAAG 654

Query Match 34.0%; Score 1066.8; DB 7; Length 2559;
Best Local Similarity 66.4%; Pred. No. 5.6e-180;
Matches 1729; Conservative 0; Mismatches 782; Indels 93; Gaps 10;

Db 340 AACACACAGTACCAAGTTCTTCTCAAGACCATACCCCTCCATGATGTCCTGGCTGT 399
QY 655 GGCACCGTCTGTTCCGTCGCCAACTCGTGGGTCTACCCGCACAAGCTCTACTCCAGGAA 714
Db 400 GACACTATTGTTGTTGCCAACTCCTGGATCTACCTGTTGGAAGTACCACTACAAT 459
QY 715 CGCATCTTCTTCGCCAACGACACCTATCTGCCGAGCAAAATGCCGGCGGTTGGTGCCT 774
Db 460 CGTATCTTCTTTCGAAAACAATTCTTACCTTCCAGGCCAAATGCCAAGCACTGAGGCCA 519
QY 775 TATCGGCAAGATGAGCTCAAGATTCTCCGTGGCGCAGCAATATCTTGGACCATACAGGAG 834
Db 520 TACCGTGAAGACGAGCTGAGGTACCTCAGAGGGGAGGACAGGCAAGGCCGTATCAAGAG 579
QY 835 CATGATCGCTCTACCGTTACGACTACTACAATGACCTTGGTGATCCCGACAAGGGCGAA 894
Db 580 CATGACCGCATCTACCGGTACGATGTTTACAATGACCTCGGTGAACCCAGACAGG- 633
QY 895 GACACAGCTCGGCCGATCTTCGGTGGCAGCCAAAGAACACCCGATCCCGCTCGCTGCAGA 954
Db 634 GACAAACCCACGCCCTGTCTAGGTGGCTCGCAGAAAGCACCCCTACCCGCGCTCGTGGCCGT 693
QY 955 ACTGGCCGGCACCCAAAGAAAGAACCCAAATTCGGAGAGCAGGCTTTTCTGCTGAAC 1014
Db 694 ACTGGCCGAATTCCGACCCAAAAGAACCCAACTCGGAGAGCAGATTATCACTGCTGGAA 753
QY 1015 CTGAACATCTACGTCGCCGTGACGAACGCTTTGGGCATCTCAAGATGTCGGACTTCCCT 1074
Db 754 C---AAATTACGTGCCAAGCGATGAGCGCTTCGCGCACCTCAAGATGTCAGACTTTGCT 810
QY 1075 GGGTACTCGCTGAAGACGATCATCGAGGCTGTTCTTCCAACACTGGGACTTTCGTCGAT 1134
Db 811 GGGTACTCGATCAAGGCAATTGTTCAAGGACATCTTGCCCTGCCATTCGCACATATGTTGAT 870
QY 1135 GACACGCCCAAGGAGTTGATTCGTTTGGAGTATCTCGGGCTCTACGAGCTGGGCCCA 1194
Db 871 CTCACACCTGGTGAATTGACTCGTTTCGAGGACATCTTGAAGCTCTACAGGGGAGGCCCTG 930
QY 1195 GAGGCACCCAAACCCACTGATAGCAGAGATCAGGAAGAAGATCCCGACGAGTTCCCT 1254
Db 931 AAGCTTCCAGCATCCCGACACTAGAGGAGCTGCGCAAGAGCTTCCCTGCTCCAACTTATC 990
QY 1255 CGAAGCATTTCTGCCGAACGGTAGCCATGACCCCGCTAAAGATGCCCTTCCAATGTC 1314
Db 991 AAGGACCTGCTTCCGGTTGGAGGC--AGCTACTGCTCAAGTTCCCAAACTGATATC 1047
QY 1315 ATCAAATCAGATGTTGTAAGAAAGGCTCCGAGTTTAAAGTTGGCTGGAGGACTGACGAA 1374
Db 1048 ATCAA-----GAGAAGAGGTTGCTTGGAGGACAGATGAG 1083
QY 1375 GAGTTCGGAGAGAGACACTTGCAGGCGTGAACCCAGTAATCATCAACGCTCTGACGGAG 1434
Db 1084 GAATTGCACGAGAGA-----TTCTGCTGGAA 1110
QY 1435 TTCCCGCTAAAGCACCTTGACCCCAAGGAGTACGGAGACCAACAGCAAGATCACT 1494
Db 1111 TTCCACCAAAAGTACTCTTGATCCTAGCAAGTACGGTGACCAAGTAGCAATCAAC 1170
QY 1495 GAAGCTCACATCCGGCATAAACATGGGAGGCCCTGTCGGTGCAGAACGCACTGAGGAACAAG 1554
Db 1171 CCAGCTCACATTGAGAAGAACCTCGAAGGCCCTCAGCGTGCAACAGGCACTGGATAGCAAC 1230
QY 1555 AGGCTCTTCATCCTAGACCAACCATGACCAATTCATGCCGTACCTCGACGAGATCAACGAG 1614
Db 1231 AGGCTCTACATTTCTGGATCATCATGATCATTTATGATGCCATTCCTCATTAACAGC 1290
QY 1615 CTGGAGGGGAATTTCATCTACGCCAGCAGGACCCCTACTGTTCTGTAAGGACGATGGCAG 1674
Db 1291 CTTGATGGTATCTTCACTATGCCACAAGGACCCCTGTTGTTCTTACGTGATGATATACC 1350
QY 1675 CTGAAGCCCTGGCCATCGAGCTGAGCCCTGCCCCACCCCTGACGGCAGCAGCGCGCGG 1734

Db 1351 CTGAAGCCACTAGCAATTGAACTGAGCTTGCCACACATCGAGGGCAACCTAACATCTGCA 1410
QY 1735 GTCAGCAAGGTGTACACCCCGGCTCACACCCGGCGTGCAGGGCCACGTTCTGGCAGCTCGCC 1794
Db 1411 AAGAGCAAGGTCCATACACCTGTCATCAAGTGGCAATTGAGTCTTGGGTGTGGCAGCTGCC 1470
QY 1795 AAGGCTTATGCTGCTGCTAAACGACTCTGCCTGGCATCAGCTGATCAGCCACTGGCTGAAC 1854
Db 1471 AAGGCTTATGTTGCTGTTAATGACTCCGGTTGGCACCAGCTTATCAGCCACTGGCTCAAC 1530
QY 1855 ACGACGCGGTGATCGAGCCGTTCTGTAATCGCGACAAACCGGAGCTCAGCTGCTGATCAT 1914
Db 1531 ACACATGCTGTGATGAGCCCTTCTGATCGCTACAAACCGCCAGCTCAGTGTGACACAC 1590
QY 1915 CCGTGCACAAGCTGCTGAGCCCGCACTACCGTGACACGCTGAACATCAACGCCCTGGCA 1974
Db 1591 CCTGTGTACAAGCTCCTCCAGCCACACTATCGCGACACGATGACAATCAATGCTATGGCA 1650
QY 1975 CGCCAGACACTCATCAACGCGCGGCGCTCTTCGAGCGCACCGTGTTCCTGCAAGTAC 2034
Db 1651 CGCCAGACACTCATCAACGCGCGTGGCATTTTCGAACAACTGTCTTCTTCTGGCAACAT 1710
QY 2035 GCGCTGGGGATGTGCGGCAGACGTGTACAAGAGCTTGAATTTCAACGAGCAGGCTCTCCCA 2094
Db 1711 GCTCTGGCAATGTCTTTCAGCAGTTTACAAGAACTTGAACCTTCAACGGAACAGGCTTCCG 1770
QY 2095 GCAGATCTCTCAAGAGAGGTGTGGCTGTGCCGACCAAGCTCAAGCCCATATGTTGTTCCGA 2154
Db 1771 GATGATCTAATAAGAGAGGCAATTGCCATCAAGGACCCATCAAGCCCATCCAAAGGTGAAG 1830
QY 2155 CTGCTGATCAAGGACTACCCCTATGCCGTTTGACGGGCTGTCATCTGGTGGGCGATCGAG 2214
Db 1831 CTACTGATCAAGGACTACCCCTTATGCAACAGATGGCTGGCGATCTGGCAAGCAATCGAG 1890
QY 2215 CGTGGGTCAAGGAGTACTTGGACATCTACTACCTAACGACGGCGAGCTCCAGCGTGCAC 2274
Db 1891 CAGTGGGTCACTGAGTACTGTGCCATCTACTACCCAAACGATGGTGTCTCCAGGAGAT 1950
QY 2275 GTGAGCTGCAGGCGTGGTGAAGGAGGTGCTGAGGAGGCGCACGGCGACCTCAAGGAC 2334
Db 1951 GTGAGCTGCAAGCATGGTGAAGGAGGTGCGGGAAAGTTCGGGCAATGGTATCTCAAGGAC 2010
QY 2335 CGAGACTGGTGGCCCCAGGATGGACACCGTCCAGCAGCTGGCTAGGGGTGACAGCCATC 2394
Db 2011 GCGGACTGGTGGCCCAAGATGCAGAGCTTGCCTGAGCTCACCAAGGCTTCACCAATC 2070
QY 2395 ATCTGGGTGGCATCCGGCTGCACGCGGTGTCAAACTTTGGGAGTACCCATACGCCGG 2454
Db 2071 ATCTGGATTGCATCAGCACTCCACGAGCCGCTCAATTTTCGGGCAATACCCATACGCCGGC 2130
QY 2455 TACCTCCCGAACCCGCGACCGCCAGCCGCGGCCCGGCTGATCCCGAGCCAGGCGCACCGAC 2514
Db 2131 TATCTTCCAAACCCGTCGACCATTAAGCCGCGCGCGGCTGATCCCGAGCCGGGTTCCAAGGAG 2190
QY 2515 TACAAGAAGCTGGAGCGGGGCGAGAGGAGCGGCGACATGGTGTTCATCCGCAACCATCAC 2574
Db 2191 TACACAGAGCTGG-----ACGAGAACCCAGAGAAAGTTCTTCTACCGCACCATCAC 2241
QY 2575 AGCCAGTTCAGACCATCTGGGCATCTCGCTCATCGAGATCTCTCTCAAGCACTCTCTCC 2634
Db 2242 AGCCAATTCCAAACCATCTCGGTGTCTCGCTCATTTGAGATTCTATCAAAGCACTCAGCG 2301
QY 2635 GACGAGGTGTACCTCGGCCAGCGTGACGAGCCTGATCGCTGGACGTGACAGCCCAAGGG 2694
Db 2302 GATGAGATCTATCTTGGCAGCGTGACACGCCAGA--GTGGACATCAGACCCCAAGGCA 2358
QY 2695 CTGGATGCGTTCAAAAGATTTCGGGAGCCCGCTGGTGCAGATTGAGAAATCGGATCAAGACG 2754
Db 2359 CTGGAAGCATTCAGAGGTTTTCAGCAGGCGAGTGGTGGAGATTGAGAGCAAGTGTGAAC 2418
QY 2755 ATGAACGACAGTCCGCACTTGAAGAACCCGGAAGGGGCTGTGGAAATGCCGTACATGCTG 2814
Db 2419 ATGAACAAGGACCCCTGCTCAAGAACCCGGGTGGTCCAGCCAATTTCCCTTACACACTG 2478

QY 2815 CTGTACCCCAACACGTCGGACGTTACCGCGAGAGCGCGGCTTACTGCCATGGC 2874
|||
Db 2479 ATGTTCCCAACACGTCAGACAATAAGG---GGCGCTAGGGGATCACTGCCAGGGC 2535
QY 2875 ATTCCCAACAGCATCTCCATATGA 2898
|||
Db 2536 ATCCCAATAGCATCTCAATATGA 2559

RESULT 11

ABX13452
ID ABX13452 standard; DNA; 2562 BP.

XX AC ABX13452;

XX DT 04-JUN-2003 (first entry)

XX DE A. thaliana LOX5 DNA corresponding to Genbank AJ302043.

XX KW Expression cassette; transgenic; promoter; LOX5; plant; food production;
XX KW animal feed; seed; stress resistance; disease resistance; starch content;
XX KW lipid content; dormancy; fibre content; pharmaceutical production;
XX KW fine chemical production; sterile plant; vitamin; flavouring; perfume;
XX KW dye; cotyledon; embryonic tissue; stress factor; LOX; ds.

XX OS Arabidopsis thaliana.

XX PN DE10127882-A1.

XX PD 12-DEC-2002.

XX PF 11-JUN-2001; 2001DE-01027882.

XX PR 11-JUN-2001; 2001DE-01027882.

XX PA (BADI) BASF PLANT SCI GMBH.

XX PI Bischoff F, Feussner I, Loyall LP;

XX DR WPI; 2003-279966/28.

XX PT Cassette for expressing transgene, useful e.g. in production of
XX PT pharmaceuticals and fine chemicals, contains promoter from the LOX5 gene
XX PT of Arabidopsis, provides cotyledon-specific expression.

XX PS Claim 5; Page; 28pp; German.

XX CC This invention describes a novel cassette for the transgenic expression
XX CC of nucleic acid containing the promoter of the LOX5 gene from Arabidopsis
XX CC thaliana or deletion variants of the LOX5 promoter which are functionally
XX CC linked to the nucleic acid of the invention. The cassette is used to
XX CC prepare transgenic organisms, especially plants, for production of foods,
XX CC animal feeds, seeds (including those with increased resistance to stress
XX CC and disease, altered starch/lipid contents or dormancy, or altered fibre
XX CC content), pharmaceuticals (especially antibodies, vaccines, enzymes and
XX CC pharmaceutical proteins) and fine chemicals (especially enzymes,
XX CC vitamins, amino acids, sugars, (un)saturated fatty acids, flavourings,
XX CC perfumes and dyes), also to produce sterile plants. The LOX5 promoter
XX CC provides strong and specific expression in cotyledons and/or other early
XX CC embryonic tissue, so can degrade, or protect against, stress factors to
XX CC which these tissues are particularly sensitive. Since cotyledons are the
XX CC main storage organs of seeds, expressing transgenes in them produces
XX CC targeted increases/modifications in nutritional value. Expression in the
XX CC cotyledons is homogeneous, there are no side effects on other plant
XX CC organs (pollen) and the promoter is functional in a wide variety of
XX CC plants (ornamentals or crops). This sequence represents a nucleic acid
XX CC sequence associated with the Arabidopsis thaliana LOX gene described in
XX CC the disclosure of the invention

SQ Sequence 2562 BP; 733 A; 624 C; 596 G; 609 T; 0 U; 0 Other;

Query Match 24.8%; Score 777.6; DB 7; Length 2562;

Best Local Similarity 58.9%; Pred. No. 1.2e-128;
Matches 1539; Conservative 0; Mismatches 1004; Indels 69; Gaps 9;
QY 298 AAGATCCGCGGCACGGTGGTGGTCAAGAGAGGAGGTGCTGGACGCTGGCGCACTTCAAC 357
|||
Db 4 AAGATAGAAGGAGAAGTTGTTGTGATGAAGAAGATCTCCTTGATTTCAAAGACGTTATG 63
QY 358 GCCTCGCTCCTCGACGGCGTCCACAGGATCCTCGGCTGGGACGACGGCGTCGCTTCCAG 417
|||
Db 64 GCTTCTCTTCTTGATCGTGTCAATGAGCTTCTTGTCG-----TCGTGTCTCTCTCCAC 117
QY 418 CTCGTACGCGCCACCGCGGCCGACCCACGAAACGGGGCGGTGGCAAGGTGGGAAGGCG 477
|||
Db 118 CTCATCAGCTCTCACCAACCCGACCCGGCCAATGAGAAGAGAGGAGACCTTGAAGCA 177
QY 478 GCGCACCTGGAGGAGGGGTGGTGTGCTCAAGTCCACGG---CGGACGGGAGACCGTG 534
|||
Db 178 GCACATCTGGAAAAATGGGTAAACAAAATAAAGCTAGTAACCGCTGAGGAAAACCTGCG 237
QY 535 TACCGGTGAGCTTCGAGTGGGACGAGTCGAGGGCATCCGGGCGCCGTCCTGTGTCAGG 594
|||
Db 238 TTTGAGTAACGTTTGTATGGGACGAGTCAATGGGACCAACCGGTGCATTGTGATCAAG 297
QY 595 AACTGCAGCACGCCGAGTCTTCTCAAGACGCTCACCTCGAGGGCGTCCAGGCAAG 654
|||
Db 298 AACCAACCATAGTCAATTTCTACCTTAAGTCCCTCACCTCCGCGGCTTCCCTGATGGC 357
QY 655 GGCACCGTCTGTC-----TTCGTGCGCAACTCGTGGGTCTACCCGCAAGCTC 702
|||
Db 358 GAAGGTGGTGCCACTGCGATACATTTTCATCTGCAATTTCTGGATTTACCCGAATCATCGA 417
QY 703 TACTCCAGGAACGATCTTTCGCCAACGACACCTATCTGCCGAGCAAAATGCCGCG 762
|||
Db 418 TACCGTCCGACCGCGTTTCTTCTCTAAACAGGCATATCTTCCAAGTGAACACCGGAG 477
QY 763 GCCTTGGTGCCTTATCGCAAGATGAGCTCAAGATTCTCCGTGGCGACGATAATCCTGGA 822
|||
Db 478 CTAATCAAAGAGCTAAGAGAAGAGAGCTAAAGATCTAAGAGGCAATGAGAAGAGGAGA 537
QY 823 CCATACCAGGAGCATGTCGCTCTACCGTTACGACTACTACAATGACCTTGGTGATCCC 882
|||
Db 538 GAATTCAAAGAAATGGGACAGAGTTTACGACTACGCTTATTACAACGACTTGGGTGCTCCT 597
QY 883 GACAAGGCGAAGACGCTCGGCCGATCTCGTGGCGAGCCAAAGAACACCGGTATCCC 942
|||
Db 598 GACAAGGTCCTGACTCAGTTGCTCGGTTCTTGGCGGTTTCACTGAGCTGCCTTATCCT 657
QY 943 CGTCGCTGCAGAACTGGCGGCACCCCAACAAAGAAAGACCCAAATTCGGGAGACAGGCTT 1002
|||
Db 658 CGCGGTGCAAAACCGGCGTAATCCACCAATCAGACCCCTAAGTCTGAAAGCAGGCTG 717
QY 1003 TTCTGTCTGAACCTGAACATCTACGTCGCCGCGTACGAAACGCTTTGGGCATCTCAAGATG 1062
|||
Db 718 GCTTTACTAAACCTAAACATATACGTGCCAAGGACGAGCGATTTAGCCATGTGAAGTTT 777
QY 1063 TCGGACTTCTTGGGTACTCGCTGAAGACGATCATCGAGGCTGTTCTTCCAACACTGGGG 1122
|||
Db 778 TCAGACTTCTCGCTTATGCACTCAAGTCCGCTCAAGTGTCTTGTCTCTGAGATCGCC 837
QY 1123 ACTTTCGTGATGACACGCCCAAGGAGTTTCGATTCTGTTGAGGATATCTCGGGCTCTAC 1182
|||
Db 838 TCTGTTGGACAAGACCATCAACGAGTTTGACTCTCTCGAAGATGTTTTCACCTCTAT 897
QY 1183 GAGCTGGGCCCCAGAGGACCCCAACACCCACTGATAGCAGAGATCAGGAAGAAGATCCCC 1242
|||
Db 898 GACGGTAGTATTAAAGCTCGCCAAATGGTCAACACCATTTCTAAGCTCCGTGATGTTATCCG 957
QY 1243 AGCGAGTTCTTCGAGACGATCTGCGGAACGGTAGCCATGACCAACCGCTAAAGATGCC 1302
|||
Db 958 TGGAGATGTTTAGAGAGCTAGTTTCGCAACG---ACGGAGAACGGTCTTGAAGTATCCC 1014
QY 1303 CTTCCAAATGTCATCAATCAGATGTGTTGAAAAAGGCTCCGGAGTTTAAAGTTTGGCTGG 1362
|||

Db 1015 TTGCCTGACATCCTCAAA-----GAGAGCAGATCGGCTTG 1050

QY 1363 AGGACTGACGAAGAGTTCCGAGAGAGACACTTGCAGGCGTGAAACCCAGTAATCATCAAA 1422

Db 1051 AGGACTGACGAAGAGTTTGTCTCGAGAAATGTCGCCCGTCTTAATCCGGTGGTATTAGC 1110

QY 1423 CGTCTGACGGAGTTCCCGCTAAAGACCCCTGGACCCAAAGGACGAGTACGGAGACCACAC 1482

Db 1111 CGTCTTCAAGAAATTCACCAAGAGAGCTGTCTGGACTCTGCAAGATATGGAACCAACAC 1170

QY 1483 AGCAAGATCACTGAAGCTCACATCCGGCAFAACATGGGAGGCGCTGTGGTGCAAGACGCA 1542

Db 1171 TCTTCCATACGAACAGACACATAGAAATCAAAACATGAACGGCCTCAATGTCCAAGAAGCT 1230

QY 1543 CTGAGGAACAAGAGGCTCTTCACTCTAGACCAACATGACCAATTTTCATGCCGTACCTCGAC 1602

Db 1231 TTGGAACAGAAATAAGCTATACATATTGGATCATCACGACGCAATTGATGCCTTACCTGACA 1290

QY 1603 GAGATCAACGAGTGGAGGGGAACCTTCACTACGCCAGCAGGACCCCTACTGTTTCTGAG 1662

Db 1291 CGGATAAACTCAACAAACACTAA---AACCTATGCGACCCGAAACCCCTGCTGTGCTTCAA 1347

QY 1663 GACGATGGCACGCTGAAGCCCTTGCCATGAGCTGAGCCTGCCACCCCTGACGGCCAG 1722

Db 1348 GCAGACGGAACACTGAAGCCTCTCGCCATAGAGCTGAGTCTTCCACACGCACAAGGCGAA 1407

QY 1723 CAGCGCGCGGCTCAGCAAGGTGTACACCCCGGCTCACACCGSGCTCGAGGGCCACGTC 1782

Db 1408 TCATATGGATCGTCAAGCTTATGCTGCGGTCAATGACTCTGCTTATCATCAGCTTATAAGC 1467

QY 1783 TGGCAGCTCGCAAGGCTTATGCCTCGGTAACAGACTCTGCTTGGCATCAGCTGATCAGC 1842

Db 1468 TGGCAACTTGTAAAGCTTATGCTGCGGTCAATGACTCTGCTTATCATCAGCTTATAAGC 1527

QY 1843 CACTGGCTGAACACGCACGCGGTGATCGAGCCGTTTCTGTAATCGCGACAAACCGGCAGCTC 1902

Db 1528 CATTTGGTTGCAACGCATGCGGTGATTGAACCGTTTCAATAATCGGTTCCAATAGGCAGCTC 1587

QY 1903 AGCGTGGTGTATCCCGTGCACAAGCTGTGTAGCCCGGCTCACTACCGTGACACGCTGAACATC 1962

Db 1588 AGCGTGGTCCATCCGATCCATAAACTTACATCCTCATTTCCGTGACACTATGAACATC 1647

QY 1963 AACGCCCTGGCACGCCAGACACTCATCAACGCCCGGCGGTCTTCGAGCGCACCGTGTTC 2022

Db 1648 AACGCATTAGCGGTCTATGTACTCATAACTCAGACGGAGTCTTTGAGAGAACAGTCTTC 1707

QY 2023 CCTGCAAAAGTACCGGCTGGGATGTCCGACAGACGTGTACAGAGCTGGAATTTCAACGAG 2082

Db 1708 CCTAGTCGATACGCCATGGAATGTCTTCTTCAATTTACAGAAATGGGTTTTCACCGAG 1767

QY 2083 CAGGCTCTCCAGCAGATCTCGTCAAGAGAGGTGTGGCTGTGCGGACCAAGTCAAGGCCA 2142

Db 1768 CAGGCTCTCCCAAAAGACCTCTCAACAGGAGGTGTGCTGTGAAGATCCAAACAGTGAC 1827

QY 2143 TATGGTTCGAGCTGCTGATCAAGGACTACCCCTATGCCGTTGACGGGCTCGTCACTGG 2202

Db 1828 AACGGCGTTAAGCTTCTGATCGAAGATTACCCGTTTTCGCGTCGACGGTTTAGAGATTGG 1887

QY 2203 TGGGCGATCGAGCGGTGGGTCAAGGAGTACCTTGACATCTACTACCCCTAACGACGCGAG 2262

Db 1888 TCAGCGATCAAAACATGGGTTCACAGAGTACTGCACATTTCTACTACAATAATGACAAAACC 1947

QY 2263 CTCCAGCTGACGTGGAGCTGCAGGGGTGGTGAAGAGGTGGTGAGGAGGCGCACGGC 2322

Db 1948 GTCCAAACGATACAGAGATCCAAATCATGGTGGACCGGAGTCCGAACCAAGGCCACGGC 2007

QY 2323 GACCTCAAGGACCGAGACTGGTGGGCCAGGATGGACACCCCTCCAGCAGCTGGCTAGGGCG 2382

Db 2008 GACAAACGACACGAGTCAATGGTGGCTTCGATGCAAAACCCGCGACGACCTAATCGAAACC 2067

QY 2383 TGCACGACCATCATCTGGGTGGCATCCGGCTGCACGCGGCTGTCAACTTTGGGCGAGTAC 2442

Db 2068 TGCACGATCATCTGGATCGCCTCTGCTCTTCAACGACGACAGTAAATTTCCGACAGTAC 2127

QY 2443 CCATACGCCGGGTACTCCGAAACCGGCGCAGCGCCAGCCGCGCCGATGCGCGAGCCA 2502

Db 2128 CCTTACGCCGGTTTCTCCCTAACCGTCTTACCGTCAGCCGCGGTTTATGCTGAACCA 2187

QY 2503 GGCAGCCACGACTACAAGAAAGCTGGGAGCGGGGCAGAAAGGAGCGGACATGGTGTTCATC 2562

Db 2188 GGTACGGATGATGATCTGAGCTGG-----AGGAAGATGCTGACGTAGCTTCTTG 2238

QY 2563 CGCACCATCACCGCAGTTCAGACCATCTCTGGGCATCTCGCTCATCGAGATCTCTCC 2622

Db 2239 AAGACGATCACCGCCAGTTACAGACTCTACTTGGTATCTCCATCATAGAGATATTGTCT 2298

QY 2623 AAGCACTCCTCCGACGAGGTGTACTCTCGGCCAGCGTGACGAGCCTGATCGCTGGACGTCA 2682

Db 2299 ATGCATTCAACGGACGAGATCTACTTAGGGCAAGAGATTCAACCGAAT--TGGACGGCG 2355

QY 2683 GACGCCAAGGCGTGGATGCGTTCAAAAGATTTCGGGAGCCGGCTGTGTCAGATTGAGAAT 2742

Db 2356 GATGATGAGCCTTTGGAGCGCTTTAAGCGGTTTGGGAAAGAACTTGAGCTGATAGAGAAC 2415

QY 2743 CGGATCAAGACGATGAACGACAGTCCCGACTTGAAGAACCGGAAGGGGCTGTGGAATG 2802

Db 2416 AATATTATACGAAGAAACAATGACAAGAGGTTCAAGAACAGAACCCGACCGGTTAACATA 2475

QY 2803 CCGTACATGCTGCTGTACCCCAACACGTCGGACGTTACCGGCGAGAAAGCCGAGGGGCTT 2862

Db 2476 CCGTACACATTTGTTGTACCCGAATACTAGGATTATAC-----GAGAGAAGGTGGGATT 2529

QY 2863 ACTGCCATGGGCATTCCTCAACAGCATCTCCAT 2894

Db 2530 ACTGGGAAAGGGATCCCGAACAGTGTCTCAAT 2561

RESULT 12

ID ABZ68210 standard; DNA; 3390 BP.

XX AC ABZ68210;

XX DT 07-APR-2003 (first entry)

XX DE Nucleotide sequence comprising CaMV 35S promoter and tobacco LOX1.

XX KW Lipoxigenase-1; LOX-1; enzyme; plant; dioxygenation;
KW polyunsaturated fatty acid; pentadiene; disease resistance; Solanacea;
KW tobacco; tomato; potato; pepper; gene; ss.

XX OS Nicotiana tabacum.

Key	Location/Qualifiers
promoter	1..532
	/*tag= a
	/note= "CaMV 35S promoter"
CDS	543..3131
	/*tag= b
	/product= "LOX1"
	/note= "6"
terminator	3138..3390
	/*tag= c
	/note= "Nos terminator"

XX WO200299112-A2.

XX PD 12-DEC-2002.

XX PF 06-JUN-2002; 2002WO-FR001943.

XX PR 07-JUN-2001; 2001PR-00007470.

XX PR 07-NOV-2001; 2001PR-00014358.

XX PA (RHOB-) RHOBIO.

XX

Db 589 GACAGAGTATATGACTATGCTTACTACAATGATTAGGGGTCCC-----ACCAAAG 639
QY 898 CACGCTCGGCGGATCCTCGGTGGCAGCCAAAGAACACCCGGTATCCCGCTCGCTGCAGAACT 957
Db 640 AACCCACGGCCTGTACTTGGAGGGACACAGGAGTATCCTTACCCAAAGAGAGGAAGAAC 699
QY 958 GGCCTGGCACCCAAACAAAGAAAGACCCAAATTCGGAGAGCAGGCT---TTTCTGTGTAAC 1014
Db 700 GGGCGGAAACCAACTAAAGAAAGATCCTCAAAACCGAGAGCAGGCTACCGATCACATCGAGC 759
QY 1015 CTGAACATCTACGTCCTCGGCTGACGAACGCTTTGGGCATCTCAAGATGTCTGGACTTCCTT 1074
Db 760 CTAGACATATATGTTCCACGAGATGAGAGATTGGACACTTGAAGATGTCTGATTTCCTT 819
QY 1075 GGGTACTCGCTGAAGACGATCATCGAGGCTGTCTTCCAAACACTGGGACTTTTCGTCGAT 1134
Db 820 GCTTATGCTCTAAAAGCGATTGCTCAGTTTCAACCTGCACCTTGAGGCTGTATTTCGAC 879
QY 1135 GACACGCCCAAGGATTGCTGTTTGGAGTATCTCTCGGGCTCTACGAGCTGGGCCCA 1194
Db 880 GATACTCCTAAAGATTGATTCTTTTGAAGATGTCTTAAAGATCTATGAAGGAATC 939
QY 1195 GAGGCACCCAAACCACTGATAGCAGAGATCAGGAAGAAGATCCCGAGCGAGTTCCTT 1254
Db 940 GATCTACCAACCAAGCTTGTATGATAGTATCGTTAAAGATATACCGCTTGAGATGTTA 999
QY 1255 CGAAGCATCTGCGCAACGGTAGCCATGACCAACCGCTAAAGATGCCCTTCCAAATGTC 1314
Db 1000 AAGGAGATATTAGAACAGATGGCCAGAAATTC---CTTAAGTTTCCAGTGCCTCAGGTC 1056
QY 1315 ATCAAAATCAGATGTGTGTAAGAAAGGCTCCGGAGTTTAAAGTTTGGCTGGAGGACTGACGAA 1374
Db 1057 ATCAAA-----GAGGACAAAACTGCTATGGAGAACAGATGAG 1092
QY 1375 GAGTTCGGAGAGAGACACTTGCAGGCGTGAACCCAGTAATCATCAAAAGCTCTGACGGAG 1434
Db 1093 GAATTTGCTAGAGAAATGTTGGCTGGACTTAAACCTGTTGTTATTCAACTTCTTAAGGAG 1152
QY 1435 TTCCCGCTAAAAGCACCCCTGGACCCAAAGGAGTACGGAGACCAACACAGCAAGATCACT 1494
Db 1153 TTTCTCCAAAGAGTAAGCTTGACAGTGAATCATACGGTAACCCAGAACAGTACATCACT 1212
QY 1495 GAAGCTCACATCCGGCATAAATCATGGAGGCTGTGCGTGACAAACGCACTGAGGAACAAG 1554
Db 1213 AAAAGCCACATAGAACACAATTTGGATGGACTCACTGTTGAAGAGGCTCTGGAGAAGGAG 1272
QY 1555 AGGCTCTTATCCTAGACCAACCATGACCAATTTTCATCCGTACCTCGACGAGATCAACGAG 1614
Db 1273 AGGTTGTTTATATTAGACCACCATGACACACTGATGCCATCTTGGGACCGGTAAACACC 1332
QY 1615 CTGGAGGGGAACCTTATCTACGCCAGCAGGACCCCTACTGTTCCTGAAGGACGATGSCACG 1674
Db 1333 ACCACGACCAAG---ACTTATGCAAGCAGGACACTTCTGTCTTCTTGAAGATGATGGGACC 1389
QY 1675 CTGAAGCCCTTGGCCATCGAGCTGAGCCTGCCCCACCCCTGACGGCCAGCAGCGCGCGG 1734
Db 1390 TTGAAGCCGTTGGTGATAGAGCTGAGCTTGGCTTGCCTCATCTTAATGGAGACAAATTTGGAGCA 1449
QY 1735 GTCAGCAAGGTGTACACCCCGGCTCACACCGGCGTCCAGGGCCACGCTCTGGCAGCTCGCC 1794
Db 1450 GTGAGTGAAGTATATACGCTGTTGA---AGGTGTCTACGACTCGCTATGGCAGTTGGCT 1506
QY 1795 AAGGCTTATGCTGCTAAACGACTCTGCTGGCATCAGCTGATCAGCCACTGGCTGAAC 1854
Db 1507 AAGGCTTTTGTGCTGTAATGACTCCGGAAATCATCAGCTTATTAGCCACTGGATGCA 1566
QY 1855 ACGCACGGGTGATCGAGCCGTTTCGTAATCGCGACAAACCGGACGCTCAGCGTGGTGCAT 1914
Db 1567 ACACACGATCGATTGAACCGTTTGTGATTGCCACAAACAGACAGCTGAGTGTCTTCAC 1626
QY 1915 CCGGTGCACAGTGTGAGCCCGCACTACCGTGACACGCTGAACATCAACGCCCTGGCA 1974
Db 1627 CCGGTCTTTAAGCTCCTTGAACCTCACTTCCGTGATACGATGAATATCAATGCACITGCT 1686

QY 1975 CGCCAGACACTCATCAACCGCGCGGGCTCTTCGAGCGCACCGTGTTCCTGCAAGTAC 2034
Db 1687 AGGCAATCTTGATCAATGGTGGTATATTGAAATCACTGTGTTTCTTCTAAATAC 1746
QY 2035 GCGCTGGGATGTCGCGAGACGCTGTACAAGA---GCTGGAATTTCAACGAGCAGGCTCTC 2091
Db 1747 GCCATGGAGATGTCATCTTTTCAAAAACCACTGGACCTTCCCTGACCAAGCATTA 1806
QY 2092 CCAGCAGATCTCGTCAAGAGAGGTGTGGCTGTGCTGCTCCGACCAAGTCAAGCCCATATGCTC 2151
Db 1807 CCAGCAGAACTTAAAAAGAGAGGATGGCCGTGAGGATCCAGAAGCACACACGATTA 1866
QY 2152 CGACTGCTGATCAAGGACTACCCCTATGCCCCTGACGGGCTCGTCACTGCTGGTGGCGATC 2211
Db 1867 CGTCTGAGGATAAAGACTATCCTTACGAGTGGATGGGCTTGAGGTTGGTATGCTATT 1926
QY 2212 GAGCGGTGGTCAAGGAGTACCTGGACATCTACTACCTTAACGACGGCGAGCTCCAGCGT 2271
Db 1927 GAATCATGGGTCCGAGACTACATTTTCTTGTCTACAAGATAGAGGAGATATCCAAACC 1986
QY 2272 GACGTGGAGCTGCAGCGTGGTGAAGGAGGTGCGTGAGGAGCGCACGGCGACCTCAAG 2331
Db 1987 GACACAGAGCTCCAAGCCTGGTGAAGGAGGTGCGGAGGAGGTCTATGGAGACAAAAG 2046
QY 2332 GACCGAGACTGGTGGCCAGGATGGACACCGTCCAGCAGCTGGCTAGGCGTGCACGACC 2391
Db 2047 TCAGAACCATGGTGGCCTAAATGCAACCCGTGAAGAACTTGTGAGTCTTGCACCATC 2106
QY 2392 ATCATCTGGTGGCATCCGCGCTGCACCGGCTGTCAACTTTGGGAGTACCCATACGCC 2451
Db 2107 ATTATTTGGTGGCTTCTGCTCTTCTCATGACGCTGTTAACTTCGGACAGTATCCAGTTGCT 2166
QY 2452 GGGTACCTCCCGAACCGCGCGACCGCCAGCGCGCGCCCGATGCCGAGCCAGGCGACCCAC 2511
Db 2167 GGGTACCTCCCAACAGACCGACTATAAGCGCTCAGTACATGCCAAAGAAACACTCCA 2226
QY 2512 GACTACAAGAGCTGGAGCGGGGAGAGAGGAGCGGACATGCTGTGTTTCATCCGACCATC 2571
Db 2227 GAGTTTGAAGAACTTG-----AGAAAGAACTCTGATAAAGTGTGTTTGAAGACCATC 2277
QY 2572 ACCAGCCAGTTCAGACCATCCTGGGCACTCTCGCTCATCGAGATCTCTCTCCAAGCACTCC 2631
Db 2278 ACAGCTCAGCTTCAGACACTTCTAGGATATCTCTGATTGAGATTCTCTCTACTATTCT 2337
QY 2632 TCCGACGAGGTGTAACCTCGGCCAGCGTGACGAGCCTGTATCGTGGACGTGAGCGCCAAG 2691
Db 2338 AGCGACGAGGTCTATTGGGACAGAG---AGATTCTAAAGAAATGGCGGCTGAGAAAGAA 2394
QY 2692 GCGCTGGATGCTTCAAAAAGATTTCGGAGCCCGGCTGGTGCAGATTGAGAAATCGGATCAAG 2751
Db 2395 GCGTTGGAGCGTTCGAGAAGTTTGGAGAGAAAGTAAAGGAGATTGAGAAAGAACATTGAT 2454
QY 2752 ACGATGAACGACAGTCCGAGCTTGAAGAACCGGAAGGGCGCTGTGAAAATGCCGTACATG 2811
Db 2455 GAGAGGAACGACGACGAGACTCTCAAGAACAGGACTGGTTTGGTTAAGATGCCATACACT 2514
QY 2812 CTGCTGTACCCCAACACAGTCGGACGTTTACCGGCGAGAAAG 2851
Db 2515 TTATTGTTTCCGAGCAGTGAAGCGGAGTCAACCGGCGAGG 2554

RESULT 14

ADA67958

ID ADA67958 standard; DNA; 2580 BP.

XX ADA67958;

AC ADA67958;

XX

DT 20-NOV-2003 (first entry)

XX

DE Arabidopsis thaliana gene, SEQ ID 206.

XX

KW Plant; bacterial infection; fungal infection; viral infection; ds.

QY	1855	ACGACACGGGTGATCGAGCCGGTTTCGTAATCGCGACAAACCGGCAGCTCAGCGTGGTGCAT	1911
Db	1567	ACACACGCATCGAATTGAACCGTTTGTGATTGCCACAAACAGACAGCTGAGTGTCTTCAC	1626
QY	1915	CCCGTGACAAAGCTGCTGAGCCCGCAGCTACCCGTGACACGCTGAACATCAACGCCCTGGCA	1974
Db	1627	CCGGTCTTTAAGCTCCTTGAACTCACTTCCGTGATACGATGAATATCAATGCACCTTGCT	1686
QY	1975	CGCCAGACACTCATCAACGCCCGCGCGCTCTTCGAGCGCACCGTGTTCCTGCAAAAGTAC	2034
Db	1687	AGGCAAAATCTTGATCAATGGTGGTGATATTTGAAATCACTGTGTTTCCCTTCTAAATAC	1746
QY	2035	GCGCTGGGGATGTCGGCAGACGCTGTACAAGA--GCTGGAATTTCAACGAGCAGGCTCTC	2091
Db	1747	GCCATGGAGATGTCATCTTTCATTTACAAAAACCACTGGACCTTCCCTGACCAAGCATTA	1806
QY	2092	CCAGCAGATCTCGTCAAGAGAGGTGTGGCTGTGCCGACCAAGTCAAGCCCAATATGGTGTCT	2151
Db	1807	CCAGCAGAACTTAAAAAGAGAGGGATGGCCGTTGAGGATCCAGAAGCACCAACGAGATTA	1866
QY	2152	CGACTGCTGATCAAGGACTACCCCTATGCCGTTGACGGGCTCGTCACTCTGGTGGGCGATC	2211
Db	1867	CGTCTGAGGATAAAAGACTATCCTTACGCAGTGGATGGGCTTGAGGTTTGGTATGCTATT	1926
QY	2212	GAGCGGTGGTCAAGGAGTACTTGACATCTACTACCTTAACGACGGCGAGCTCCAGCGT	2271
Db	1927	GAATCATGGTCCGAGACTACATTTTCTTGTCTACAAGATAGAGGAGGATATCCAAACC	1986
QY	2272	GACGTGGAGCTGCAGGCGTGGTGAAGGAGGTGCGTGAGGAGGCGCACGCGGACCTCAAG	2331
Db	1987	GACACAGAGCTCCAAGCCTGGTGAAGGAGGTGCGGAGGAAGGTCAATGGAGACAAAAAG	2046
QY	2332	GACCGAGACTGGTGGCCAGGATGGACACCGTCCAGCAGCTGGCTAGGGCGTGACGACCC	2391
Db	2047	TCAGAACCATGTTGGCTTAAATGCAACCCGCTGAAGAACTTGTGAGTCTTGACCATC	2106
QY	2392	ATCATCTGGTGGCATCCGCGCTGCACGCGGCTGTCAACTTTGGGCAGTACCCATACGCC	2451
Db	2107	ATTATTTGGTGGCTTCTGCTCTTCATGCAGCTGTAACTTCGGACAGTATCCAGTTGCT	2166
QY	2452	GGTACCTCCCGAACCGGCGACGGCCAGCCGCGCGCGATGCCGAGCCAGGAGCCAC	2511
Db	2167	GGGTACCTCCCAACAGACCGACTATAAGCCGCTAGTACATGTCCTCAAGGAAACACTCCA	2226
QY	2512	GACTACAAGAAGCTGGAGCGGGGCAGAAAGGAGGCGGACATGGTGTTCATCCGACCATC	2571
Db	2227	GAGTTTGAAGAACTTG-----AGAAGAACTCTGATAAAGTGTCTTGTGAGACCATC	2277
QY	2572	ACCAGCCAGTTCAGACCATCTCTGGGCATCTCGCTCATCGAGATCCTCTCCAGGACTCC	2631
Db	2278	ACAGCTCAGCTTCAGACACTTCTAGGGATATCTCTGATTGAGATTCTCTCTACTCATCT	2337
QY	2632	TCCGACGAGGTGTACCTCGGCCAGCGTGACGAGCCTGATCGCTGGAAGTCAAGCGCCAAG	2691
Db	2338	AGCGACGAGGTCTATTTGGGACAGAG--AGATTCTAAAGAAATGGCGGCTGAGAAAGAA	2394
QY	2692	GCGCTGGATGCGTTCAAAGATTTCGGGAGCCGGCTGGTGCAGATTGAGAAATCGGATCAAG	2751
Db	2395	GCGTTGGAGGCGTTTCGAGAAAGTTTGGAGAGAAAGTAAAGGAGATTGAGAAAGCAATTGAT	2454
QY	2752	ACGATGAACGACAGTCCGGAATTGAAGAACCGGAAGGGGCTGTGTGGAATGCCGTACATG	2811
Db	2455	GAGAGGAACGACGACGAGACTCTCAAGAACAGGACTGGTTTGGTTAAGATGCCATACACT	2514
QY	2812	CTGCTGTACCCCAACACGTCGGACGTTTACCGGCGGAGAAGG	2851
Db	2515	TTATTGTTTCCGAGCAGTGAAGGCGGAGTCAACCGGCAGGG	2554

RESULT 15
AAT60429
ID AAT6
XX

AC AAT60429;
XX
XX
DT 27-AUG-2003 (revised)
DT 08-JUL-1997 (first entry)
XX
XX Tomato fruit ripening specific lipoxygenase gene fragment.
DE
XX
XX LOX gene; fruit ripening specific lipoxygenase; FRS-LOX; tomato;
KW transgenic plant; ss.
XX
XX Lycopersicon esculentum.
OS
XX WO9713851-A1.
XX
XX 17-APR-1997.
XX
XX 11-OCT-1996; 96WO-US016387.
XX
XX 13-OCT-1995; 95US-0005404P.
XX
XX (PURD) PURDUE RES FOUND.
XX
XX Handa AK, Kausch KD;
PI
XX WPI; 1997-235887/21.
DR
XX
XX New transgenic plants with fruits having improved quality - obtained by
PT transforming plant cells so as to inhibit production of fruit ripening
PT specific lipoxygenase in fruits.
XX
XX Claim 6; Fig 1; 38pp; English.
PS
XX
XX A tomato fruit ripening specific lipoxygenase (FRS-LOX) gene fragment
CC (AAT60429) comprises nucleotides 158-2598 of the FRS-LOX gene (see also
CC AAT60428). It was isolated from partial LOX cDNA clone 8-27-1, and can be
CC inserted into the multiple cloning site present between the CaMV 35S
CC promoter and rbc 3' terminator sequences in pTZ35rbss in both
CC orientations, yielding pTZSL (sense) and pTZAL (antisense). These vectors
CC can be used to create transgenic fruit-bearing plants, esp. tomato, in
CC which native FRS-LOX gene expression is inhibited. These transgenic
CC plants can provide fruits having improved quality and texture, greater
CC firmness, longer shelf life, better packaging and storage characteristics
CC and improved processing characteristics. (Updated on 27-AUG-2003 to
CC correct OS field.)
XX
SQ Sequence 2441 BP; 742 A; 496 C; 544 G; 659 T; 0 U; 0 Other;

Query Match	21.2%;	Score 664.2;	DB 2;	Length 2441;
Best Local Similarity	57.7%;	Pred. No. 1.6e-108;		
Matches 1367; Conservative	0;	Mismatches 953;	Indels 51;	Gaps 8;

QY	460	GGCAAGTGGGAAAGCGCGCGCACCTGGAGGAGCGCGTGGTTCGCTCAAGTCCACGGCG	519
DB	89	GGGAAACTGAGCAATCCAGCATACTTAGAGAGTTGGCTTACAGACATCACCCCAATAACA	148
QY	520	GACGGGGAGACCGTGTACCGGGTGAGCTTCGAGTGGGA--CGAGTCGCAGGGGCATCCCG	576
DB	149	GCAGGGGAATCAACTTTTAGTGTACATTTGACTGGGATCGTGACGAGTTTGGAGTTCCA	208
QY	577	GGCGCCGTCTTGTCAGGAACCTGCAGCACGCGCAGTTCCTTCTCAAAGACGCTCACCCCTC	636
DB	209	GGAGCATTCATCATCAAGAATCTTCATCTTAATGAGTTCCTTCTCAAGTCACCTCACACTC	268
QY	637	GAGGGCGTCCCAGGCAAGGGCACCGTCGTCTTCGTGCGCAACTCGTGGGTCTACCCGAC	696
DB	269	GAAGATGTTCTTAATTATGGAAAATCCATTTGTATGCAATCTTGGGTTTATCCTGTCT	328
QY	697	AAGCTCTACTCCAGGAACGCATCTTCTTCGCAACGACACCTATCTGCCGAGCAAAATG	756
DB	329	TTTAGATACAAGTCTGACCGCATTTTCTTTTGCCAATCAGGCTTATCTCCCAAGTGAACA	388
QY	757	CCGGCGGCGTTGGTGCCTTATCGGCAAGATGAGCTCAAGATTCTCCGTGGCGACGATAAT	816

Db 389 CCACAACCATTCGGAATAATACAGAGAAATGAACTGGTAGCTTTCGAGGAGATGGAA-- 446
QY 817 CCTGGACCAATACCAGGAGCATGATCGCGTGTACCGTTACGACTACTACAATGACCTTGGT 876
Db 447 -CTGGAAGCTTGAAGAAATGGGACAGGGTTATGATTATGCTTGTCTACATGACTTGGGT 505
QY 877 GATCCCGACAAGGGCGAAGAGCACCGTCGGCCGATCCTCGGTGGCAGCCAAAGAACACCCG 936
Db 506 GAACCAAGATAAGGGGAAGAGTATGCTAGGCCCTATCCTTGGAGGGTCTCTGAGTACCCG 565
QY 937 TATCCCCGTCGTCAGAACTGGCCGGACCCCAACAAAGAAAGACCCAAATTCGGAGAGC 996
Db 566 TATCCTCGTAGAGCAGGACAGGCCCGGAAACCAAGCAGATCCTAATTCGGAGAGC 625
QY 997 AGG---CTTTTCTGCTGAACCTGAACATCTACTCGTCCCGGTGACGAACGCTTTGGGCAT 1053
Db 626 AGGAACCCATTGCTATGAGCTTAGACATATATGTCCCAAGGACGAGGATTTGGTCAAT 685
QY 1054 CTCAAGATGTCGACTTCCTTGGGTACTCGGTGAAGACGATCATCGAGGCTGTTCTTCCA 1113
Db 686 GTGAAGAAGTCAGACTTTTGTACGTGCTTAAATCCTCTTTGCAAAACGCTTCTCCCT 745
QY 1114 AACTGGGGACTTTCGTTCGATGACACGCCCAAGGAGTTCGATTCTGTTTGGAGATATCCTC 1173
Db 746 GCGTTTAAGGCTTTGTGCGATAACACGCCTAATGAGTTCAATAGCTTTCGGATGTACTT 805
QY 1174 GGGCTCTACGAGCTGGGCCCGAGGACCCCAACCAACCCACTGATAGAGAGATCAGGAAG 1233
Db 806 AATCTCTATGAAGGAGGAATCAAGTTGCTGAAAGGCCCTTGGTTGAAGCCATTACTGAT 865
QY 1234 AAGATCCCCAGCGAGTTCCTTCGAAGCATCTGCGGAACCGGTAGCCATGACCAACCCGCTA 1293
Db 866 AACATTTCTCAGAGATACTAAAGACATCCTTCAACCGGATGCTCAAG---GCCTACTT 922
QY 1294 AAGATGCCCCCTTCCAAATGTCTCAATCAATCAGATGTGTTGAAAAGGCTCCGGAGTTTAAG 1353
Db 923 AAGTACCCAACTCCTCAGGTTATTCAAGSCGA-----TAAA 958
QY 1354 TTTGGCTGGAGGACTGACGAAGAGTTTCGGAGAGAGACACTTGCAGSGGTGAACCCAGTA 1413
Db 959 ACTGCATGGAGGACGATGAAGAAATTTGGGAGAGAAATGTTGGCAGGATCCAATCCTGTC 1018
QY 1414 ATCATCAAAACGTCGAGGAGTTCCCGCTTAAAGCACCCCTGGACCCCAAGGCAGTACGGA 1473
Db 1019 TTAATCAGTAGACTCCAAGAATTTCTCCGAAGAGCAAGTTGGATCCAACCATATATGGA 1078
QY 1474 GACCACACCAGCAAGATCACTGAAGCTCACATCGGCATACATGGAAGGAGGCTGTCGGTG 1533
Db 1079 AACCAAAACAGTACAATTAACACAGAACATGTACAGGATAAGTTGAATGGATTAAACAGTG 1138
QY 1534 CAGAACGCATGAGGAACAAGAGGCTTTCATCCTAGACCAACCATGACCATTTTCATGCCG 1593
Db 1139 AATGAGGCAATCAAGAGTAACAGGTTATTATATTGAACCAACCATGACATCGTGTATGCCA 1198
QY 1594 TACCTCGACGAGATCAACGAGCTGGAGGGAACTTCACTACGCCAGCAGGACCCCTACTG 1653
Db 1199 CTATTGAGGAAATTTAATCATGTTCAGCAACACAAAAGCCTATGCCCTCAAGAACTCTGCTC 1258
QY 1654 TTCCTGAAGGACGATGGCAGCGCTGAAGCCCTTGGCCATCGAGCTGAGCTGCCCAACCCCT 1713
Db 1259 TTCCTACAAGATGATAGAACTTTGAAGCCACTAGCAATTTGAACCTAAGCTTGCACATCCA 1318
QY 1714 GACGGCCAGCAGCGCGGGCGGTGAGCAAGGTGTACACCCCGGTACACCGGCGTTCGAG 1773
Db 1319 GACGGAGATCAATTTGGTACTGTTAGTAAAGTATATACACCAAGCTGACCAAGGTTGTAA 1378
QY 1774 GGCCACGTCCTGGCAGCTCGCAAGGCTTATGCTCGGTAAACGACTCTGCTGGCATCAG 1833
Db 1379 GGTCTATCTGGCAGTTTGCAAAAGCCTATGTAGCAGTGAATGACATGGGCATTTCATCAG 1438
QY 1834 CTGATCAGCCACTGGCTGAACACGACGCGGTGTATCGAGCCGTTTCGTAATCGGACAAAC 1893
Db 1439 CTCATTAGCCACTGGTTTGAATACACACGCGGTGTATCGAACCATTGTTGTGATTGCAACAAAT 1498

QY 1894 CGGCAGCTCAGCGTGGTGATCCCGTGTGACAAAGCTGCTGAGCCCGCACTACCGTGACACG 1953
Db 1499 AGGCATCTAAGTGTGCTTTCATCCCATTCATAAACTTCTTCATCCTCATTTCCGTAAACAG 1558
QY 1954 CTGAACATCAACGCCCTGGCAGCGCCAGACACTCATCAACGCCCGCGGCGTCTTCGAGCGC 2013
Db 1559 ATGAACATAAATGCTTTAGCAAGAGAGACCTTGACCTATGATGGTGG---TTTTGAGACG 1615
QY 2014 ACCGTGTTCCCTGCAAAAGTACGCCCTGGGATGTGGCAGACGTTGTACAAAGAGCTGGAAT 2073
Db 1616 TCTCTTTTCTGCAAAATATTCCATGGAATGTGACGACGCTTACAAAGATTGGGTT 1675
QY 2074 TTCAACGAGCAGGCTCTCCAGCAGATCTCGTCAAGAGAGGTGTGGCTGTGCGGACCCAG 2133
Db 1676 TTCCCTGAACAAGCACTTCTGCTGATCTCCTCAAAAGAGGAGTGGCTGTGAGGACTTG 1735
QY 2134 TCAAGCCCATATGTTGTCGACTGCTGATCAAGGACTACCCCTATGCCGTTGACGGGCTC 2193
Db 1736 AGCTCCCAACATGGCATTCGTTTACTGATTTCTGGACTATCCATATGCTGTTGATGGCTTG 1795
QY 2194 GTCATCTGGTGGCGATCGAGCGGTGGGTCAAGGAGTACCTGGACATCTACTACCCCTAAC 2253
Db 1796 GAAATTTGGCAGCAATCAAAAGTTGGGTAAACAGAATATTGCAAGTTCATTATCAAATCT 1855
QY 2254 GACGGCGAGCTCCAGCGTGACGTGGAGCTGCGAGCGTGGTGAAGAGGTGCGTGAGGAG 2313
Db 1856 GACGAGACAGTAGAGAAAGACACTGAACCTCAAGCTTGGTGAAGGAGCTCCGCGAAGAA 1915
QY 2314 GCGCACGGCGACCTCAAGGACCGGAGACTGGTGGCCCGCAGGATGGACACCGCTCCAGCAGCTG 2373
Db 1916 GGACATGGCGACAAGAAAGATGAGGCTTGGTGGCCTAAACTGCAAACTCGACAAGAGCTC 1975
QY 2374 GCTAGGGCGTGCAACGACCATCATCTGGGTGSCATCCGCGCTGCACCGCGCTGTCAACTTT 2433
Db 1976 AGAGATTGTTGCACCATCATTATATGGATAGTTTCAGCACTTCATGCAGCACTCCATTTT 2035
QY 2434 GGGCAGTACCCATACCGCGGTACTCTCCGHAACCGGCGCAGCGGCCAGCGCGGCCGATG 2493
Db 2036 GGCTTATACTCTTACGCTGGTTATCTCCCTTAATCGCCCTACTTTAAGCTGTAATTTGATG 2095
QY 2494 CCGGAGCCAGGCGACCACTACAAGAAAGCTGGGAGCGGGGCGAGAGGCGGAGACATG 2553
Db 2096 CCAGAGCCAGGAAGTGTGAGTATGAAGAGCT-----CAAGACAAATCCAGACAAG 2146
QY 2554 GTGTTTCATCCGACCATCACAGCCAGTTCCAGACCATCTCTGGGCATCTCGCTCATCGAG 2613
Db 2147 GTATTCTCTAAAACAATTTGTTCTCTCAGTTGCAATCACTGCTTGAAATTTCCATCTTTGAG 2206
QY 2614 ATCCTCTCAAGCACTCTCTCCGACGAGGTGTACTCGGCCAGCGTGACGAGCCTGATCGC 2673
Db 2207 GTCTCGTCAAGGCATGCTTCAGATGAGGTTTACTTGGGACAAAGGAGCTCAATTGA---A 2263
QY 2674 TGGACGTCAGACGCCCAAGCGCTGGATGCGTTTCAAAAGATTTCGGGAGCGCGCTGGTGCAG 2733
Db 2264 TGGACAAAGGATAAAGAACCACTTGTAGCTTTTTCAGAGGTTTGGAAAGATGCTAAGTGAT 2323
QY 2734 ATTGAGAATCGGATCAAGACGATGAACGACAGTCCCGGACTTGAAGAACCCGGAAGGGGCCT 2793
Db 2324 ATCGAGAATCGAATTATGATAATGAATAGTATGAAGAGTTGGAAGAACAGGTCAGGGCCT 2383
QY 2794 GTGGAATGCCGTACATGCTGTGTACCCCA 2824
Db 2384 GTTAAAGTTCCATATACGTTGCTCTTTTCCCA 2414

Search completed: March 22, 2004, 22:20:43
Job time : 1156 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 22:00:16 ; Search time 210 Seconds
(without alignments)
8281.981 Million cell updates/sec

Title: US-10-059-909-15
Perfect score: 3134
Sequence: 1 ccacgcgtccggccggaggcg.....aaaaaaaaaaaaaaaaaaag 3134

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PCITUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1326	42.3	3007	4	US-09-810-268-1
2	1324	42.2	2595	4	US-09-810-268-2
3	1222.2	39.0	2818	4	US-09-751-687-10
4	664.2	21.2	2441	4	US-09-051-465-1
5	664.2	21.2	2871	4	US-09-051-465-2
6	664.2	21.2	2871	4	US-09-051-465-4
7	599.2	19.1	4663	4	US-09-751-687-11
8	599	19.1	4663	4	US-09-751-687-8
9	270.2	8.6	302	4	US-09-313-294A-3908
10	160.4	5.1	282	4	US-09-313-294A-6360
11	155.8	5.0	298	4	US-09-313-294A-4946
12	135	4.3	340	1	US-08-181-271A-40
13	135	4.3	340	1	US-08-449-315-40
14	135	4.3	340	1	US-08-444-803-40
15	135	4.3	340	1	US-08-449-043-40
16	135	4.3	340	1	US-08-456-265A-40
17	135	4.3	340	1	US-08-455-416-40
18	135	4.3	340	1	US-08-455-244-40
19	135	4.3	340	1	US-08-454-876-40
20	135	4.3	340	2	US-08-457-364-40
21	135	4.3	340	2	US-08-456-262-40
22	135	4.3	340	2	US-08-456-240-40
23	135	4.3	340	2	US-08-455-736-40
24	135	4.3	340	2	US-08-971-217-40
25	135	4.3	340	3	US-09-350-600-40
26	135	4.3	340	4	US-09-906-234-40
27	133.2	4.3	155	4	US-09-313-294A-3677

28	107.6	3.4	2236	4	US-09-547-435-5	Sequence 5, Appli
29	107.6	3.4	2604	4	US-09-547-435-23	Sequence 23, Appl
30	107.6	3.4	2701	4	US-09-547-435-1	Sequence 1, Appli
31	107.6	3.4	3384	4	US-09-547-435-29	Sequence 29, Appl
32	104.6	3.3	1383	4	US-09-547-435-11	Sequence 11, Appli
33	104.6	3.3	1848	4	US-09-547-435-9	Sequence 9, Appli
34	104.6	3.3	2316	4	US-09-547-435-27	Sequence 27, Appl
35	102.6	3.3	2497	4	US-09-023-655-1155	Sequence 1155, Ap
36	98	3.1	252	4	US-09-313-294A-2555	Sequence 2555, Ap
37	84.6	2.7	1441	4	US-09-547-435-13	Sequence 13, Appl
38	83.4	2.7	2079	4	US-09-252-991A-3097	Sequence 3097, Ap
39	83.2	2.7	2685	3	US-09-061-768A-1	Sequence 1, Appli
40	83.2	2.7	2685	4	US-09-764-246-1	Sequence 1, Appli
41	82.4	2.6	2343	4	US-09-641-638-652	Sequence 652, App
42	81.6	2.6	588	4	US-09-547-435-19	Sequence 19, Appl
43	75	2.4	1005	4	US-09-547-435-7	Sequence 7, Appli
44	75	2.4	1470	4	US-09-547-435-3	Sequence 3, Appli
45	75	2.4	1938	4	US-09-547-435-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-09-810-268-1
; Sequence 1, Application US/09810268
; Patent No. 6627797
; GENERAL INFORMATION:
; APPLICANT: Duvick, Jon
; APPLICANT: Maddox, Joyce R.
; APPLICANT: Keller, Nancy P.
; TITLE OF INVENTION: Maize Lipoxigenase Polynucleotide and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 1269
; CURRENT APPLICATION NUMBER: US/09/810,268
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/190,950
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3007
; TYPE: DNA
; ORGANISM: Zea mays
US-09-810-268-1

Query Match	42.3%	Score	1326;	DB	4;	Length	3007;
Best Local Similarity	71.7%	Pred. No.	2e-264;				
Matches	1906;	Conservative	0;	Mismatches	680;	Indels	72;
Gaps	10;						
Qy	246	CGGGGTCCGGACCGGCTGACGGGAAGAAACAGGAGCGGTGGAGCGGCAAGATCCG	305				
Db	73	CGGGATCATCGACGGGCTGACGGGGCGGAACAGCATGCGGGCTCAAG-----	121				
Qy	306	CGGCACGGTGAGGCTGGTCAAGAAAGAGGTGCTGGACGTCGGCGACTTCAACGCCCTCGCT	365				
Db	122	-GGCACGGTGGTGCTCATGCGCAAGAACCGTGTGGACCTCAACGACTTCGGCGCCACCGT	180				
Qy	366	CCTCGACGGCGTCCACAGGATCCTCGGCTGGGACGACGGCGTCGCCCTTCCAGCTCGTCAG	425				
Db	181	CGTTGACAGCATCAGCGAGTTCTTCGGCA-----AGGGGTACCTGCCAGCTCATCAG	234				
Qy	426	CGCCACCGCGCCGACCCAGCAACCGGGGCGGTGGCAAGGTGGGAAGCGCGGCACCT	485				
Db	235	CTCCACCTCTGTCGACGCCCAACACGGCAACCGCGGGCGGGTTCGGGGCGGAGCGAACCT	294				
Qy	486	GGAGGAGCGGTGGTGTGCTCAAGTCCACGGCGGACCGGGGAGACCGGTGACCGGGGTGAG	545				
Db	295	GGAGCAGTGGTGACGAGCCTGCCGTGCTGACGACCGCGGAGTCCAGTTCGGCGTCCAC	354				
Qy	546	CTTCGAGTGGGA---CGAGTCGAGGGCATCCCGGGCGCGCTCTGTGTCAGGAACCTGCA	602				
Db	355	GTTGACTGGGAGGTGGAGAAGCTGGGAGTGGCGGGGGCGCTCGTCTGTCAGGAACAACCA	414				

QY 603 GCACGCCGAGTTCTTCTCAAGACGCTCACCCTCGAGGGCGTCCAGGGCAAGGGCACCGT 662
Db 415 CGCCGCCGAGTTCTTCTCAAGACAATCACCTCTGACGACGTGCGCGCGCGCGCGT 474
QY 663 CGTCTTCTGTCGCAACTCGTGGGTCTACCCGCAACAAGCTCTACTTCCAGGAACGCACTT 722
Db 475 CACCTTCTGTCGCAACTCTGCGGTCTACCCGCGGGCAAGTACCGCTACAACCGCGTCTT 534
QY 723 CTTCGCCAACGACACCTATCTGCGGAGCAAAATGCCGGCGGTGGTGGCTTATCGGCA 782
Db 535 CTTCCTCAACGATACGTACTCTGCCAAGCCAGATGCCGGCGGTGAAGCCGTACCGCGA 594
QY 783 AGATGAGCTCAAGATCTCTCGTGGCGACGATTAATCCTGGACCAATACCAGGAGCATGATCG 842
Db 595 CGACGAGCTCCGCAACCTCCGCGGCGACGACGAGGCGCCCTACAGGAGCACGACCG 654
QY 843 CGTCTACCGTTACGACTACTACAATGACCTTGGTGATCCCGACAAAGCGCGAAGACGCG 902
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QY 903 TCGGCCGATCCTCGTGGCAGCCAAAGAACCCGATCCCGTATCCCGTCTGTCAGAACTGGCCG 962
Db 709 GCGCCCCATCCTCGCGGCTCCGCGGACCCGACCCGTAACCGCGCGCTGCGCACGGGCGG 768
QY 963 GCACCCAAACAAAGAAAGACCCAAATTCGGAGAGCAGGCTTTCTGCTGAACCTGAACAT 1022
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Db 826 CTACGTCCCGCGGACGAGCGCTTCGGCCACCTCAAGATGTCCGACTTCTTGGGTACTC 885
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Db 946 GGGCGAGTTCGACTCTCTCCAGGACATCATCAACCTGTACGAGGCGSGGATCAAGCTGCC 1005
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QY 1443 TAAAGCACCTTGACCCCAAGGCAGTACGGAGACCAACAGCAAGATCACTGAAGCTCA 1502
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QY 1623 GAACTTCTACCGCAGCAGGACCCCTACTGTTCTTGAAGGACGATGGCAGCGCTGAAGCC 1682
Db 1399 CAACTTCTACCGCACCGACGCTCTTCTTCTGCGCGGACCGGAGGCTCGCGCC 1458

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QY 1743 GGTGTACACCCCGGCTCACACCGGCGTTCAGGGGCCACGTCTGGCAGCTCGCCAAGGCTTA 1802
Db 1519 GGTCTACACCGCGCGTCCAGCGGCGTTCAGGGCTGGGTGTGGAGCTCGCCAAGGCTTA 1578
QY 1803 TGCCCTGCTAAACGACTCTGCTTGGCATCAGCTGATCAGCCACTGGTGAACACGACGCG 1862
Db 1579 TGTCCCGTCAACGACTCTGGCTGGCACCAACTCGTACGCCACTGGTGAACACCCACGCG 1638
QY 1863 GGTGATCGAGCGCTTCGTAATCGCGACAAACCGGCGAGCTCAGCGTGGTGCATCCCGTGCA 1922
Db 1639 GGTGATGGAGCGCTTCGTGATCGCGACGAACCGGCGAGCTGAGCGTACGCCACCCGCTGCA 1698
QY 1923 CAAAGCTGCTGAGCCCGCACTACCGTGACACGCTGAACATCAACGCCCTGGCAGCCAGAC 1982
Db 1699 CAAAGCTCCTGAGCTCGCACTTCCGCGACCACTGACCATCAACCGCTGGCGCGGAGAC 1758
QY 1983 ACTCATCAACGCCGCGCGCTTTCGAGCGCACCGTGTTCCTGCAAGTACGCGTGGG 2042
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QY 2043 GATGTCGGCAGACGTGTACAAGAGCTGGAATTTCAACGAGCAGGCTTCTCCAGCAGATCT 2102
Db 1819 CATGTCTCCTGCTGTGTACAAGAGCTGGAATTTCAACGAGCAGGCGCTTCCCGCGCACCT 1878
QY 2103 CGTCAAGAGAGGTGTGGCTGTGCCGACCCAGTCAAGCCCATATGTTGTCGCACTGTGAT 2162
Db 1879 CGTCAAGAGGGCGGTGGCGGACCCGCTCAGCCCGTACAAGGTGCGGTGCTGAT 1938
QY 2163 CAAAGACTACCCCTATCCGTTGACGGGCTCGTCTATCTGGTGGCGATCGAGCGGTGGGT 2222
Db 1939 CGAGGACTACCCGTAACGAGCGACGCGGTGGCTGCTGTCATCTGGCACGCCATCGAGCAGTGGGT 1998
QY 2223 CAAGGAGTACCTGGACATCTACTACCCCTAACGACGGCGAGCTCCAGCGTACGTTGAGCT 2282
Db 1999 GGGCGAGTACCTGGCCATCTACTACCCCGACGACGGCGCGCTGCGGGCGACGAGGAGCT 2058
QY 2283 GCAGGCGTGGTGAAGAGGTGCGTGAGGAGGCGCACGGCGACCTCAAGGACCGAGACTG 2342
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QY 2343 GTGGCCAGGATGGACACCGTCCAGCAGCTGCTAGGGCGTGCACGACCATCATCTGGGT 2402
Db 2119 GTGGCCCAAGATGACGCGCTGTGCGAGCTGCCAGCGCTGCACCCACCATCATCTGGAT 2178
QY 2403 GGCATCCGCGCTGCAACGGGCTGTCAAATTTGGGCGAGTACCCCATACGCCGGGTACCTCCC 2462
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Db 2239 GAACAGGCGCCACGCTGAGCGCGCGCGGATGCGCGAGCGCGGAGCAAGGAGTACGAGGA 2298
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Db 2527 CGACCGCAGCTGAGGAACAGGAACGGCCCGCGAGTTCCCTACATGTTGCTCTATCC 2586
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Db 2587 CAACACCTCTGACCACACAGTGGC---CCGCCGCAGGGGCTCACTGCCAAGGGCATCCCCAA 2643
Qy 2883 CAGCATCTCCATATGAGC 2900
Db 2644 CAGCATCTCCATCTGAGC 2661

RESULT 2

US-09-810-268-2
; Sequence 2, Application US/09810268
; Patent No. 6627797
; GENERAL INFORMATION:
; APPLICANT: Duivick, Jon
; APPLICANT: Maddox, Joyce R.
; APPLICANT: Keller, Nancy P.
; TITLE OF INVENTION: Maize Lipoxigenase Polynucleotide and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 1269
; CURRENT APPLICATION NUMBER: US/09/810,268
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/190,950
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2595
; TYPE: DNA
; ORGANISM: Zea mays
US-09-810-268-2

Query Match 42.2%; Score 1324; DB 4; Length 2595;
Best Local Similarity 71.7%; Pred. No. 5e-264;
Matches 1904; Conservative 0; Mismatches 680; Indels 72; Gaps 10;
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Db 9 CGGGATCATCGACCGGCTGACGGGGCGGAACAAGCATGCGGGCTCAAG----- 57
Qy 306 CGGCACGGTGAGGCTGGTCAAGAAAGGAGGTGCTGGAGCTCGGCGACTTCAACGCTCGCT 365
Db 58 -GGCAGGTGGTGCTCATGCGCAAGAAAGTGTGGACCTCAACGACTTGGCGGCCACCGT 116
Qy 366 CCTCAGCGGCTCCACAGGATCCTCGGCTGGGACGACGGGCTGCGCTTCCAGCTCGTCAG 425
Db 117 CGTTGACAGCATCAGCGAGTTCTCTGGCA-----AGGGGGTCACTGCCAGCTCATCAG 170
Qy 426 CGCACCGCGCGCCGACCCACGAAACGGGGCGGTGGCAAGTGGGGAAGCGGCGCACCT 485
Db 171 CTCCACCCTCGTCGACGCCAACAAACGGCAACCGCGGCGGGTTCGGGCGGAGGCGAACCT 230
Qy 486 GGAGAGGCGGTGGTGTGCTCAAGTCCACGGCGGACGGGGAGACCGGTGACCGGGTGAG 545
Db 231 GGAGCAGTGGCTGACGAGCGCTGCGGTGACGACCGGCGAGTCCAAGTTCGGCGTCAC 290
Qy 546 CTTGAGTGGGA---CGAGTGGCAGGGCATCCCGGGCGCGCTCTGTTGTCAGAAACCTGCA 602
Db 291 GTTGACTGGGAGGTGGAGAAGCTGGGAGTGCCTGGGGGCGCTGCTCGTCAAGAAACAACCA 350
Qy 603 GCACGCGAGTTCTTCTCAAGACGCTCACCCCTCGAGGGCGTCCCGAGGCAAGGCGACCGT 662
Db 351 CGCCGCGGAGTTCTTCTCAAGACAATCACCCCTCGACGACGTGCCCGGCGGCGCGCT 410
Qy 663 CGTCTCGTCGCCAACTCGTGGGTCTACCCGACAAAGTCTACTCCAGGAACGCACTTT 722
Db 411 CACCTTCGTGCGCAACTCTGCGTCTACCCCGCGGGCAAGTACCGGTACAAACCGGCTCT 470
Qy 723 CTTGCGCAACGACACCTATCTGCCGAGCAAAATGCCGCGGCGTGGTGGCTTATCGGCA 782

Db 471 CTTCTCAAACGATACGTACTGCTGCTCAAGCCAGATGCGCGGGCGCTGAAGCCGTACCGCGA 530
Qy 783 AGATGAGCTCAAGATTCTCGTGGCGACGATAATCTGGACCATACCAGGAGATGATCG 842
Db 531 CGACGAGCTCCGCAACCTCGCGGCGACGACCCAGAGGGCCCCCTACCAGGAGCAGCAGCG 590
Qy 843 CGTCTACCGTTACGACTACTACAAATGACCTTGTGTATCCCGACAAGGGCGAAGAGCAGC 902
Db 591 CGTGTACCGCTACGACGTCTACAAACGACCTCGGCGAGCCCGACGGCGC-----AACCC 644
Qy 903 TCGGCGGATCCTCGGTGGCAGCAAGAAACACCCCGTATCCCGTGTGTCAGAACTGGCCG 962
Db 645 GCGCCCATCTCTCGGCGGCTCCGCGGACCAACCCGTACCCGCGCGCTGCGCGCAGGGCG 704
Qy 963 GCACCCAAACAAAGAACCCAAATTCGGAGAGCAGGCTTTTCTGTGTAACCTGAACAT 1022
Db 705 CAAGCCCAACAAACCGACCCCAACTCGGATAGCCGACTGTGCTGGTGA---GCAGAT 761
Qy 1023 CTACGTCCCGCGTGACGAACGCTTTGGGCATCTCAAGATGTGGACTTCTCTTGGGTACTC 1082
Db 762 CTACGTCCCGCGGACGAGCGCTTCGGCCACCTCAAGATGTCCGACTTCTCTGGGTACTC 821
Qy 1083 GCTGAAGACGATCATCGAGGCTGTTCTTCCAAACACTGGGACTTTCGTCGATGACACGCC 1142
Db 822 CATCAAGGCCATCACGCGAGGCGATCATCCCGCGGTGGCAGCTACGTGGACACACCC 881
Qy 1143 CAAGGAGTTCGATTTCGTTGAGGATATCCTCGGGCTCTACGAGCTGGGCCCCAGAGCACC 1202
Db 882 GGGCGAGTTCGACTCTCTCCAGGACATCATCAACCTGTACGAGGGCGGATCAAGCTGCC 941
Qy 1203 CAACAACCCACTGATAGCAGAGATCAGGAAGAGATCCCCAGCGAGTTCTTTCGAAGCAT 1262
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Qy 1263 TCTGCGGAACGGTAGCCATGACCAACCCGCTAAAGATGCCCCCTTCCAAATGTCAATAATC 1322
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Qy 1323 AGATGTGTTGAAAAAGGCTCCGAGTTTAAAGTTTGGCTGGAGGACTGACGAGAGTTCCG 1382
Db 1057 -----GAGGACAAGAACGCGTGGAGGACCGACGAGGAGTTCCG 1094
Qy 1383 GAGAGAGACATTGACGGCTGAACCCAGTAATCATCAAAAGTCTGACGAGGTTCCCGCG 1442
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Qy 1443 TAAAGCACCTGGACCCAAAGGCGAGTACGGAGACCAACAGCAAGATCACTGAAGCTCA 1502
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Qy 1503 CATCCGGCATAACATGGGAGGCTGTGCGGTGACAGACGCACTGAGGAACAAGAGGCTCTT 1562
Db 1215 CATGAGAAAGAACCTCGAGGGCTCACGGTGCAGAGGCGCTGGACGGCAACAGGCTCTA 1274
Qy 1563 CATCTAGACCAACCATGACCATTTTCATGCCGTACCTCGACGAGATCAACGAGCTGGAGGG 1622
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Qy 1803 TGCTGCGTAAACGACTCTGCTGGCTGGCATCAGTGTATCAGCCACTGGCTGAACACGACGC 1862
Db 1515 TGTCGCGGTCAACGACTCTGGCTGGACCAACTCGTCAAGCCACTGGCTGAACACCCACGC 1574

QY 1863 GGTGATCGAGCCGTTTCGTAAATCGCGACAAACCGGAGCTCAGCGTGGTGGTCAATCCCGTGC 1922
Db 1575 GGTGATGAGCCGTTTCGTGATCGCGACGAAACCGGAGCTGAGCGTGACGACCCCGGTGCA 1634
QY 1923 CAAGCTGCTGAGCCCGCTACCTGACGCTGACACGCTGAAATCAACGCTTCCGACGCGCAGAC 1982
Db 1635 CAAGCTCCTGAGCTCGCACTTCCGCGACACCATGACCATCAACGCGTGGCGCGCAGAC 1694
QY 1983 ACTCATCAACGCGCGGCTGCTTTCGAGCGCACCGTGTTCCTGCAAGTACGCGCTGGG 2042
Db 1695 GCTCATCAACGCGCGGCTGCTTTCGAGATGACCGTCTCCGCGCAAGTACGCGCTGGG 1754
QY 2043 GATGTCGCGACAGCTGTACAAGAGCTGGAATTTCAACGAGCAGGCTCTCCAGCAGATCT 2102
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Db 1815 CGTCAAGAGAGGTGTGGCTGTGCGGACCGCTCCAGCCCGTACAAGTGGCTGCTGAT 1874
QY 2163 CAAGGACTACCCCTATGCGGTGACGGGCTGCTCATCTGGTGGCGATCGAGCGGTGGT 2222
Db 1875 CGAGGACTACCCGTTACGAGCGAGCGGCTGGCTGCTGCGACGCTGCGCATCGAGCAGTGGT 1934
QY 2223 CAAGGAGTACCTGGACATCTACTACCTTAACGACGCGGAGCTCCAGCGTGACGTGGAGCT 2282
Db 1935 GGGCGAGTACCTGGCCATCTACTACCCCGACGACGCGCGCTGCGGGCGACGAGGAGCT 1994
QY 2283 GCAGGCGTGTGGAAGAGGTGCTGAGGAGGCGCACGCGGACCTCAAGGACCGAGACTG 2342
Db 1995 GCAGGCGTGTGGAAGAGGTGCGGAGGTGCGGACGCGGACCGACCAAGGACGCGCCCTG 2054
QY 2343 GTGGCCAGGATGACACCGTCCAGCAGCTGGCTAGGGCGTGACGACGACCATCATCTGGT 2402
Db 2055 GTGGCCCAAGATGACGCGCGTGTGCGAGCTGCGAGCGCTGCGACGCGCTGCGACCATCATCTGGAT 2114
QY 2403 GGCATCCGCGCTGCACGCGCTGTCAACTTTGGGCGAGTACCCATACGCGGGGTACCTCCC 2462
Db 2115 CGCGTCGCGCTCCACGCGCGCTCAACTTCGCGCAGTACCCGTAACGCGGGGTACCTCCC 2174
QY 2463 GAACGCGCGACGCGCGCGCGCGCGCGATGCGGAGCGGAGCGGACCGACGACTACAAGAA 2522
Db 2175 GAACAGGCGCGCGCGCGCGCGCGATGCGGAGCGCGGAGCGCGGAGGAGTACGAGGA 2234
QY 2523 GCTGGAGCGGGGACGAGGAGGCGGACATGTTGTTTCATCCGACCATCATCAGCGCGGTT 2582
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QY 2583 CCAGACCATCTCGGCGATCTCGCTCATCGAGATCTCTCCAAGACTCTCTCCGACGAGGT 2642
Db 2286 CCAGACCATCATCGGCGATCTCGCTCATCGAGATCTCTCCAAGACTCTCTCCGACGAGGT 2345
QY 2643 GTACCTCGGCGAGCGAGCGCTGATCGCTGGACGTCAGACGCGCAAGCGCGCTGGATGC 2702
Db 2346 GTACCTCGGCGAGCGCGACACCCCGA---GTGACCTCCGACCGCGCGCTGGCGGC 2402
QY 2703 GTTCAAAAGATTTCGGGAGCGCGCTGGTGCAGATTGAGAAATCGGATCAAGACGATGAACGA 2762
Db 2403 GTTCAAGAGGTTTCAGCGACGCGTGGTCAAGATCGAGGCAAGGTGGTGGCGGAGAACCG 2462
QY 2763 CAGTCCGGAATTGAAGAACCGGAAGGGCGCTGTGGAAATGCCGTACATGCTGTATCCC 2822
Db 2463 CGACCCGCGAGCTGAGGAACAGGAACGCGCCCGCGGAGTTCCCTTACATGCTGTCTATCC 2522
QY 2823 CAACACGTCGGACGTTACCGGCGAGAAAGCGCGGCGGCTTACTGCGATGGGCTATCCCAA 2882
Db 2523 CAACACCTCTGACCAAGTGGCG---CCGCGCGAGGGCTCACTGCCAAGGGGCTATCCCAA 2579
QY 2883 CAGCATCTCCATATGA 2898
Db 2580 CAGCATCTCCATCTGA 2595

RESULT 3
US-09-751-687-10
; Sequence 10, Application US/09751687
; Patent No. 6660915
; GENERAL INFORMATION:
; APPLICANT: Douma, Anneke
; APPLICANT: Doderer, Albert
; APPLICANT: Cameron-Mills, Verena
; APPLICANT: Skadhauge, Birgitte
; APPLICANT: Bech, Lene
; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY
; FILE REFERENCE: 11225.11US01
; CURRENT APPLICATION NUMBER: US/09/751,687
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 2818
; TYPE: DNA
; ORGANISM: Hordeum vulgare
US-09-751-687-10

Query Match 39.0%; Score 1222.2; DB 4; Length 2818;
Best Local Similarity 69.0%; Pred. No. 5.2e-243;
Matches 1868; Conservative 0; Mismatches 758; Indels 81; Gaps 11;

QY 210 GGAGCGAGAAAAGCGAAGAGCGGCCATGTTCTGGCACGGGTCGCGGACCGGCTGACGGG 269
Db 32 GGAGCAGTGAAAGCGAGAGAGGAGGCGCAAGAACAAAGATGCTGCTGGAGGGCTGATCGA 91
QY 270 AAAGAACAAAGGAGGCGTGGAGCGAGGGCAAGATCCGCGGACCGTGGTGGTCAAGAA 329
Db 92 CACCCTCACGGGGCGAACAAGAGCGCCCGCTCAAGGGCACGGTGGTGGTCAATGCGCAA 151
QY 330 GGAGGTGCTGGACGTCGGCGACTTCAACGCTTCGCTCCTCGACGCGGCTCCACAGATCCT 389
Db 152 GAACGTGCTGGACCTCAACGACTTGGCGGCCACCATCATCGACGGCATCGGCGAGTTCCT 211
QY 390 CGGCTGGGACGACGCGCTGCGCTTCCAGTCTGTCAGCGCCACCGCGGCGGACCCAGCAA 449
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QY 450 CGGGGGCGCTGGCAAGGTGGGGAAGGCGGCGCACCTGGAGGAGCGGCTGGTGGTCAAA 509
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QY 510 GTCCACGCGGACGCGGAGACCGGTGTACCGGCTGAGCTTCGAGTGGGA---CGAGTCGCA 566
Db 326 GTGCTGACGACGCGGGAGTCCAAGTTTGGCGCTCACCTTCGACTGGGAGGTGGAGAGCT 385
QY 567 GGGCATCCCGGCGCGCTCCTGTGTGAGGAACCTGCAGCACCGCGAGTCTTCTCCTCAAGAC 626
Db 386 CGGGGTGCGGGCGCGCATCGTCTCAACAACTACCAAGTCCGAGTTCCTGCTTAAAC 445
QY 627 GCTCACCTCGAGGCGTCCCAG---GCAAGGGCACCGTCTGCTTCGTCGCGCAACTCGTG 683
Db 446 CATCACCTCCACGACGTCCTCCGCGCGGCGGCAACCTCACCTTCGTCGCGCAACTCATG 505
QY 684 GGTCTACCCGCAAGCTCTACTCCAGGAACGCTATCTTCTCGGCAACGACACCTATCT 743
Db 506 GATCTACCCCGCGCGCAACTACCGATACAGCCGCTCTTCTTCGCAACGACACGATACCT 565
QY 744 GCGAGCAAAATGCGCGGCGGTGGTGGCTTATCGGCAAGATGAGTCAAGATCTCCG 803
Db 566 GCGGAGCCAGATGCGCGGCGGTGAAGCGGTACCGCGACGACGAGCTCCGGAACCTGCG 625
QY 804 TGGCGACGATATCTTGGACCATACCGAGGAGCATGATCGCGTCTACGTTACGACTACTA 863
Db 626 TGGCGACGACGAGGCGGCGGTACCGAGGAGCACGACCGCATCTACCGCTACGACGCTCTA 685
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QY 924 CCAAGAAACACCCGTATCCCGCTGCTGCGAAGTGGCCGGCACCCCAACAAAGAACCC 983
Db 725 CTCGACCACTTACCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 784
QY 984 AAATTCGGAGAGCAGGCTTTCTCTGCTGAACCTGAACATCTACGTCGCGCTGACGAACG 1043
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QY 1104 TGTTCCTTCCAACTGGGACTTTCTGTCGATGACACGCCCAAGGAGTTCTGTTTGA 1163
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QY 1584 TTTTCATGCCGTACCTGACGAGATCAACGAGCTGGAGGGGAACCTTCTACGCCAGCAG 1643
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QY 1821 TGCTTGGCATCAGCTGATCAGCCACTGGCTGAACACGACGCGGCTGATCGAGCCGTTCTG 1880
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QY 1881 AATCGCGACAAACCGGCGAGCTCAGCGTGGTGGCTCCCGTGCACAGCTGCTGAGCCCGCA 1940
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QY 2001 CGTCTTCGAGCGCACCGTGTTCCTCTGCAAAAGTACGCGCTGGGATGTTCGGCAGACGTGTA 2060
Db 1775 CATCTTCGAGATGACCGTGTTCCTCGGGAAGTTCGGTGGGATGTTCGGCGTGTGTA 1834
QY 2061 CAAGAGCTGGAATTTCAACGAGCAGGCTCTCCAGCAGATCTCTGTCAGAGAGGTTGTGGC 2120
Db 1835 CAAGACTGGAAGTTACCGAGCAGGACTGCGGACGATCTCATCAAGAGGGGCTATGGC 1894
QY 2121 TGTGCCGACACAGTCAAGCCCATATGTTGTCGACTGCTGATCAAGGACTACCCCTATGC 2180
Db 1895 GGTGAGGACCCGTCGAGCCCGTACAAGTTCGGTGTCTGTTGTCGACTACCCGTACGC 1954
QY 2181 CGTTGACGGGCTGTCATCTGTTGGGCGATCGAGCGGTGGGTCAAGAGTACCTGGACAT 2240
Db 1955 GCGGACGGGCTGGCATCTGGCACGCCATTGAGCAGTACGTAGCGAGTACCTGECCTAT 2014
QY 2241 CTACTACCCCTAACGACGGCGAGCTCCAGCTGACGTGGAGTGCAGGCTGGTGAAGGA 2300
Db 2015 CTACTACCCGAACGACGGCGTGTGTCAGGGCGATACGAGGTGCAGGCTGGTGAAGGA 2074
QY 2301 GGTGCTGAGGAGGCGCACGGCGACCTCAAGGACCGAGACTGTTGGCCAGGATGGACAC 2360
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QY 2361 CGTCCAGCAGCTGGCTAGGGCGTGCAGCACCATCATCTGGTGGCATCCGCGCTGCACGC 2420
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QY 2541 GGAGCGGAGCATGTTGTTTCATCCGCACTTACAGGCGGCTTCCAGACCATCTTGGGCG 2600
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Db 2603 GGGCG---CGGCTGCGGCGCTTACCGGCAAGGCGCATCCCAACAGCATCTCCATCTAATC 2659
QY 2901 CTGGGCA 2907
Db 2660 TAAGCCA 2666

RESULT 4
US-09-051-465-1
; Sequence 1, Application US/09051465A
; Patent No. 6355862
; GENERAL INFORMATION:
; APPLICANT: Handa, Avtar K.
; APPLICANT: Kausch, Kurt D.


```

; TITLE OF INVENTION: Improvement of Fruit Quality by Inhibiting
; TITLE OF INVENTION: Production of Lipoxigenase in Fruits
; FILE REFERENCE: 7024-297

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;; CURRENT APPLICATION NUMBER: US/09/051,465A

CURRENT FILING DATE: 1998-07-31

; PRIORITY APPLICATION NUMBER: PCT/US96/16387

PRIOR FILING DATE: 1996-10-11

PRIOR APPLICATION NUMBER: 60/005,404

PRIOR FILING DATE: 1995-10-13

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: ASCII

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; SEO ID NO 1
; SEO ID NO 1
; SEO ID NO 1

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LENGTH: 2441

TYPE: DNA

ORGANISM: Lycopersicon esculentum

US-09-051-465-1

Query Match	21.2%;	Score 664.2;	DB 4;	Length 2441;
Best Local Similarity	57.7%;	Pred. No. 6.6e-128;		
Matches 1367;	Conservative	0;	Mismatches 953;	Indels 51;
				Gaps 8;

Qv 460 GGCAAGGTGGGGAAGCGCGGCACCTGGAGGAGGCGGTGGTGTGGCTCAAGTCCACCGCG 519

Db 89 GGGAACTGAGCAATCCAGCATACTTAGAGAGTTGGCTTACAGACATCACCCCAATAACA 148

520 GACGGGGAGACCGGTGTACCGGGTGAGCTTCGAGTGGGA--CGAGTCGCAGGGCATCCCCG 576

Db 149 GCAGGGAATCAACTTTTAGTGTTACATTTGACTGGGATCGTGACGAGTTTGGAGTTCCA 208

577 GGCGCCGTCCTGGTCAGGAACCTGCAGCAGCCGAGTTCTTCCTCAGACGCTCACCCCTC 636

Db 209 GGAGCATTTCATCAAGAATCTTCATCTTAATGAGTCTTTTCTCAAGTCATCACACTC 268

QY 637 GAGGCGTCCCAGGCAAGGCACCGTCGTCTTCGTGCGCACTCGTGGTCTACCCGCAC 696

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Db 329 TTTAGATACAAGTCTGACCGCATTTCTTTGCCAATCAGGCTTATCTCCCAAGTGAACA 388

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Db 447 - CTGGAAGCTTGAAGAAATGGGACAGGGTTTATGATTATGCTTGTACAAATGACTTGGGT 505

QV 877 GATCCGACAGGGCGAAGAGCACGCTCGGCCGATCCTCGGTGGCAGCCAAAGAACACCCG 936

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506 GAACAGATAAGGGGGAAGATATGCTAGGCCTATCCTTGGAGGTCTCTGAGTACCCG 565

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Qy 1174 GGGCTCTACGAGCTGGGCCAGAGGCCAACCAACCCACTGATAGCAGAGATCAGGAAG 123

Db 806 AATCTCTATGAAGGAGGAATCAAGTTCCTGAAGGCCCTTGGTTGAAAGCCATTACTGAT 865

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QY 2374 GCTAGGGCGTGCACGACCATCATCTGGTGGCATCCGCGTGCACGCGGTGTCAACTTT 2433
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Db 2036 GGCTTACTCTTACCGTGTATCTCCCTAATCGCCCTACTTTAAGCTGTAAATTTGATG 2095
QY 2494 CCGGAGCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2553
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QY 2554 GTGTTTATCCGACCATCACCAGCCAGTTCAGACCATCTCTGGGCGATCTCGCTCATCGAG 2613
Db 2147 GTATTCCTAAACAACTTTGTTCTCAGTTGCAATCACTGCTTGAATTTCCATCTTTGAG 2206
QY 2614 ATCTCTCCAAGCACTCTCCGACGAGGTGTACCTCGGCGGCGGCGGCGGCGGCGGCGG 2673
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QY 2794 GTGGAATGCCGTACATGCTGTGTACCCCA 2824
Db 2384 GTTAACGTTCCATATACGTTGCTCTTTCCCA 2414

RESULT 5

US-09-051-465-2
; Sequence 2, Application US/09051465A
; Patent No. 6355862
; GENERAL INFORMATION:
; APPLICANT: Handa, Avtar K.
; APPLICANT: Kausch, Kurt D.
; TITLE OF INVENTION: Improvement of Fruit Quality by Inhibiting
; TITLE OF INVENTION: Production of Lipoxigenase in Fruits
; FILE REFERENCE: 7024-297
; CURRENT APPLICATION NUMBER: US/09/051,465A
; CURRENT FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: PCT/US96/16387
; PRIOR FILING DATE: 1996-10-11
; PRIOR APPLICATION NUMBER: 60/005,404
; PRIOR FILING DATE: 1995-10-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: ASCII
; SEQ ID NO 2
; LENGTH: 2871
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-09-051-465-2

Query Match 21.2%; Score 664.2; DB 4; Length 2871;
Best Local Similarity 57.7%; Pred. No. 6.9e-128;
Matches 1367; Conservative 0; Mismatches 953; Indels 51; Gaps 8;
QY 460 GGCAAGGTGGGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 519
Db 246 GGGAACTGAGCAATCCAGCATACTTAGAGAGTTGGCTTACAGACATCACCCCAATAACA 305
QY 520 GACGGGGAGACCGGTACCGGGTACGCTTGGAGTGGGA---CGAGTCGAGGCGGCGGCGG 576
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QY 577 GGCGCGGCTCTGGTCAAGAACCTGCAGCAGCGGCGGAGTTCTTCTCAAGACGCTCACCCCTC 636

Db 366 GGAGCATTCATCATCAAGAAATCTTCACTTAATGAGTTCTTTCTCAAGTCACTACACTC 425
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Db 486 TTTAGATACAAGTCTGACCGCAATTTCTTTGGCCAAATCAGGCTTATCTCCCAAGTGAACA 545
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QY 877 GATCCCGACAAGGGCGAAGAGCACGCTCGGCGGATCTCTCGGTGGCAGCCAAAGACACCCG 936
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Qy 2254 GACGGCGAGCTCCAGCGTGACGTGGAGCTGCGAGCGGTGGTGGAGAGGTGCGTGAGGAG 2313
Db 2013 GACGAGACAGTAGAAGAAACACTGAACCTCAAGCTTGGTGGAGGAGCTCCGCGAAGAA 2072
Qy 2314 GCGCAGCGGACCTCAAGGACCGGAGACTGGTGGCCAGGATGGACACCGTCCAGCAGCTG 2373
Db 2073 GGACATGGCGACAAGAAAGATGAGGCTTGTGTGCTTAACTGCAAACTCGACAAGAGCTC 2132
Qy 2374 GCTAGGGCGTGACGACCATCATCTGGTGGATCCGCGTGCACGGGCTGTCAACTTT 2433
Db 2133 AGAGATTGTTGCACCATCATATATGATAGCTTTCAGCACTTTCATGAGCACTCCATTTT 2192
Qy 2434 GGGCAGTACCCATACGCGGGTACCTCCGAAACCGCGCCGACGGCCAGCGCGCGCGATG 2493
Db 2193 GGCTTATCTCTTACGCTGGTTATCTCCCTATCGCCCTACTTTAAGTGTAATTGATG 2252
Qy 2494 CCGGAGCCAGGCACGACTACAAGAAGCTGGGAGCGGGGCGAGAGGAGCGGACATG 2553
Db 2253 CCAGAGCCAGGAAGTGTGATGATGAAGAGCT-----CAAGACAAATCCAGACAAG 2303
Qy 2554 GTGTTTCATCCGACCATCACCAGCCAGTTCCAGACCATCTCGGGCATCTCGCTCATCGAG 2613
Db 2304 GTATTCCTAAACAAATTTGTTCTCTCAGTTGCAATCACTGCTTGAATTTCCATCTTTGAG 2363
Qy 2614 ATCCTCTCAAGCACTCTCCGACGAGGTGTACTCGGCCAGCGTGACGAGCCCTGATCGC 2673
Db 2364 GTCTCGTCAAGGCATGCTTCAGATGAGGTTTACTTGGGACAAAGGGACTCAATTGA--A 2420
Qy 2674 TGGAGCTCAGACGCCAAGCGCTGGATGCGTTCAAAAGATTCCGGAGCGCGCTGGTGCAG 2733
Db 2421 TGGACAAAGGATAAAGAACCACTTGTAGCTTTTGTAGAGGTTTGGAAAGATGCTAAGTGAT 2480
Qy 2734 ATTGAGAATCGGATCAAGACGATGAACGACAGTCCGGACTTTGAAGAACCGGAGGGCCT 2793
Db 2481 ATCGAGAATCGAATTTATGATAATGAATAGTATCAAGAGTTGGAAGAACAGTCAAGGCGCT 2540

Qy 2794 GTGGAATGCCGTACATGCTGCTGTACCCCA 2824
Db 2541 GTTAACGTTCCATATACGTTGCTCTTTCCCA 2571

RESULT 6

US-09-051-465-4
; Sequence 4, Application US/09051465A
; Patent No. 6355862
; GENERAL INFORMATION:
; APPLICANT: Handa, Avtar K.
; APPLICANT: Kausch, Kurt D.
; TITLE OF INVENTION: Improvement of Fruit Quality by Inhibiting
; TITLE OF INVENTION: Production of Lipoxigenase in Fruits
; FILE REFERENCE: 7024-297
; CURRENT APPLICATION NUMBER: US/09/051.465A
; CURRENT FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: PCT/US96/16387
; PRIOR FILING DATE: 1996-10-11
; PRIOR APPLICATION NUMBER: 60/005,404
; PRIOR FILING DATE: 1995-10-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: ASCII
; SEQ ID NO 4
; LENGTH: 2871
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-09-051-465-4

Query Match 21.2%; Score 664.2; DB 4; Length 2871;
Best Local Similarity 57.7%; Pred. No. 6.9e-128;
Matches 1367; Conservative 0; Mismatches 953; Indels 51; Gaps 8;

Qy 460 GGCAAGGTGGGAAAGCGCGCACCTGGAGGAGCGGTGGTGGTCAAGTCCACGGCG 519
Db 246 GGGAACTGAGCAATCCAGCATACCTTAGAGAGTTGGCTTACAGACATCACCCCAATAACA 305
Qy 520 GACGGGAGACCGTGTACCGGGTGAGCTTCGAGTGGGA--CGAGTCGAGGGCATCCCG 576
Db 306 GCAGGGGAATCAACTTTTAGTGTACATTTGACTGGGATCGTGACGAGTTGGAGTTCCA 365
Qy 577 GCGCGCGTCTGTGTCAGGAACCTGCGAGCAGCGCGAGTTCTTCTTCAAGACGCTCACCCCTC 636
Db 366 GGAGCATTCATCAAGAAATCTTCAATGAGTTCTTTCTCAAGTCACTCACACTC 425
Qy 637 GAGGGCGTCCAGCAAGGCGCACCGTCTTCTGTCGCCAACCTGTCGGGTCTACCCGCAC 696
Db 426 GAAGATGTTCTTAATATGGAATAATCCATTTGTATGCAATCTTGGGTTTATCCTGCT 485
Qy 697 AAGCTCTACTCCAGGAACGCTATCTTTCGCCAACGACACCTATCTCCGAGCAAAATG 756
Db 486 TTAGATACAAGTCTGACCGCATTTTCTTGGCAATCAGGCTTATCTCCCAAGTGAACA 545
Qy 757 CCGGGCGGTTGGTGGCTTATCGGCAAGATGAGCTCAAGATTCTCGTGGCGAGCATAAT 816
Db 546 CCACAACCATTCGCAAAATACAGAGAAATGAACTGGTAGCTTTGCGAGGAGATGGAA-- 603
Qy 817 CCTGGACCATACAGGAGCATGATCGCGTCTACCGTTACGACTACTACATGACCTTGGT 876
Db 604 -CTGAAAGCTTGAAGATGGGACAGGTTTATGATTATGCTTGTCTACAAATGACTTGGGT 662
Qy 877 GATCCCGACAAGGCGAAGAGCAGCGCTCGGCGCATCTCGGTGGCAGCAAGAACACCCG 936
Db 663 GAACCAGATAAGGGGGAAGAGTATGCTAGGCTATCTTGGAGGCTCTCTGTAGTACCCG 722
Qy 937 TATCCCGCTCGCTGAGAACTGGCCGCGCACCGTCCGCGCATCTACCTCCGCGTACGAAACGCTTGGGAT 996
Db 723 TATCTCGTAGAGGAGGACAGCGCCGCAACCAACCAAGCAGATCCTTAATTCGAGAGC 782
Qy 997 AGG--CTTTTCTGCTGAACCTGAACATCTACCTCCCGGTGACGAACTTGGGAT 1053
Db 783 AGGAACCCATTGCCCTATGAGCTTAGACATATATGTCCCAAGGAGCGGATTTGGTCAAT 842

QY 1054 CTAAGATGTCGACTTCTTGGGTACTCGGTGAAGACGATCATCGAGGCTGTTCTTCCA 1113
Db 843 GTGAAGAAGTCAGACTTTTGGACGTGCTTAAATCCTCTTTGCAACGCTTCTCCCT 902
QY 1114 AACTGGGACCTTTCGTGATGACACGCCCAAGGAGTTCGATTCTGTTGAGGATATCCTC 1173
Db 903 GCGTTTAAGGCTTTGTCGATAACACGCCCTAATGAGTTCAATAGCTTTGCGGATGTACTT 962
QY 1174 GGGCTCTACGAGCTGGGCCCAGAGGCCACCCAAACCCACTGATGACGAGATCAGGAAG 1233
Db 963 AATCTCTATGAAGGGAATCAAGTTGCCTGAAGGCCCTTGGTTGAAAGCCATTACTGAT 1022
QY 1234 AAGATCCCAGCGAGTTCCTTCGAAGCATCTGCGCGAACCGGTAGCCATGACCCCGCTA 1293
Db 1023 AACATTTCTCAGAGATACTAAAGACATCCTTCAAAACGGATGGTCAAG--GCCTACTT 1079
QY 1294 AAGATGCCCTTCCAAATGTTCATCAAAATCAGATGTGTTGAAAAAGGCTCCGGAGTTTAA 1353
Db 1080 AAGTACCCAACTCCTCAGGTTAATCAAGGCGA-----TAAA 1115
QY 1354 TTTGGCTGGAGGACTGACGAAGATTTCCGAGAGAGACACTTGCAGGCGTGAACCCAGTA 1413
Db 1116 ACTGCATGGAGGACGGATGAAGAAATTTGGGAGAGAAATGTTGGCAGGATCCAATCCTGTC 1175
QY 1414 ATCATCAAAACGTCTGACGAGTTCCTCCGCTTAAAGACACCTTGACCCCAAGCAGTACGGA 1473
Db 1176 TTAATCAGTAGACTCCAAAGAAATTTCTCCGAGAGCAAGTTGGATCCCAACCATATATGGA 1235
QY 1474 GACCACACGACGATCACTGAAGCTCACATCCGCGCATAAACATGGGAGCCTGTCCGGTG 1533
Db 1236 AACCAAAACAGTACAATTACCACAGAACATGTACAGGATAAGTTGAATGGATTAACAGTG 1295
QY 1534 CAGAACGCACTGAGGAACAAGAGGCTCTTCATCTCTAGACCAACCATGACCATTTTCATGCCG 1593
Db 1296 AATGAGGCAATCAAGAGTAACAGGTTATTTCATATTGAACCAACCATGACATCGTGATGCA 1355
QY 1594 TACCTCGACGAGATCAACGAGCTGGAGGGAACITTCATCTACGCCAGCAGGACCTTACTG 1653
Db 1356 CTATTGAGGAAATTAACATGTTCAGCAACACAAAAGCCTATGCCCTCAAGAACTCTGCTC 1415
QY 1654 TTCCTGAAGGACGATGGACGCTGAAGCCCCCTGGCCATCGAGCTGAGCCTGCCCCACCCCT 1713
Db 1416 TTCCTACAAGATGATAGAACTTTGAAGCCACTAGCAATTGAACCTTCCACATCCA 1475
QY 1714 GACGCGCAGCAGCGCGCGGTGAGCAAGGTGTACACCCCGCTCACACCGCGGTGAG 1773
Db 1476 GACGAGATCAATTTGGTACTGTTAGTAAAGTATATACACAGCTGACCAAGGTGTTGAA 1535
QY 1774 GGCCACGTCTGGCAGCTCGCAAGGCTTATGCTGCTAAACGACTCTGCTGGCATCAG 1833
Db 1536 GGTCTATCTGGCAGTTTGCCAAAGCCTATGTAGCAGTGAATGACATGGGCAATTCATCAG 1595
QY 1834 CTGATCAGCCACTGGCTGAACACGACGCGGTGATCGAGCCGTTCTGTAATCGGACAAAC 1893
Db 1596 CTCATAGCCACTGGTTGAATATACACACGCGGTGATCGAACCATTTGTGATTGCAACAAAT 1655
QY 1894 CGGACGCTCAGCGTGGTGATCCCGTGCACAAAGCTGCTGAGCCCGCACTACCGTGACACG 1953
Db 1656 AGGCATCTAAGTGTGCTTCAATCCCATTCATAAACTTCTTCATCCTCATTTCCGTAACACG 1715
QY 1954 CTGAACATCAACGCCCTGGCAGCCAGACACTCATCAACCGCGCGGTCTTCGAGCGC 2013
Db 1716 ATGAACATAAATGCTTTAGCAAGAGAGACCTTGACCTATGATGGTGG---TTTGAGACG 1772
QY 2014 ACCGTGTTCCCTGCAAGTACGCGCTGGGGATGTGCGCAGACGCTGTACAGAGCTGGAAT 2073
Db 1773 TCTCTTTTCTGCGCAATATTCCATGGAAATGTACAGCAGCAGCTTACAAAGATGGGTT 1832
QY 2074 TTCACGACGAGGCTCTCCAGCAGATCTCGTCAAGAGAGGTTGGCTGTGCGGACCCAG 2133
Db 1833 TTCCCTGAACAAGCACTTCCGTGATCTCCTCAAAAGAGGAGTGGCTGTTGAGGACTTG 1892

QY 2134 TCAAGCCCATATGTTGTCGACTGCTGATCAAGGACTACCCCTATGCGGTTGACGGGCTC 2193
Db 1893 AGCTCCCAACATGGCATTCGTTTACTGATTTCTGGACTATCCATATGCTGTTGATGGCTTG 1952
QY 2194 GTCATCTGTTGGCGATCGAGCGGTGGTCAAGGAGTACCTGGACATCTACTACCCCTAAC 2253
Db 1953 GAATTTGGGCGAGCAATCAAAAGTTGGGTAAACAGATATTGCAAGTCTTATTACAAATCT 2012
QY 2254 GACGGCGAGCTCCAGCGTGACGTGGAGCTGAGGCTGGTGAAGGAGGTGCGTGAGGAG 2313
Db 2013 GACGAGACAGTAGAGAAAGACACTGAACCTCCAAAGCTTGGTGAAGGAGCTCCGCGAAGAA 2072
QY 2314 GCGCACGGCGACCTCAAGGACCGAGACTGTTGGTGGCCCAAGGATGGACACCCGTCAGCAGCTG 2373
Db 2073 GGACATGGCGACAAAGAAAGATGAGGCTTGGTGGCCCTAAACTGCAAACTCGACAAGAGCTC 2132
QY 2374 GCTAGGGCGTGACGACCATCATCTGGTGGGATCCGCGCTGCACCGCGCTGTCAACTTT 2433
Db 2133 AGAGATTGTTGCACCATCATATATGATAGCTTCAGCACTTCATGACGACTCCATTTT 2192
QY 2434 GGGCAGTACCCATACGCGGGGTACTCTCCGAAACGCGCCAGCGCGCCCGGATG 2493
Db 2193 GGGTTATCTCTTACGCTGGTTATCTCCCTAATCGCCCTACTTTAAGCTGTAAATTTGATG 2252
QY 2494 CCGAGCCAGGACGACCAAGGACTCAAGAAAGCTGGGAGCGGGGAGAGGAGCGGACATG 2553
Db 2253 CCAGAGCCAGGAAGTGTGAGTATGAAGAGCT-----CAAGACAAATCCAGACAAG 2303
QY 2554 GTGTTTCATCCGCAACCATCACAGCCAGTTCAGAGACCATCTCGGCACTCTCGCTCATCGAG 2613
Db 2304 GTATTCTTAAACAATTTGTTCTCAGTTGCAATCAGTGTGAAATTTCCATCTTTGAG 2363
QY 2614 ATCTCTCCAAGCACTCCTCCGACGAGGTGTACCTCGGCCAGCGTGACGAGCCTGATCGC 2673
Db 2364 GTCTCGTCAAGGCATGCTTCAGATGAGGTTTACTTGGACAAAGGAGCTCAATTGA--A 2420
QY 2674 TGACGTCAGACGCGCAAGCGCTGGATGCGTTCAAAAGATTTCGGGAGCGCGGTGGTGAG 2733
Db 2421 TGGACAAAGGATAAAGHACCACTTGTAGCTTTTGGAGAGGTTTGGAAAGATGCTAAGTGAT 2480
QY 2734 ATTGAGAATCGGATCAAGACGATGAACGACAGTCCGGAATTGAAGAACCGGAAGGGGCT 2793
Db 2481 ATCGAGAATCGAATTATGATAATGAATAGTCAATAGAGTTGGAAGAACAGGTCAGGCT 2540
QY 2794 GTGAAATGCGGTACATGCTGCTGTACCCCA 2824
Db 2541 GTTAACGTTCCATATACGTTGCTCTTTCCCA 2571

RESULT 7

US-09-751-687-11
; Sequence 11, Application US/09751687
; Patent No. 6660915
; GENERAL INFORMATION:
; APPLICANT: Douma, Anneke
; APPLICANT: Doderer, Albert
; APPLICANT: Cameron-Mills, Verena
; APPLICANT: Skadhauge, Birgitte
; APPLICANT: Bech, Lene
; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY
; FILE REFERENCE: 11225.11US01
; CURRENT APPLICATION NUMBER: US/09/751,687
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 4663
; TYPE: DNA
; ORGANISM: Hordeum vulgare
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2346)..(2348)
; OTHER INFORMATION: "n" is a, c, t, or g encoding an acidic, basic, or polar amino ac

; OTHER INFORMATION: i									
US-09-751-687-11									
Query Match		19.1%;		Score 599.2;		DB 4;		Length 4663;	
Best Local Similarity		59.2%;		Pred. No. 2.1e-114;					
Matches 1511;		Conservative 0;		Mismatches 621;		Indels 421;		Gaps 12;	
QY	734	ACACCTATCTGCGAGCAAAATGCCGCGGCTTGGTGCCTTATCGGCAAGATGAGCTCA	793						
Db	2020	AGACGTACCTGCGAGCCAGATGCCGCGCGCTGAAGCCGTACCGGACGACGAGCTCC	2079						
QY	794	AGATTCTCGTGGGACGATAATCCTGGACCATACGAGGACGATCGCTACCGTT	853						
Db	2080	GGAACCTGCGTGGGACGACGACGAGGCGCTACGAGGACGACGACCGCATCTACCGCT	2139						
QY	854	ACGACTACTACAAATGACCTTGGTGATCCCGACAAGGGCGAAGAGCAGCTCGGCCGATCC	913						
Db	2140	ACGACGTCTACAACGACCTCGGCG	2178						
QY	914	TCGGTGGCAGCCAAAGAACACCCGTATCCCGCTCGCTGCAGAACTGGCCGGCACCCCAACAA	973						
Db	2179	TCGGCGGCAACTCCGACCAACCTTACC CGCGCGCGCGCGCACGAGCGCAAGCCCAACG	2238						
QY	974	AGAAAGACCCAAATTCGGAGAGCAGGCTTTCTCTGCTGAACCTGAACATCTACGTCCCGC	1033						
Db	2239	CCAGCAGCCCGAGCTGGAGAGCCGCTGCTGCTGCTGA	2295						
QY	1034	GTGACGAACGCTTTGGGCATCTCAAGATGTCGGACTTCTCTGGTACTCGCTGAAGACGA	1093						
Db	2296	GGGACGAGAAAGTTCGGCCACCTCAAGACGTCGACTTCTCTGGGTACTCTCATCAAGGCCA	2355						
QY	1094	TCATCGAGGCTGTTCTTCCAAACACTGGGGACTTTCGTGATGACAGCCCAAGGATTG	1153						
Db	2356	TCACGAGGGCATCTCTCGCGCCGCTGCGCACTACGTGGACACCAACCCCGCGGAGTTG	2415						
QY	1154	ATTGTTTGAGGATATCTCTGGGCTCTACGAGCTGGGCCCCAGAGGACCCCAACACCCAC	1213						
Db	2416	ACTCCTCCAGGACATCATCAACCTCTATGAGGGCGGCATCAAGTGCCCAAGGTGGCCG	2475						
QY	1214	TGATAGCAGAGATCAGGAAGAAGATCCCGAGCGAGTTCTCTCGAAGCATTTCTGCCGAACG	1273						
Db	2476	CCCTGGAGGAGCTCCGTAAAGCAGTTCCCGCTCCAGCTCATCAAGGACCTCTCCCGCTG	2535						
QY	1274	GTAGCCATGACCAACCCGCTAAAGATGCCCTTCCAAATGTCTCAATCAATCAGATGTGTTGA	1333						
Db	2536	GCGGC---GACTCCCTGCTTAAGCTCCCGCTGCCCCACATCATCCAGGAGAACAAAGCAGG	2592						
QY	1334	AAAAGGCTCCGAGTTTAAGTTTGGCTGGAGG-----ACTGACGAAGAGTTTCGCGA	1384						
Db	2593	CGTGGAGGACCGACGAGGAGTTTCGACCGGAGGTTGCTCGCCNNNGTCAACCCGCTCATGA	2652						
QY	1385	GAGAGACACTTGAGCGGTGAACCCAGTAATCATCAA-----	1421						
Db	2653	TCACGCGTCTCACGCTGAGTCAGCGATTATTGTTTCATTGTTGTTGTTATGTTGCCATGG	2712						
QY	1422	-----ACGTTCTGACG	1431						
Db	2713	TGAGAAAGTGCAGATCTTGAATTTGCGTTGGTTCGCATGCACGATGCTGCATGCAG	2772						
QY	1432	GAGTTCCCGCTAAAGCACCTCTGGACCCCAAGGCAGTACGGAGACACACCAAGATC	1491						
Db	2773	GAGTTCCCGCCAAAAGTAGTCTTGACCCCTAGCAAGTTTGGTGACACACCAACCAATC	2832						
QY	1492	ACTGAAGCTCACATCCGGCATAAACATGGGAGGCTGTGCGTGCAGAACGCA-----	1542						
Db	2833	ACGGCGGAGCACATAGAGAAGAACCTTCGAGGSCCTCACGGTGCAGCAGGTAATTGGTTCCA	2892						
QY	1543	-----	1542						
Db	2893	AGCCATCGACATCAACTATGATTACCTAGGAGTAATTGGTAGCTGTAGATAAATTTGGCT	2952						
QY	1543	-----	1542						

Db	2953	TCGTTGCAATTAAATTTGATGCTGGCCGATCAAGTGATCGTATTGGGTTTGAATTTGCAG	3012
QY	1543	---CTGAGGAACAAGAGGCTCTTTCATCTCTAGACCACCATGACCATTTTCATGCCGTACCTC	1599
Db	3013	GCGCTGGAAGCAACAGGCTGTACATCTTGATCACCATGACCGGTTTCATGCCGTTCTCTG	3072
QY	1600	GACGAGATCAACGAGCTGGAGGGAACTTCTACGCCAGCAGGACCCCTACTGTTCTCTG	1659
Db	3073	ATCGAGCTCAACAACCTGCCCGCAACTTCACTACGCCACGAGGACCCCTCTTCTTCTCTG	3132
QY	1660	AAGGACGATGGCAGCTGAAGCCCTTGCCCATCGAGCTGAGCCTGCCCCACCCCTGACGGC	1719
Db	3133	CGCGCGACCGCAGGCTCACGCCGCTCGGCATCGAGCTGAGCGAGGCCCATCATCCAGGGC	3192
QY	1720	CAGCAGCGCGCGGCTCAGCAAGGTGTACACCCCGGCTCACACCGG---CGTCGAGGGC	1776
Db	3193	GGCCTTACACGCGCAAGAGCAAGTTTACACGCCGCTGCCAGCGGCTCCGTCGAAGGC	3252
QY	1777	CACGTCTGGCAGCTCGCAAGGCTTATGCTGCTGCTAAACGACTCTGCTTGGCATCAGCTG	1836
Db	3253	TGGGTGTGGAGCTCGCAAGGCTTACGTGCCGCTCAATGACTCCGGGTGGCACCAGCTC	3312
QY	1837	ATCAGCCACT-----	1846
Db	3313	GTACGCCACTGTACGTTCTCCACGCTCGATGTGATTACGTACGTACGACCAACT	3372
QY	1847	-----GGCTGAACAACGACCGCGGTGATCGAGCCGTT	1877
Db	3373	GATCGAAATATGATTGATTGAACCGCGAGGCTGAACACTCACCGGTGATGGAGCCGTT	3432
QY	1878	CGTAATCGGACAAACCGGAGCTCAGCGTGGTGATCCCGTGACAAGCTGCTGAGCCC	1937
Db	3433	CGTGATCTCGACGAACCGGACCTTAGCGTGACCAACCGGTGCAAGCTGCTGAGCCC	3492
QY	1938	GCACCTACCGTGACACGCTGAACATCAACGCGCTGGCACGCCAGACACTCATCAACGCCG	1997
Db	3493	GCACCTACCGGACACCATGACCATCAACGCGCTGGCGCGGACGCTCATCAACGCCG	3552
QY	1998	CGGCGTCTTCGAGCGCACCGTGTTCCTGCAAAAGTACGCGTGGGATGTGGCAGACGT	2057
Db	3553	CGGCATCTTCGAGATGACGGTGTTCCTCGGCAAGTTTCGCGTTGGGATGTGGCCCGTGT	3612
QY	2058	GTACAAAGAGCTGGAATTTCAACGAGCAGGCTCTCCAGCAGATCTCGTCAAG-----	2109
Db	3613	GTACAAAGGACTGGAAGTTTCAACGAGCAGGACTGCCGACGATCTCATCAAGAGGTACGT	3672
QY	2110	-----	2109
Db	3673	ACCTGGTAAATGTTATGAATGTGTAATAAACAATTTGGCGTCTCGCTCACTGACAGGAACG	3732
QY	2110	-----AGAGGTGTGGCTGTGCGCGGACCAAGTCAAGCCCATATGGTGTCCGA	2154
Db	3733	TGGTAAAAAATGACAGGGGCTATGGCGTGGAGGACCCGTCGAGCCGTTACAAGTGGCG	3792
QY	2155	CTGCTGATCAAGGACTACCCCTATGCCGTTGACGGGCTCGTCACTCTGGTGGCGATCGAG	2214
Db	3793	TTGCTGGTGTCCGACTACCCGTACGCGGCGGACGGGCTGGCGATCTGGCACGCCATTGAG	3852
QY	2215	CGGTGGGTCAAGGAGTACCTGGACATCTACTACCCCTAACGACGCGGAGCTCCAGCGTGAC	2274
Db	3853	CAGTACGTGAGCGAGTACCTGGCCATCTACTACCCGAAACGACGCGGCTGTCAGGGCGAT	3912
QY	2275	GTGAGCTGCAGCGTGTGGAAGGAGGTGCTGAGGAGCGCACGCGGACCTCAAGGAC	2334
Db	3913	ACGAGGTGCAGCGTGTGGAAGGAGACGCGGAGGTTCGGGCACGCGGACCTCAAGGAC	3972
QY	2335	CGAGACTGGTGGCCAGGATGGACACCCGTCAGCAGCTGGCTAGGGGCTGCACGACCATC	2394
Db	3973	GCCCCATGGTGGCCCAAGATGCAAAAGTGTCCCGAGCTGGCCAAAGGCGTGCACCCATC	4032
QY	2395	ATCTGGGTGGCATCCGCGCTGCACCGGCTGTCAACTTTGGGCGAGTACCCATACGCCGG	2454
Db	4033	ATCTGGATCGGGTGGCGCTGCATCGGCGAGTCAACTTCGGGCGAGTACCCCTACGCCGG	4092

QY	2455	TACCTCCCGAACC	CGCGCAGCGCC	CGCCAGCCCGCGCCCGGATCCCGGAGCCAGGCAGCCACGAC	2514
DB	4093	TTCTCTCCGAAC	CCCGCCGACGGT	GAGCCGGCGCCCGATCCGGAGCCCGGACGCGAGGAG	4152
QY	2515	TACAAGAAGCT	GGGAGCGGGC	CAGAAAGGAGGCGGACATGGTGTTCATCCGACCATCACC	2574
DB	4153	TACGCGGAGCT	GG-----	AGCGGACCCCGGAGCGGGCCTTCATCCACACCATCAG	4203
QY	2575	AGCCAGTTC	CAGACCATCT	TGGGCATCTCGCTCATCGAGATCCTCTCCAAGCACTCCTCC	2634
DB	4204	AGCCAGATC	CAGACCATCAT	CGCGGTGTGCTGTGAGGCTGCTGCGAAGCACTCCTCC	4263
QY	2635	GACGAGGTG	TACCTCGGCC	ACGCTGACGAGCCTGATCGCTGGACGTCAGACGCCAAGGCG	2694
DB	4264	GACGAGCTG	TACCTCGGGC	ACGGGACACGCCCGA---GTGGACCTCGGACCCCAAGGCC	4320
QY	2695	CTGGATCGG	TTCAAAAGAT	TCGGGAGCCGGCTGGTTCAGATTGAGAAATCGGATCAAGACG	2754
DB	4321	CTGGAGGTG	TTCAACCGGT	TACGACCGGCTGGTGGAGATCGAGAGCAAGGTGGTGGC	4380
QY	2755	ATGAACGAC	AGTCCG	GACTTGAAACCGGAACCGGAGCGGCTGTGGAAATGCCGTACATGCTG	2814
DB	4381	ATGAACCAT	GAACCCG	AGCTCAAGAACCGCAACCGGCCGGCTAAGTTTCCCTACATGCTG	4440
QY	2815	CTGTACCCCA	ACACGT	CGGACGTTACCGGCGAGAAAGCCGAGGGGCTTACTGCCATGGGC	2874
DB	4441	CTCTACCCCA	ACACCT	CCGACCAAGGGCG---CCGCTGCCGGGCTTACCGCCAAGGGC	4497
QY	2875	ATTCCCAAC	AGCATCT	CCCATATGAGCCTGGGCA	2907
DB	4498	ATCCCCAAC	AGCATCT	CCCATCTAATCTAAGCCA	4530

RESULT 8

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US-09-751-687-8
; Sequence 8, Application US/09751687
; Patent No. 6660915
; GENERAL INFORMATION:
; APPLICANT: Douma, Anneke
; APPLICANT: Doderer, Albert
; APPLICANT: Cameron-Mills, Verena
; APPLICANT: Skadhauge, Birgitte
; APPLICANT: Bech, Lene
; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY
; FILE REFERENCE: 11225.11US01
; CURRENT APPLICATION NUMBER: US/09/751,687
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 4663
; TYPE: DNA
; ORGANISM: Hordeum vulgare
US-09-751-687-8

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	Query Match	19.1%;	Score 599;	DB 4;	Length 4663;
	Best Local Similarity	59.5%;	Pred. No. 2.3e-114;		
	Matches 1533;	Conservative 0;	Mismatches 575;	Indels 469;	Gaps 12;
QY	734	ACACCTATCTGCCGAGCAAAATGCCGGCGGCTTGCTGCTTATCGGCAAGATGAGTCA	793		
DB	2020	AGACGTACCTGCCGAGCCAGATGCCGGCGGCTGAAGCCGTACCGCGACGACGAGTCC	2079		
QY	794	AGATTCTCCGTGGCGAGCATAAATCTTGGACCATACCGAGCATGATCGCGTCTACCGTT	853		
DB	2080	GGAACCTGCGTGGCGAGCACAGCAGGGCCCGTACCAGGAGCACGCCGCATCTACCGCT	2139		
QY	854	ACGACTACTACAATGACCTTGGTGATCCCGACAAGGGCGAAGAGCACGCTCGGCCGATCC	913		
DB	2140	ACGACGTCTACAACGACCTCGGCG-----AGGGCCGCCCCCATCC	2178		
QY	914	TCGGTGGCAGCCAGCAACACCCCGTATCCCGCTCGCTGCAGAACTGGCCGGCACCCCAACAA	973		

Db	2179	TCGGCGGCAACTCCGACCACCCCTTACCCGCGCGCGCGCCGACGGAGCGCAAGCCCAACG	2238
Qy	974	AGAAAGACCCAAATTCGGAGAGCAGGCTTTTCCTGCTGAACCTGAACATCTACGTCCCGC	1033
Db	2239	CCAGCGACCCGAGCCTGGAGAGCCGGCTGTCCGTGCTGGA--GCAGATCTACGTGCCGC	2295
Qy	1034	GTGACGAACGCTTTGGGCATCTCAAGATGTCGGACTTCTTGGGTACTCGCTGAAGACGA	1093
Db	2296	GGGACGAGAAGTTCGGCCACCTCAAGACGTCCGACTTCTCTGGGTACTCCATCAAGGCCA	2355
Qy	1094	TCATCGAGGCTGTCTTCCAACACTGGGACTTTCGTGATGACACGCCCAAGGAGTTTCG	1153
Db	2356	TCACGCGAGGCACTCTGCCGCCGTGCGCACTACGTGGACACCAACCCCGCGGAGTTTCG	2415
Qy	1154	ATTCTGTTGAGGATATCTCTCGGGCTCTACGAGCTGGGCCACGAGGCCACCAACACCCAC	1213
Db	2416	ACTCTTCCAGGACATCATCAACCTCTATGAGGGCGGCATCAAGCTGCCCAAGGTGGCCG	2475
Qy	1214	TGATAGCAGAGATCAGGAAGAAGATCCCGAGCTGCGAGTTCCTTCGAAGCATTCGCGCAACG	1273
Db	2476	CCCTGGAGGAGTCCGTAAGCAGTTCCCGTCCAGCTCATCAAGGACCTCTCCCGCTCG	2535
Qy	1274	GTAGCCATGACCACCCGCTAAAGATGCCCTTCCAAATGTCTCAAAATCAGATGTGTGA	1333
Db	2536	GCGGC--GACTCCCTGCTTAAGCTCCCGTGCGCCACATCATC-----	2576
Qy	1334	AAAAGGCTCCGAGTTTAAGTTTGGCTGGAGGACTGACGAAGAGTTCGCGAGAGACAC	1393
Db	2577	-----CAGGAGAACAGCAGGCGTGGAGGACCGACGAGGAGTTCGCACGGGAGGTGC	2628
Qy	1394	TTGCAGGCGTGAACCCAGTAATCATCAAAAGTCTGAC-----	1430
Db	2629	TCGCCGCGTCAACCCGGTTCATGATCACGGCTCTCACGGTGAGTCAGCGATTATTGTTC	2688
Qy	1431	-----	1430
Db	2689	ATTGTGTGTATGGTGTCCATGGTGAGAAAGTCAGATCTTGATTTTGGTTGGTTCGCA	2748
Qy	1431	-----GGAGTTCCTCCCGCTAAAAGCACCCCTGGACCCCAAGGCAG	1467
Db	2749	TGCACGCATGCTGCATGCATGCAGGAGTTCCCGCCAAAAGTAGTCTGACCCCTAGCAAG	2808
Qy	1468	TACGGAGACCAACAGCAAGATCACTGAAGCTCACATCCGGCATACATGGGAGGCGCTG	1527
Db	2809	TTTGGTGACCAACAGCACCATCACGCGGAGCACATAGAGAAGAACCTCGAGGGGCTC	2868
Qy	1528	TCGGTGCAGA-----	1537
Db	2869	ACGGTGCAGCAGGTAATTGGTCCAAGCCATCGACATCAACTATGATTTACCTAGGAGTAA	2928
Qy	1538	-----	1537
Db	2929	TTGGTAGCTGTAGATAAATTGGCTTCGTTGCAATTAATTGATGCTGGCCGATCAAGTGA	2988
Qy	1538	-----ACGCATGAGGAACAAGAGGCTCTTCATCTCTAGACCCAC	1575
Db	2989	TCGTATTGGGTTGAAATTTGCAGGCGCTGGAAAGCAACAGGCTGTACATCTTGTATCAC	3048
Qy	1576	CATGACCAATTTCATGCCGTACCTCGACGAGATCAACGAGCTGGAGGGGAATTCATCTAC	1635
Db	3049	CATGACCCGGTTTCATGCCGTTTCCCTGATCGACGCTCAACAACCTGCCCCGCAACTTCATCTAC	3108
Qy	1636	GCCAGCAGGACCCCTACTGTTTCCCTGAAGGACGATGGCACGCTGAAGCCCTGGCCATCGAG	1695
Db	3109	GCCACGAGGACCCCTCTTCTTCCCTGCGGCGCAGCGAGGCTCACGCCGCTCGCATCGAG	3168
Qy	1696	CTGAGCCTGCCACCCCTGACGGCCAGCAGCGCGGCGGGTCAAGAGGTGTACACCCCG	1755
Db	3169	CTGAGCGAGCCCATCATCCAGGGCGGCTTACCACGGCCAAAGAGCAAGGTTTACACGCCG	3228
Qy	1756	GCTCACACCCG--CGTCGAGGGCCACGCTGGCAGCTCGCCAAGGCTTATGCTCGGTA	1812

Db 3229 GTGCCCAGCGGCTCCGTGCGAAGGCTGGGTGGGAGCTCGCCCAAGGCCTACGTGCGCCGTC 3288
QY 1813 AACGACTCTGCTGGCATCAGCTGATCAGCCACT----- 1846
Db 3289 AATGACTCCGGGTGGCACCAGCTCGTCAGCCACTGGTACGTTCTCCACGGTCGATGTGAT 3348
QY 1847 -----GGCTGAA 1853
Db 3349 TCAGTCAGTCGATGCACAACAACACTGATCGAATAATGATTGATTGAAACGCCAGGCTGAA 3408
QY 1854 CACGCACCGGGTATCGAGCCGTTTCGTAATCGCGACAAACCCGCAGCTCAGCGTGGTGCA 1913
Db 3409 CACTCACGCGGTGATGGAGCCGTTTCGTGATCTCGACGAACCCGCACCTTAGCGTGACGA 3468
QY 1914 TCCCGTGCACAAGCTGCTGAGCCCGCACTACCGTGACACGCTGAACATCAACGCCCTGGC 1973
Db 3469 CCCGGTGACAAGCTGCTGAGCCCGCACTACCGGCACACCATGACCATCAACGCCGTGGC 3528
QY 1974 ACGCCAGACACTCATCAACCGCCGGCGGTCTTCGAGCGCACCGTGTTCCTGCAAACTA 2033
Db 3529 GCGGCAGACGCTCATCAACCGCCGGCGGCATCTTCGAGATGACGGTGTTCCTGGGCAAGTT 3588
QY 2034 CGCGCTGGGGATGTGGCAGACGCTGTACAAGAGCTGGAATTTCAACGAGCAGGCTCTCC 2093
Db 3589 CGCGTTGGGGATGTGGCCCGTGGTGTACAAGGACTGGAAGTTACCGAGCAGGGACTGCC 3648
QY 2094 AGCAGATCTCGTCAAG----- 2109
Db 3649 GGACGATCTCATCAAGAGGTACGTACTGTGTAATGTTATGAATGTGTAAACAATTTGG 3708
QY 2110 -----AGAGTGTGGCTGTGCCGGAC 2130
Db 3709 GCGTCTCGCTCACTGACAGGAACGTGGTAAAAAATGCAAGGCGCATGGCGGTGGAGGAC 3768
QY 2131 CAGTCAAGCCCATATGGTGTCCGACTGCTGATCAAGGACTACCCCTATGCCGTTGACGGG 2190
Db 3769 CCGTCGAGCCCGTACAAGGTGCGGTTGCTGTTGTCGGACTACCCGTACCGCGCGGACGGG 3828
QY 2191 CTGCTCATCTGGTGGCGGATCGAGCGGTGGTCAAGGAGTACCTGGACATCTACTACCTT 2250
Db 3829 CTGGCGATCTGGCACGCCATTGAGCAGTACGTGAGCGAGTACCTGGCCATCTACTACCCG 3888
QY 2251 AACGACGGCGAGCTCCAGCGTGACGTGGAGCTGCAGGCGTGGTGAAGGAGGTGCGTGAG 2310
Db 3889 AACGACGGCGTGTGACGGCGATACGGAGGTGCAGGCGTGGTGAAGGAGACGCGCGGAG 3948
QY 2311 GAGCGCACGGGACCTCAAGGACCGAGACTGGTGGCCCAAGATGGACACCGTCCAGCAG 2370
Db 3949 GTCGGGCACGGGACCTCAAGGACGCCCATGTTGGTGGCCCAAGATGCAAAAGTGTGCGGGAG 4008
QY 2371 CTGGCTAGGGCGTGACGACCATCATCTGGTGGCATCCGCGCTGCACGCGGTGTGTCAAC 2430
Db 4009 CTGGCCAAAGCGTGCACCAACCATCATCTGATCGGTCGCGCTGCATCGCGCAGTCAAC 4068
QY 2431 TTTGGGAGTACCCTATACCGCGGTACCTCCGAACCGCGCGACGGCCAGCCGCGCCCG 2490
Db 4069 TTCGGGCACTACCCCTACGCGGGTTCCTCCGAACCGCGCGACGGTGAAGCCGCGCGC 4128
QY 2491 ATGCGGAGCGCAGGCACCGACTACAAGAAGCTGGGAGCGGGGCGAGAGGAGCGGAC 2550
Db 4129 ATGCGGAGCGCGGACCGAGGAGTACGCGGAGCTGG-----AGCGGACCGCGGAG 4179
QY 2551 ATGGTGTTCATCCGCACCATCACGAGCCAGTTCAGACCATCTCTGGCATCTCGTCAATC 2610
Db 4180 CGGGCTTCATCCACACCATCACGAGCCAGATCCAGACCATCATCGCGTGTGCTGTG 4239
QY 2611 GAGATCTCTCAAGCACTCTCTCCGACGAGGTGTACCTCGCCAGCGTGCAGGACCTGAT 2670
Db 4240 GAGGTGTGTGAAGCACTCTCTCCGACGAGTGTACTCTGGGACGCGGACACCGCGGA- 4298
QY 2671 CGCTGAGCTCAGACGCCCAAGGCGTGGATGCGTTCAAAAGATTCGGGAGCGCGCTGGTG 2730
Db 4299 --GTGACCTCGGACCCCAAGGCCCTGGAGGTGTTCAAGCGGTTTCAGCGGTTCCAGCGGCTGGTG 4356

QY 2731 CAGATTGAGATCGGATCAAGACGATGAACGACAGTCCGGACTTGAAGAACCGGAAGGG 2790
Db 4357 GAGATCGAGAGCAAGGTGGTGGCATGAACCATGACCCGGAGCTCAAGAACCGCAACGGC 4416
QY 2791 CCTGTGAAATGCGGTACATGCTGTGTACCCCAACACACGTCGGAAGTTACCGGCGAGAAG 2850
Db 4417 CCGGCTAAGTTTCCCTACATGCTGTCTACCCCAACACACCTCCGACCAACAGGGCG--CC 4473
QY 2851 GCCGAGGGGCTTACTGCCATGGGCAATCCCAACAGCATCTCCATATGAGCCTGGCA 2907
Db 4474 GCTCCGGGCTTACCGCAAGGGCATCCCAACAGCATCTCCATTAATCTAAGCCA 4530

RESULT 9

US-09-313-294A-3908
; Sequence 3908, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 3908
; LENGTH: 302
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700282343H2
; NAME/KEY: unsure
; LOCATION: 30, 38, 50, 73, 85, 104, 224, 246, 259, 278, 281, 294
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-3908

Query Match 8.6%; Score 270.2; DB 4; Length 302;
Best Local Similarity 94.6%; Pred. No. 6.6e-47;
Matches 283; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

QY 2545 GCGGACATGGTGTTCATCCGACCATCACCAGCCAGTTCAGACCATCTCTGGGCACTCG 2604
Db 1 GCGGACATGGTGTTCATCCGACCATCAGNAGCCAGTNCAGACCATCCNGGGCATCTCG 60
QY 2605 CTATCGAGATCCTCTCCAAGCACT-CCTCCGACGAGGTGTACCTCGGCCAGCGTGACGA 2663
Db 61 CTATCGAGATCCTCTCCAAGCACTCCGAGAGGTGTACNTCGGCCAGCGTGACGA 120
QY 2664 GCCTGATCGTGGACGTCAGACGCAAGGGCGCTGGATGCGTTCAAAAGATTCCGGAGCCG 2723
Db 121 GCCTGATCGTGGACGTCAGACGCAAGGGCGCTGGATGCGTTCAAAAGATTCCGGAGCCG 180
QY 2724 GCTGGTGCAGATTGAGAATCGGATCAAGACGATGAACGACAGTCCGGACTTGAAGAACC 2783
Db 181 GCTGGTGCAGATTGAGAATCGGATCAAGACGATGAACGACAGTNCGGACTTGAAGAACC 240
QY 2784 GAAGGGCCCTGTGGAATGCCGTACATGCTGTGTACCCCAACACAGTTCGGACGTTACCG 2842
Db 241 GAAGNGCCTGTGGAATNCCGTACATGCTGTGTACNCCNACACGTCGGGCGNTACCG 299

RESULT 10

US-09-313-294A-6360
; Sequence 6360, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.

; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 6360
; LENGTH: 282
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700351661H1
; NAME/KEY: unsure
; LOCATION: 55, 64, 68, 85, 241, 246, 250-251, 253-254
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-6360

Query Match 5.1%; Score 160.4; DB 4; Length 282;
Best Local Similarity 77.0%; Pred. No. 2.9e-24;
Matches 214; Conservative 0; Mismatches 61; Indels 3; Gaps 2;

QY 2247 CCCTAACGACGGGAGCTCCAGCGTGCAGTGGAGCTGCAGGCGTGGTGAAGGAGTGCG 2306
Db 1 CCCCAACGACGGGAGCTCCAGCGTGCAGGCGTGGTGAAGGAGTGCG 60

QY 2307 TGAGGAGGCGGACGGGACCTCAAGGACCGAGA--CTGGTGGCCAGGATGGACACCGTC 2364
Db 61 CGANGTCNGGACGGCGGACCTCAANAGACCGGAACCTGGTGGCCCAAGATGCAGACGCTG 120

QY 2365 CAGCAGCTGGTAGGGCGTGCAGCAGCATCATCTGGTGGCATCCGCGTGCACGGCGT 2424
Db 121 GCCGAGCTGGTCAAGGCGCTGCACCACCATCATCTGGATCGCTGGCGCTCCACGGCGCC 180

QY 2425 GTCAACTTTGGGAGTACCCATACCGCGGTACCTCCCGAACCGCCGACGGCCAGCGG 2484
Db 181 GTCAACTTCGGGAGTACCCGTCAGCGCGGTA-CTCCCGAACCGCCGCTCCGTCAGCGG 239

QY 2485 CGCCCGATGCCGAGCCAGGCGAGCCAGCCAGCTACAGAA 2522
Db 240 ANGCGNTGCGNNGNCCGGGCGAGCGAGTACGCGGA 277

RESULT 11
US-09-313-294A-4946
; Sequence 4946, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Ialgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 4946
; LENGTH: 298
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700349323H1
US-09-313-294A-4946

Query Match 5.0%; Score 155.8; DB 4; Length 298;
Best Local Similarity 72.2%; Pred. No. 2.6e-23;
Matches 216; Conservative 0; Mismatches 82; Indels 1; Gaps 1;

QY 1993 GCCGGCGGCTCTTCGAGCGCACCGTGTTCCTGTCAAAGTACCGCTGGGGATGTCGGCA 2052
Db 1 GCCGGCGGCTCTTCGAGATGACCGGTATTCGCGGCAAGTACCGCATCGAGATCTCTCTCC 60

QY 2053 GACGTGTACAAGAGCTGGAATTTCAACGAGCAGGCTCTCCGAGCAGATCTCGTCAAGAGA 2112
Db 61 AAAGTCTACGGCAGCTGGAATTTTCAACGAGCAGGCTCTCCGAGCAGATCTCATCAAGCGA 120

QY 2113 GGTGTGGCTGTGCGGACCAAGTCAAGCCCATATATGGTGTCCGACTGTCTGATCAAGGACTAC 2172
Db 121 GGATGGCGCTTCCAGATCCGTCGAGCCCTACAAGTGGCGTGTGATCGAGGACTAC 180

QY 2173 CCCTATGCCGTTGACGGGCTCGTCAATCTGGTGGCGATCGAGCGGTGGTCAAGGAGTAC 2232
Db 181 CCGTACGCTCGAGCGGCTGGCGGTGGG-CAGCCATCGAGCAGTGGGTGACGGAGTAC 239

QY 2233 CTGGACATCTACTACCTTAACGACGGCGAGCTCCAGCGTGCAGCTGCAGGCGTG 2291
Db 240 CTGGCCATCTACTACCCCAACGACGGCGTGTGCAGGCCGAGCTGCAGGCGTG 298

RESULT 12
US-08-181-271A-40
; Sequence 40, Application US/08181271A
; Patent No. 5614395
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/181,271A
; FILING DATE: 13-JAN-94
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667

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; FILING DATE: 8-MAR-1988
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT 1989
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 340 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-181-271A-40

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Query Match	4.3%;	Score 135;	DB 1;	Length 340;
Best Local Similarity	65.3%;	Pred. No. 5.3e-19;		
Matches 226;	Conservative 0;	Mismatches 112;	Indels 8;	Gaps 2;
QY	1352	AGTTTGGCTGGAGGACTGACGAAGAGTTTCGCGAGAGAGACACACTTGCAGGCGCTGAACCCAG	14111	
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QY	1412	TAATCATCAAAACGCTGACGGAGTTCCCGCTAAAGACACCCCTGGACCCCAAGGCAGTACG	14711	
Db	61	ACATCATCACCCGCTGAACGTGTTCCCTCCGAGGAGCACGNTTGA-----AGGCTACG	114	
QY	1472	GAGACCACACCAGCAAGATCACTGAAGCTCACATCCGGGCATAACATGGGAGGCCCTGTGCGG	15311	
Db	115	GTGACCAGACGAGCAAGATCACGGTGGAGCACATCCAACACAACCTCGGNAAGCTCAACG	174	
QY	1532	TGCAGAAACGCACTGAGGAACAAGAGGCTCTTTCATCCTAGACCACCATGACCATTCATGC	15911	
Db	175	TCGACAAAGGCAATCGACGCCAAGAGGCTCTTTCATCCTAGACCACCAACGACATTCATGC	234	
QY	1592	CGTACCTCGACGAGATCAACGAGCTGGAGGGGAATTTC--ATCTACGCCAGCAGGACCTT	16499	
Db	235	CTCACCTGTAAAGATCAACAGTCTCCCAAACACATTCGGTCTTACGNCAACGAGCGCT	294	
QY	1650	ACTGTTCTTGAAAGACGATGGCACGCTGAAGCCCTGGCCCATCGAG	1695	
Db	295	GCTCTTCCTGCAAGATGACGGGACTCTCAAGNCAATCGNCATCGAG	340	

RESULT 13
US-08-449-315-40
; Sequence 40, Application US/08449315
; Patent No. 5650505
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,315
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT 1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991


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QY 1352 AGTTTGGCTGGAGGACTGACGAAGAGTTCCGGAGAGAGACACTTGAGGCGTGAACCCAG 1411
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Db 1 AGCTCGNGTGGCGAACGGACGAGGAGTTCCGCCGGGAGATGCTCGCCGNGNCTCAACCCAC 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1412 TAATCATCAAAAGCTCTGACGGAGTTCCCGCTAAAGCACCCCTGGACCCAAAGGCAGTACG 1471
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 ACATCATCACCCGCTGAACGTCGTGTTCCCTCCGAGGAGCACGNTTGA-----AGGTACG 114
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1472 GAGACCACACCAGCAAGATCACTGAAGCTCAATCCGGGCATAACATGGGAGGCGCTGTCCG 1531
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 115 GTGACCAGACGAGCAAGATCACGGTGGAGCACATCCAAACAACTCGGNAAGCTCAACG 174
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1532 TGCAGAACGCACTGAGGAACAAGAGGCTCTTATCCTAGACCACTGACCATTTTCATGC 1591
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 175 TCGACAAGGCAATCGACGCCAAGAGGCTCTTATCCTAGACCACTGACCAACTTCATGC 234
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1592 CGTACCTCGACGAGATCAACGAGCTGGAGGGGAACTTC--ATCTACGCCAGCAGGACCCCT 1649
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 235 CTCACCTGCTAAAGATCAACAGTCTCCCAAAACACATTCGTCCTTACGNCACCCAGGACGCT 294
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1650 ACTGTTCTGAAAGGACGATGGCACGCTGAAGCCCTGGCCATCGAG 1695
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 295 GCTCTTCTGCAAGATGACGGGACTCTCAAGNCAATCGNCATCGAG 340
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Search completed: March 23, 2004, 03:49:15
Job time : 232 secs

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QY	1141	CCCAAGGAGTTCGATTCTGTTTGGAGATATCCTCGGGCTCTACGAGCTGGGCCACAGAGGCA	1200
Db			
QY	1201	CCCAAGGAGTTCGATTCTGTTTGGAGATATCCTCGGGCTCTACGAGCTGGGCCACAGAGGCA	1260
Db			
QY	1261	CCCAACAACCCACTGATAGCAGAGATCAGGAAGAAGATCCCCAGCGAGTTCCTTCGAAGC	1320
Db			
QY	1321	ATCTGCGGAACGGTAGCCATGACCAACCCGCTAAAGATGCCCTTCCAAATGTCATCAAA	1380
Db			
QY	1381	TCAGATGTGTGAAAAAGGCTCCGGAGTTTAAAGTTTGGCTGGAGGACTGACGAAGAGTTC	1440
Db			
QY	1441	GCGAGAGACACTTGACGGCGTGAACCCAGTAATCATCAACCGTCTGACGGAGTTCCTCC	1500
Db			
QY	1501	GCTAAAGCACCCCTGGACCCAAAGGCAGTACCGAGACCAACAGCAAGATCACTCAAGCT	1560
Db			
QY	1561	CACATCCGGCATTAACATGGGAGGCCCTGTCTGGTGCAGAACGCACCTGAGGAACCAAGAGGCTC	1620
Db			
QY	1621	TTCATCTTAGACCAACCATGACCATTTTCATGCCGTACCTCGACGAGATCAACGAGCTGGAG	1680
Db			
QY	1681	GGGAACCTTCATCTACGCCAGCAGGACCCCTACTGTCTCTGAAGGACGATGGCACCGCTGAAG	1740
Db			
QY	1741	AGGTGTACACCCCGGCTCACACCGGCGTCGAGGGCCACGTCCTGGCAGCTCGCCAAAGCT	1800
Db			
QY	1801	TATGCTGCGTAAACGACTCTGCCCTGGCATCAGCTGATCAGCCACTGGCTGAACACGCAC	1860
Db			
QY	1861	GCGGTGATCGAGCCGTTTCGTAATCGCGACAAACCGGCGAGCTCAGCGTGGTGCATCCCGTG	1920
Db			
QY	1921	CACAAGCTGCTGAGCCCGCACTACCGTGACACGCTGAACATCAACGCCCTGGCACGCCAG	1980
Db			
QY	1981	ACACTCATCAACGCCCGGCGCTCTTCGAGCGCACCGTGTTCCTGTCAAAGTACGCGGTG	2040
Db			
QY	2041	GGGATGTCGGCAGACGCTGTACAAGAGCTGGAATTTCAACGAGCAGGCTCTCCAGCAGAT	2100
Db			
QY	2101	CTCGTCAAGAGAGGTGTGGCTGTGCCGACCCAGTCAAGCCCATATGGTGTCCGACTGCTG	2160
Db			
QY	2161	ATCAAGGACTACCCCTATGCCGTTGACGGGCTCGTCATCTGGTGGCGATCGAGCGGTGG	2220
Db			
QY	2221	GTCAAGGAGTACCTGGACATCTACTACCCCTAACGACGGCGAGCTCCAGCGTGCAGCTGGAG	2280

Db	2221	GTCAAGGAGTACCTGGACATCTACTACCCATAACGACGGCGAGCTCCAGCGTGACGTGGAG	2280
QY	2281	CTGCAGGCGTGGTGAAGAGGAGTCCGTGAGGAGCGGCACGGCGACCTCAAGGACCGAGAC	2340
Db	2281	CTGCAGGCGTGGTGAAGAGGAGTCCGTGAGGAGCGGCACGGCGACCTCAAGGACCGAGAC	2340
QY	2341	TGGTGGCCCAAGATGGACACCGTCCAGCAGCTGCTAGGGCGGTGCACGACCATCATCTGG	2400
Db	2341	TGGTGGCCCAAGATGGACACCGTCCAGCAGCTGCTAGGGCGGTGCACGACCATCATCTGG	2400
QY	2401	GTGGCATCCGCGCTGCACGCGGCTGTCAACTTTGGGCAGTACCCATACGCCCGGTACCTC	2460
Db	2401	GTGGCATCCGCGCTGCACGCGGCTGTCAACTTTGGGCAGTACCCATACGCCCGGTACCTC	2460
QY	2461	CCGAACCGGCCGACGGCCAGCCGGCGCCCGATGCCGGAGCCAGGCACCGACTACAAG	2520
Db	2461	CCGAACCGGCCGACGGCCAGCCGGCGCCCGATGCCGGAGCCAGGCACCGACTACAAG	2520
QY	2521	AAGCTGGGAGCGGGGCGAAGGAGGCGGACATGGTGTTCATCCGCAACATCACCGACCCAG	2580
Db	2521	AAGCTGGGAGCGGGGCGAAGGAGGCGGACATGGTGTTCATCCGCAACATCACCGACCCAG	2580
QY	2581	TTCCAGACCATCCTGGGCATCTCGCTCATTCGAGATCCTCTCCAAGCACTCCTCCGACGAG	2640
Db	2581	TTCCAGACCATCCTGGGCATCTCGCTCATTCGAGATCCTCTCCAAGCACTCCTCCGACGAG	2640
QY	2641	GTGTACCTCGGCCAGCGTGACGAGCCCTGATCGCTGGACGTCAGACGCCAAGGCGCTGGAT	2700
Db	2641	GTGTACCTCGGCCAGCGTGACGAGCCCTGATCGCTGGACGTCAGACGCCAAGGCGCTGGAT	2700
QY	2701	GCGTTCAAAAGATTCCGGAGCCGCGCTGGTGCAATTGAGAAATCGGATCAAGACGATGAAC	2760
Db	2701	GCGTTCAAAAGATTCCGGAGCCGCGCTGGTGCAATTGAGAAATCGGATCAAGACGATGAAC	2760
QY	2761	GACAGTCCGGACTTTGAAGAACCCGGAAGGGGCCCTGTGGAATGCCGTACATGCTGCTGTAC	2820
Db	2761	GACAGTCCGGACTTTGAAGAACCCGGAAGGGGCCCTGTGGAATGCCGTACATGCTGCTGTAC	2820
QY	2821	CCCAACACGTCGGACGTTACCGGCAGAAAGCCGAGGGGCTTACTGCCATGGGCATTCCC	2880
Db	2821	CCCAACACGTCGGACGTTACCGGCAGAAAGCCGAGGGGCTTACTGCCATGGGCATTCCC	2880
QY	2881	AACAGCATCTCCATATGAGCCCTGGGCAGATTGTGTCTCGTAGTAAATTTGTTGTCTGCGC	2940
Db	2881	AACAGCATCTCCATATGAGCCCTGGGCAGATTGTGTCTCGTAGTAAATTTGTTGTCTGCGC	2940
QY	2941	CGTCCGATGTGTTTCTTCATTTGGTTTTTGTTCAGTCTCAGGGTAGGGATGGAGATCATACC	3000
Db	2941	CGTCCGATGTGTTTCTTCATTTGGTTTTTGTTCAGTCTCAGGGTAGGGATGGAGATCATACC	3000
QY	3001	ATGATCTTTGTAGGTTGAGAGAGGAGTCCACCGTTGAAATATTGTTGTCTATGTATGTAAT	3060
Db	3001	ATGATCTTTGTAGGTTGAGAGAGGAGTCCACCGTTGAAATATTGTTGTCTATGTATGTAAT	3060
QY	3061	TCCTTGGTTAATAATAAGTTTCGTCACTTTCATTTCTTAAAAAATAAAAAA	3120
Db	3061	TCCTTGGTTAATAATAAGTTTCGTCACTTTCATTTCTTAAAAAATAAAAAA	3120
QY	3121	AAAAAAAAAAAAAAG	3134
Db	3121	AAAAAAAAAAAAAAG	3134

RESULT 2

RESUL 2
US-10-132-350-21

US-10-132-330-21
; Sequence 21, Application US/10132350

; sequence 21, Application US/101
; Publication No. US20030166855A1; PUBLICATION NO: US20
: GENERAL INFORMATION:
: GENERAL INFORMATION:; GENERAL INFORMATION: Pedro A. Navarro
: APPLICANT: Acevedo:

APPLICANT: Acevedo, Pedro A. N

APPLICANT: Duvick, Jonathan P

APPLICANT: DUVICK, Jonathan P.
APPLICANT: Kolomiets, Mikhailo V.

APPLICANT: KOLOMIETS, Mikhail
APPLICANT: SIMMONS, Carl R.

```

; TITLE OF INVENTION: Lipoxigenase Polynucleotides and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286,889
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 3122
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (224)...(2887)
; OTHER INFORMATION: LOX5
; US-10-132-350-21

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Query Match	99.6%	Score 3120.4	DB 14;	Length 3122;
Best Local Similarity	100.0%	Pred. No. 0;		

QY	12	GCCGAGGCGAGCAGCGCTCGCCGCGCTATATATCGCGGCGCAGGGGCGAGGAGTTCACA	71
DB	1	GCCGAGGCGAGCAGCGCTCGCCGCGCTATATATCGCGGCGCAGGGGCGAGGAGTTCACA	60
QY	72	CTTCCATACACGCGCTGCTTGTGCCCTTCCCTTCCCTTGCCTTGCCTTCGCTTATTGCCGGC	131
DB	61	CTTCCATACACGCGCTGCTTGTGCCCTTCCCTTCCCTTGCCTTGCCTTCGCTTATTGCCGGC	120
QY	132	ACATCACATCGGCAGGCGAGGGACGGAGCGAGCAGGGAAGCCCATCCACGAGCCAGCCAC	191
DB	121	ACATCACATCGGCAGGCGAGGGACGGAGCGAGCAGGGAAGCCCATCCACGAGCCAGCCAC	180
QY	192	CGCGTTCTTGAGAAGCGAGGAGCGAGAAAGCGAAGAGCGGCCCATGTTCTGGCACGGGGT	251
DB	181	CGCGTTCTTGAGAAGCGAGGAGCGAGAAAGCGAAGAGCGGCCCATGTTCTGGCACGGGGT	240
QY	252	CGCGACCGGCTGACGSGAAAGAACAGGAGGCGCTGGAGCGAGGGCAAGATCCGCGGCAC	311
DB	241	CGCGACCGGCTGACGSGAAAGAACAGGAGGCGCTGGAGCGAGGGCAAGATCCGCGGCAC	300
QY	312	GGTGAGGCTGGTCAAGAGGAGGTGCTGGACGTCGCGGACTTCAACGCCCTCGCTCCTCGA	371
DB	301	GGTGAGGCTGGTCAAGAGGAGGTGCTGGACGTCGCGGACTTCAACGCCCTCGCTCCTCGA	360
QY	372	CGGCGTCCACAGGATCCTCGGCTGGGACGACGGCGCTCGCCTTCCAGCTCGTCAGCGCCAC	431
DB	361	CGGCGTCCACAGGATCCTCGGCTGGGACGACGGCGCTCGCCTTCCAGCTCGTCAGCGCCAC	420
QY	432	CGCGGCCGACCCACGAAACGGGGGCGGTGGCAAGGTGGGAAGGCGGCGCACCTGGAGGA	491
DB	421	CGCGGCCGACCCACGAAACGGGGGCGGTGGCAAGGTGGGAAGGCGGCGCACCTGGAGGA	480
QY	492	GGCGGTGGTGTGCTCAAGTCCACGGCGGACGGGAGACCGTGTAACGGGTGAGCTTCGA	551
DB	481	GGCGGTGGTGTGCTCAAGTCCACGGCGGACGGGAGACCGTGTAACGGGTGAGCTTCGA	540
QY	552	GTGGGACGAGTCGAGGGCATCCCGGGCGCGTCTTGTCAGGAACCTGCAGCACGCCGA	611
DB	541	GTGGGACGAGTCGAGGGCATCCCGGGCGCGTCTTGTCAGGAACCTGCAGCACGCCGA	600
QY	612	GTTCTTCTCAAGACGCTCACCTTCGAGGGCGTCCAGGCAAGGGCACCGTCGTCCTCGT	671
DB	601	GTTCTTCTCAAGACGCTCACCTTCGAGGGCGTCCAGGCAAGGGCACCGTCGTCCTCGT	660
QY	672	CGCCAACTCGTGGGTTACCCGCAACAGCTCTACTCCAGGAACGCATCTTCTTCGCCAA	731
DB	661	CGCCAACTCGTGGGTTACCCGCAACAGCTCTACTCCAGGAACGCATCTTCTTCGCCAA	720

QY	732	CGACACCTATCTGCGAGCAAAATGCCGGCGTGGTGCCCTTATCGGCAAGATGAGCT	791
Db	721	CGACACCTATCTGCGAGCAAAATGCCGGCGTGGTGCCCTTATCGGCAAGATGAGCT	780
QY	792	CAAGATTCTCCGTGGCGACGATAATCCTGGACCATACCAGGAGCATGATCGCGTCTACCG	851
Db	781	CAAGATTCTCCGTGGCGACGATAATCCTGGACCATACCAGGAGCATGATCGCGTCTACCG	840
QY	852	TTACGACTACTACAATGACCTTGGTGATCCCGACAAGGCGAAGAGCACGCTCGGCCGAT	911
Db	841	TTACGACTACTACAATGACCTTGGTGATCCCGACAAGGCGAAGAGCACGCTCGGCCGAT	900
QY	912	CCTCGGTGGCAGCCAAGAACACCCGTATCCCCGTCGTGCAGAACTGSCCGGCACCCCAAC	971
Db	901	CCTCGGTGGCAGCCAAGAACACCCGTATCCCCGTCGTGCAGAACTGSCCGGCACCCCAAC	960
QY	972	AAAGAAAGACCCCAATTTCGGAGAGCAGGCTTTTCTCTGTGAACCTTGAACATCTACGTCCC	1031
Db	961	AAAGAAAGACCCCAATTTCGGAGAGCAGGCTTTTCTCTGTGAACCTTGAACATCTACGTCCC	1020
QY	1032	GCGTGACGAACGCTTTGGGCATCTCAAGATGTTCGACTTCTTGGGTACTCGCTGAAGAC	1091
Db	1021	GCGTGACGAACGCTTTGGGCATCTCAAGATGTTCGACTTCTTGGGTACTCGCTGAAGAC	1080
QY	1092	GATCATCGAGGCTGTCTTCCAACACTGGGGACTTTCGTGATGACACGCCCCAAAGGAGTT	1151
Db	1081	GATCATCGAGGCTGTCTTCCAACACTGGGGACTTTCGTGATGACACGCCCCAAAGGAGTT	1140
QY	1152	CGATTGTTGAGGATATCCTCGGGCTCTACGAGCTGGGCCCCAGAGGCACCCAAACACCC	1211
Db	1141	CGATTGTTGAGGATATCCTCGGGCTCTACGAGCTGGGCCCCAGAGGCACCCAAACACCC	1200
QY	1212	ACTGATAGCAGAGATCAGGAAGAAGATCCCGAGGAGTTCCTTGAAGCATCTCTGCCGAA	1271
Db	1201	ACTGATAGCAGAGATCAGGAAGAAGATCCCGAGGAGTTCCTTGAAGCATCTCTGCCGAA	1260
QY	1272	CGGTAGCCATGACCAACCGCTAAAGATGCCCTTCCAAATGTCTCAAAATCAGATGTGTT	1331
Db	1261	CGGTAGCCATGACCAACCGCTAAAGATGCCCTTCCAAATGTCTCAAAATCAGATGTGTT	1320
QY	1332	GAAAAAGGCTCCGGAGTTTAAAGTTTGGCTGGAGACTGACGAAGAGTTTCGCAGAGAGAC	1391
Db	1321	GAAAAAGGCTCCGGAGTTTAAAGTTTGGCTGGAGACTGACGAAGAGTTTCGCAGAGAGAC	1380
QY	1392	ACTTGCAGGCGTGAAACCCAGTAATCATCAAACGTCTGACGGAGTTCCCGCTAAAAAGCAC	1451
Db	1381	ACTTGCAGGCGTGAAACCCAGTAATCATCAAACGTCTGACGGAGTTCCCGCTAAAAAGCAC	1440
QY	1452	CCTGGACCCAAAGGCAGTACGGAGACCACACAGCAAGATCACTGAAGCTCACATCCGGCA	1511
Db	1441	CCTGGACCCAAAGGCAGTACGGAGACCACACAGCAAGATCACTGAAGCTCACATCCGGCA	1500
QY	1512	TAAACATGGAGGCCTGTCCGTGCAGAACGCACTGAGGAACAAGAGGCTCTTTCATCCTAGA	1571
Db	1501	TAAACATGGAGGCCTGTCCGTGCAGAACGCACTGAGGAACAAGAGGCTCTTTCATCCTAGA	1560
QY	1572	CCACCATGACCATTTTCATGCCGTACCTCGACGAGATCAACGAGCTGGAGGGGAACTTCAT	1631
Db	1561	CCACCATGACCATTTTCATGCCGTACCTCGACGAGATCAACGAGCTGGAGGGGAACTTCAT	1620
QY	1632	CTAGCCAGCAGGACCCCTACTGTTCTTGAAGGACGATGGCACGCTGAAGCCCTTGCCCAT	1691
Db	1621	CTAGCCAGCAGGACCCCTACTGTTCTTGAAGGACGATGGCACGCTGAAGCCCTTGCCCAT	1680
QY	1692	CGAGCTGAGCCTGCCCAACCTGACGGCCAGCAGCGCGGCGCGGTACAGCAAGTGTACAC	1751
Db	1681	CGAGCTGAGCCTGCCCAACCTGACGGCCAGCAGCGCGGCGCGGTACAGCAAGTGTACAC	1740
QY	1752	CCCGGCTCACACCGGCGTGCAGGGCCACGTTCTGGAGAGCTGCCAAGGCTTATGCTGCGT	1811
Db	1741	CCCGGCTCACACCGGCGTGCAGGGCCACGTTCTGGAGAGCTGCCAAGGCTTATGCTGCGT	1800
QY	1812	AAACGACTCTGCCTGGCATCAGCTGATCAGCCACTGGCTGAACACGCACGCGGTGATCGA	1871

Db	1801	AAACGACTCTGCTGGCATCAGCTGATCAGCCACTGGCTGAACACGACCGGCTGATCGA	1866
QY	1872	GCCGTTTCGTAATCGCGACAAACCGGCAGCTCAGCGTGGTGTCATCCCGTGCACAAGCTGCT	1931
Db	1861	GCCGTTTCGTAATCGCGACAAACCGGCAGCTCAGCGTGGTGTCATCCCGTGCACAAGCTGCT	1920
QY	1932	GAGCCCGCACTACCGTGACACGCTGAACATCAACGCCCTTGGCAGCCGACACACTCATCAA	1991
Db	1921	GAGCCCGCACTACCGTGACACGCTGAACATCAACGCCCTTGGCAGCCGACACACTCATCAA	1980
QY	1992	CGCCGGCGGCTTTCGAGCGCACCGTGTCCCTGCAAAAGTACGGCTGGGGATGTCCGGC	2051
Db	1981	CGCCGGCGGCTTTCGAGCGCACCGTGTCCCTGCAAAAGTACGGCTGGGGATGTCCGGC	2040
QY	2052	AGACGTGTACAAGAGCTGGAATTTCAACGAGCAGGCTCTCCCAGCAGATCTCGTCAAGAG	2111
Db	2041	AGACGTGTACAAGAGCTGGAATTTCAACGAGCAGGCTCTCCCAGCAGATCTCGTCAAGAG	2100
QY	2112	AGGTGTGGCTGTGCCGGACCAAGTCAAGCCCATATGGTGTCCGACTGTGTATCAAGGACTA	2171
Db	2101	AGGTGTGGCTGTGCCGGACCAAGTCAAGCCCATATGGTGTCCGACTGTGTATCAAGGACTA	2160
QY	2172	CCCTATGCCGTTGACGGGCTCGTCACTCTGGTGGCGGATCGAGCGGTGGTCAAGGAGTA	2231
Db	2161	CCCTATGCCGTTGACGGGCTCGTCACTCTGGTGGCGGATCGAGCGGTGGTCAAGGAGTA	2220
QY	2232	CCTGGACATCTACTACCCTAACGACGGCGAGCTCCAGCGTGACGTGGAGTGCAGGCGTG	2291
Db	2221	CCTGGACATCTACTACCCTAACGACGGCGAGCTCCAGCGTGACGTGGAGTGCAGGCGTG	2280
QY	2292	GTGGAAGGAGGTGCGTGAGGAGGCGCACGGGACCTCAAGGACCGAGACTGGTGGCCCCAG	2351
Db	2281	GTGGAAGGAGGTGCGTGAGGAGGCGCACGGGACCTCAAGGACCGAGACTGGTGGCCCCAG	2340
QY	2352	GATGGACACCGTCAGCAGCTGGCTAGGCGGTGCACGACCATCATCTGGGTGGCATCCGC	2411
Db	2341	GATGGACACCGTCAGCAGCTGGCTAGGCGGTGCACGACCATCATCTGGGTGGCATCCGC	2400
QY	2412	GCTGCACCGGCTGTCAACTTTGGGCAGTACCCATACGCCGGGTACCTCCGAAACCGGCC	2471
Db	2401	GCTGCACCGGCTGTCAACTTTGGGCAGTACCCATACGCCGGGTACCTCCGAAACCGGCC	2460
QY	2472	GACGGCCAGCCGGCCCCGATGCCGGAGCCAGGCAGCCACGACTACAAGAACTGGGAGC	2531
Db	2461	GACGGCCAGCCGGCCCCGATGCCGGAGCCAGGCAGCCACGACTACAAGAACTGGGAGC	2520
QY	2532	GGGGCAGAAAGGAGCGGACATGGTGTTCATCCGCACCATCACCAGCCAGTTCAGACCAT	2591
Db	2521	GGGGCAGAAAGGAGCGGACATGGTGTTCATCCGCACCATCACCAGCCAGTTCAGACCAT	2580
QY	2592	CCTGGGCATCTCGCTCATCGAGATCCTCTCCAAGCACTCCTCCGACGAGGTGTACTCGG	2651
Db	2581	CCTGGGCATCTCGCTCATCGAGATCCTCTCCAAGCACTCCTCCGACGAGGTGTACTCGG	2640
QY	2652	CCAGCGTGACGAGCCTGATCGCTGGAAGTGAATTCGGATCAAGACGATGAACAGTCCGGA	2711
Db	2641	CCAGCGTGACGAGCCTGATCGCTGGAAGTGAATTCGGATCAAGACGATGAACAGTCCGGA	2700
QY	2712	ATTCGGGAGCCGGTGGTGAGATTCGGAATTCGGATCAAGACGATGAACAGTCCGGA	2771
Db	2701	ATTCGGGAGCCGGTGGTGAGATTCGGAATTCGGATCAAGACGATGAACAGTCCGGA	2760
QY	2772	CTTGAAGAACCCGGAAGGGCCCTGTGGAAATGCGGTAATGTGTGTACCCCAACACGTC	2831
Db	2761	CTTGAAGAACCCGGAAGGGCCCTGTGGAAATGCGGTAATGTGTGTACCCCAACACGTC	2820
QY	2832	GGACGTTACCGGCAGAAAGCCGAGGGGCTTACTGCCATGGGCATTCCTCAACAGCATCTC	2891
Db	2821	GGACGTTACCGGCAGAAAGCCGAGGGGCTTACTGCCATGGGCATTCCTCAACAGCATCTC	2880
QY	2892	CATATGAGCCTGGGCAGATGTGTCTCGTAGTAAATTTGTGTGCTGCCCGCTGCATGTG	2951

Db 2881 CATATGAGCCTGGGAGATTGTGTCTCGTAGTAAATGTTGTGCTGGGCGGTGCGATGTG 2940
Qy 2952 TTTCTTCATTGGTTTGTTCAGTCTCAGGGTAGGGATGGAGATCATACCATGATCTTTGT 3011
Db 2941 TTTCTTCATTGGTTTGTTCAGTCTCAGGGTAGGGATGGAGATCATACCATGATCTTTGT 3000
Qy 3012 AGGGTTGAGAGAGGAGTCCACGCTTGAATATTTGTTCATGTATGTAATCTTGGTTAAT 3071
Db 3001 AGGGTTGAGAGAGGAGTCCACGCTTGAATATTTGTTCATGTATGTAATCTTGGTTAAT 3060
Qy 3072 AATAAAGTTCGTGAGTTCATTTCTTAAAAAACAACAAAAAATAAAAAAATAAAAAA 3131
Db 3061 AATAAAGTTCGTGAGTTCATTTCTTAAAAAATAAAAAAATAAAAAAATAAAAAA 3120
Qy 3132 AA 3133
Db 3121 AA 3122

RESULT 3
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; Sequence 1810, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 1810
; LENGTH: 2917
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700202892_FLI
US-10-425-114-1810

Query Match 88.1%; Score 2760.2; DB 12; Length 2917;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2799; Conservative 0; Mismatches 28; Indels 2; Gaps 2;

Qy 262 CTGACGGGAAAGAACAGGAGGCGTGGAGCGAGGGCAAGATCCGGGCGACGGTGAGGCTG 321
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Qy 322 GTCAAGAAGGAGGTGCTGGACGTGGCGGACTTCAACGCCTCGTCTCGACGGCGTCCAC 381
Db 150 GTCAAGAAGGAGGTGCTGGACGTGGCGGACTTCAACGCCTCGTCTCGACGGCGTCCAC 209
Qy 382 AGGATCCTCGGCTGGACGACGGCGTGGCGGCTTCCAGCTCGTCAGCGCCACCGCGCCGAC 441
Db 210 AGGATCCTCGGCTGGACGACGGCGTGGCGGCTTCCAGCTCGTCAGCGCCACCGCGCCGAC 269
Qy 442 CCCAGCAACGGGGCGGTGGCAAGGTGGGGAAGCGGGCGCACCTGGAGGAGGCGGTGGTG 501
Db 270 CCCAGCAACGGGGCGGTGGCAAGGTGGGGAAGCGGGCGCACCTGGAGGAGGCGGTGGTG 329
Qy 502 TCGCTCAAGTCCACGGGCGGACGGGAGACCGGTGTACCGGGTGAGCTTCGAGTGGGACGAG 561
Db 330 TCGCTCAAGTCCACGGGCGGACGGGAGACCGGTGTACCGGGTGAGCTTCGAGTGGGACGAG 389
Qy 562 TCGCAGGGGCATCCCGGGCGCGTCTCGTGTGAGGAACTTGCAGCACGCGGAGTTCTTCCTC 621
Db 390 TCGCAGGGGCATCCCGGGCGCGTCTCGTGTGAGGAACTTGCAGCACGCGGAGTTCTTCCTC 449
Qy 622 AAGACGCTCACCCCTCGAGGGCGTCCCAGGCAAGGGCACCGTCTGCTCGTCCGCAACTCG 681

Db 450 AAGACGCTCACCCCTGAGGGCGTCCCGGCAAGGGCACCGTGTCTTCGTCGCCAACTCG 509
Qy 682 TGGGTCTACCCGACAAAGCTCTACTCCAGGAACGCTATCTTCTTCCGCAACGACACCTAT 741
Db 510 TGGGTCTACCCGACAAAGCTCTACTCCAGGAACGCTATCTTCTTCCGCAACGACATCTAT 569
Qy 742 CTGCCGAGCAAAATGCCGGCGGGCTTGGTGCCTTATCGGCAAGATGAGCTCAAGATTCTC 801
Db 570 CTGCCGAGCAAAATGCCCTGCGGCTTGGTGCCTTACCGGCAAGATGAGCTCAAGATTCTC 629
Qy 802 CGTGGCGACGATAATCCTGGACCATACACAGGAGCATGTCGGCTCTACCGTTACGACTAC 861
Db 630 CGTGGCGACGATAATCCTGGACCATACACAGGAGCATGTCGGCTCTACCGTTACGACTAC 689
Qy 862 TACAATGACCTTGGTATCCCGACAAGGGCGAAGAGCACGCTCGGCCGATCCTCGGTGGC 921
Db 690 TACAATGACCTTGGTATCCCGACAAGGGCGAAGAGCACGCTCGGCCGCTCCTCGGTGGC 749
Qy 922 AGCCAAGAACACCCGTATCCCGCTGCTGCAAACTGGCCGGCACCCAAACAAAGAAAGAC 981
Db 750 AGCCAAGAACACCCCGTATCCCGCTGCTGCAAACTGGCCGGCATCCAAACAAAGAAAGAC 809
Qy 982 CCAAATTCGGAGAGCAGGCTTTTCTGCTGAACCTGAACATCTACGTCCCGCTGACGAA 1041
Db 810 CCAAATTCGGAGAGCAGGCTTTTCTGCTGAACCTGAACATCTACGTCCCGCTGACGAA 869
Qy 1042 CGCTTTGGGCATCTCAAGATGTGCGACTTCTTGGGTACTCGTGAAGAGCATCTCGAG 1101
Db 870 CGCTTTGGGCATCTCAAGATGTGCGACTTCTTGGGTACTCGTGAAGAGCATCTCGAG 929
Qy 1102 GCTGTTCTTCCAACTGGGACTTTTCTGCTGATGACACGCCCAAGGAGTTCGATTTCGTTT 1161
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Db 1170 CCGGAGTTTAAAGTTGGCTGGAGGACTGACGAAGAGTTTCGCGAGAGAGACACTTGCAGGC 1229
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Db 1230 GTGAACCCAGTAATCATCAAAACGCTCTGACGGAGTTCCCGCTAAAAGCACCCCTGGACCCA 1289
Qy 1462 AGGCAGTACGGAGACCAACACGAGATCACTGAAGCTCACATCCGSCATAACATGGGA 1521
Db 1290 AGGCAGTATGGAGACCAACACGAGATCACTGAAGCTCACATCCGSCATAACATGGGA 1349
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Db 1410 CATTTTCATGCCGTACCTCGACGAGATCAACGAGCTTGAGGGGAACCTTCATCTACGCCAGC 1469
Qy 1642 AGGACCCCTACTGTTCTGAGGACGATGGACGCTGAAGCCCTGAAGCCCTGGCCATCGAGCTGAGC 1701
Db 1470 AGGACCCCTACTGTTCTCAAGGACGATGGACGCTGAAGCCCTGGCCATCGAGCTGAGC 1529
Qy 1702 CTGCCCCACCCCTGACGGCCAGCAGCGCGGCGGCTCAGCAAGGTGTACACCCCGGCTCAC 1761

Db 1530 CTGCCCCACCCTGACGGCCAGCAGCGCGCGGTGAGCAAGGTGTACACCCCGGCTCAC 1589
Qy 1762 ACCGGCGTCGAGGGCCACGTCCTGGCAGCTCGCAAGGCTTATGCCTCGCTAAACGACTCT 1821
Db 1590 ACCGGCGTCGAGGGCCACGTCCTGGCAGCTCGCAAGGCTTATGCCTCGCTAAACGACTCT 1649
Qy 1822 GCCTGGCATCAGCTGATCAGCCACTGGCTGAACAGCAGCAGCGGGTGTATCGAGCCGTTTCGTA 1881
Db 1650 GCCTGGCATCAGCTGATCAGCCACTGGCTGAACAGCAGCAGCGGGTGTATCGAGCCGTTTCGTA 1709
Qy 1882 ATCGCGACAAACCGGCGAGCTCAGCGTGGTGTATCCCGTGCACAAGCTCATCAACGCCCGGC 1941
Db 1710 ATCGCGACAAACCGGCGAGCTCAGCGTGGTGTATCCCGTGCACAAGCTCATCAACGCC - GCGGC 1769
Qy 1942 TACCGTGACACCGCTGAACATCAACGCCCTGGCAGCCAGACACTCATCAACGCCCGGC 2001
Db 1770 TACCGTGACACCGCTGAACATCAACGCCCTGGCAGCCAGACACTCATCAACGCC - GCGGC 1828
Qy 2002 GTCTTCGAGCGCACCGTGTTCCTGTC - AAAGTACGCGCTGGGGATGTCGGCAGACGTGTA 2060
Db 1829 GTCTTCGAGCGCACCGTGTTCCTGTC - AAAGTACGCGCTGGGGATGTCGGCAGACGTGTA 1888
Qy 2061 CAAGAGCTGGAATTTCAACGAGCAGCGCTCTCCAGCAGATCTCTGTCGAAGAGAGGTGTGGC 2120
Db 1889 CAAGACCTGGAATTTCAACGAGCAGCTCTCTCCAGCAGATCTCTGTCGAAGAGAGGTGTGGC 1948
Qy 2121 TGTGCCGACCCAGTCAAGCCCATATGGTGTCCGACTGTGATCAAGACTACCCCTATGC 2180
Db 1949 TGTGCCGACCCAGTCAAGCCCATATGGTGTCCGACTGTGATCAAGACTACCCCTATGC 2008
Qy 2181 CGTTGACGGGCTCGTCATCTGGTGGCGATCGAGCGGTGGTCAAGAGTACCTGGACAT 2240
Db 2009 CGTTGACGGGCTCGTCATCTGGTGGCGATCGAGCGGTGGTCAAGAGTACCTGGACAT 2068
Qy 2241 CTACTACCCCTAACGACGGCGAGCTCCAGCGTACGCTGGAGCTGACGGCTGGTGAAGGA 2300
Db 2069 CTACTACCCCTAACGACGGCGAGCTCCAGCGTACGCTGGAGCTGACGGCTGGTGAAGGA 2128
Qy 2301 GGTGCGTGAGGAGCGCACGGCGACCTCAAGACCGGAGACTGGTGGCCAGGATGGACAC 2360
Db 2129 GGTGCGTGAGGAGCGCACGGCGACCTCAAGACCGGAGACTGGTGGCCAGGATGGACAC 2188
Qy 2361 CGTCCAGCAGCTGGCTAGGGCGTGCACGCCATCATCTGGTGGCATCTCCGCTGCACGC 2420
Db 2189 CGTCCAGCAGCTGGCTAGGGCGTGCACGCCATCATCTGGTGGCATCTCCGCTGCACGC 2248
Qy 2421 GGCTGTCAACTTTGGSCAGTACCCATACGCCGGGTACCTCCCGAACCGGCCGACGCCGAG 2480
Db 2249 GGCTGTCAACTTTGGSCAGTACCCATACGCCGGGTACCTCCCGAACCGGCCGACGCCGAG 2308
Qy 2481 CCGGCGCCCGATGCCGAGCCAGGCAGCCAGCTCAAGAGCTGGAGCGGGGCAGAA 2540
Db 2309 CCGGCGCCCGATGCCGAGCCAGGCAGCCAGCTCAAGAGCTGGAGCGGGGCAGAA 2368
Qy 2541 CGAGCGGACATGGTGTTCATCCGACCATCACCAGCCAGTTCAGACCATCTCTGGGCAT 2600
Db 2369 CGAGCGGACATGGTGTTCATCCGACCATCACCAGCCAGTTCAGACCATCTCTGGGCAT 2428
Qy 2601 CTCGCTCATCGAGATCCTCTCCAAGCACTCTCCGACGAGGTGTACTCGGCCAGCGTGA 2660
Db 2429 CTCGCTCATCGAGATCCTCTCCAAGCACTCTCCGACGAGGTGTACTCGGCCAGCGTGA 2488
Qy 2661 CGAGCCTGATCGCTGGACGTGAGCAAGCGCTGATGTCGTTCAAGATTCGGGAG 2720
Db 2489 CGAGCCTGAGCGCTGGACGTGAGCAAGCGCTGATGTCGTTCAAGATTCGGGAG 2548
Qy 2721 CCGGCTGGTGCAGATTGAGAAATCGGATCAAGACGATGAACGACAGTCCGACTTGAAGAA 2780
Db 2549 CCGGCTGGTGCAGATTGAGAAATCGGATCAAGACGATGAACGACAGTCCGACTTGAAGAA 2608
Qy 2781 CCGGAAGGGCCTGTGGAAATGCCGTACATGCTGTACCCCAACACAGTCCGACGTTAC 2840
Db 2609 CCGGAAGGGCCTGTGGAGATGCCGTACATGCTGTACCCCAACACAGTCCGACGTTAC 2668

RESULT 4

US-10-132-350-23
; Sequence 23, Application US/10132350
; Publication No. US2003016855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Kolomiets, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxigenase Polynucleotides and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286,889
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 2664
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2664)
US-10-132-350-23

Query Match 85.0%; Score 2664; DB 14; Length 2664;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 235 ATGTTCTGGCACGGGGTCGGGACCGGCTGACGGGAAAGAACAGAGCGCTGGAGCGAG 294
Db 1 ATGTTCTGGCACGGGGTCGGGACCGGCTGACGGGAAAGAACAGAGCGCTGGAGCGAG 60
Qy 295 GGCAAGATCCGCGCACCGGTGAGGTGGTCAAGAAAGAGAGGTGCTGGACGCTTC 354
Db 61 GGCAAGATCCGCGCACCGGTGAGGTGGTCAAGAAAGAGAGGTGCTGGACGCTTC 120
Qy 355 AACGCCTCGCTCCTCGACGGCGTCCACAGGATCCTCGGCTGGGACGACGGCCTTC 414
Db 121 AACGCCTCGCTCCTCGACGGCGTCCACAGGATCCTCGGCTGGGACGACGGCCTTC 180
Qy 415 CAGCTCGTCAGCGCACCGCGCGGACCCCGAGCAACCGGGGCGCTGGCAAGGTGGGAAG 474
Db 181 CAGCTCGTCAGCGCACCGCGCGGACCCCGAGCAACCGGGGCGCTGGCAAGGTGGGAAG 240
Qy 475 GCGGCGCACCTGGAGAGCGGTGGTGGTCAAGTCCACGGCGGAGACCGGTG 534

Db 241 GCGGCGACCTGGAGGAGCGGTGGTGTCTCGCTCAAGTCCACGGCGGACGGGGAGACCGTG 300
Qy 535 TACCGGGTGAGCTTCGAGTGGGACGAGTCGACGGGCATCCCGGGCGCGTCTCGTGGTCAGG 594
Db 301 TACCGGGTGAGCTTCGAGTGGGACGAGTCGACGGGCATCCCGGGCGCGTCTCGTGGTCAGG 360
Qy 595 AACCTGCAGACGCGCGAGTTCTTCTCAAGACGCTCACCCCTCGAGGGCGTCCAGGCAAG 654
Db 361 AACCTGCAGACGCGCGAGTTCTTCTCAAGACGCTCACCCCTCGAGGGCGTCCAGGCAAG 420
Qy 655 GGCACCGTCGTCCTTCGTCGCGCAACTCGTGGGTCTACCGGCACAAGCTCTACTCCAGGAA 714
Db 421 GGCACCGTCGTCCTTCGTCGCGCAACTCGTGGGTCTACCGGCACAAGCTCTACTCCAGGAA 480
Qy 715 CGCATCTTCTTCGCCAACGACACCTATCTCGTCGAGCAAAATGCGGGCGGCTTGGTGCT 774
Db 481 CGCATCTTCTTCGCCAACGACACCTATCTCGTCGAGCAAAATGCGGGCGGCTTGGTGCT 540
Qy 775 TATCGGCAAGATGAGCTCAAGATTCTCCGTGGCGACGATAATCTTGACCATACCGAGAG 834
Db 541 TATCGGCAAGATGAGCTCAAGATTCTCCGTGGCGACGATAATCTTGACCATACCGAGGAG 600
Qy 835 CATGATCGCGTCTACCGTTACGACTACTACAATGACCTTGGTGATCCCGACAAGGGCGAA 894
Db 601 CATGATCGCGTCTACCGTTACGACTACTACAATGACCTTGGTGATCCCGACAAGGGCGAA 660
Qy 895 GAGCACGCTCGGCGGATCCTCGGTGGCGACCAAGAACACCCGATACCCCGTCGTCGAGA 954
Db 661 GAGCACGCTCGGCGGATCCTCGGTGGCGACCAAGAACACCCGATACCCCGTCGTCGAGA 720
Qy 955 ACTGGCCGGCACCCAAACAAAGAAAGACCCAAATTCGGAGAGCAGGCTTTTCTGCTGAAC 1014
Db 721 ACTGGCCGGCACCCAAACAAAGAAAGACCCAAATTCGGAGAGCAGGCTTTTCTGCTGAAC 780
Qy 1015 CTGAACATCTACGTCCCGCGTGACGAACGCTTTGGGCATCTCAAGATGTCGGACTTCCTT 1074
Db 781 CTGAACATCTACGTCCCGCGTGACGAACGCTTTGGGCATCTCAAGATGTCGGACTTCCTT 840
Qy 1075 GGGTACTCGTGAAGACGATCATCGAGGCTGTCTTCCAACACTGGGGACTTTCGTCGAT 1134
Db 841 GGGTACTCGTGAAGACGATCATCGAGGCTGTCTTCCAACACTGGGGACTTTCGTCGAT 900
Qy 1135 GACACGCCCAAGGAGTTCGATTCTGTTGAGGATATCCTCGGGCTCTACGAGCTGGGCCCA 1194
Db 901 GACACGCCCAAGGAGTTCGATTCTGTTGAGGATATCCTCGGGCTCTACGAGCTGGGCCCA 960
Qy 1195 GAGGCACCCCAACACCCACTGATAGCAGAGATCAGGAAGAAGATCCCCAGCGAGTTCCTT 1254
Db 961 GAGGCACCCCAACACCCACTGATAGCAGAGATCAGGAAGAAGATCCCCAGCGAGTTCCTT 1020
Qy 1255 CGAAGCATTTCTGCCGAACGGTAGCCATGACACCCCGCTAAAGATGCCCTTCCAATGTC 1314
Db 1021 CGAAGCATTTCTGCCGAACGGTAGCCATGACACCCCGCTAAAGATGCCCTTCCAATGTC 1080
Qy 1315 ATCAAATCAGATGTGTTGAAAAGGGCTCCGGAGTTTAAAGTTTGGCTGGAGGACTGACGAA 1374
Db 1081 ATCAAATCAGATGTGTTGAAAAGGGCTCCGGAGTTTAAAGTTTGGCTGGAGGACTGACGAA 1140
Qy 1375 GAGTTCGCGAGAGACACTTGCAGGCGTGAACCCAGTAATCATCAAAACGTCCTGACGGAG 1434
Db 1141 GAGTTCGCGAGAGAGACACTTGCAGGCGTGAACCCAGTAATCATCAAAACGTCCTGACGGAG 1200
Qy 1435 TTCCCGCTAAAGCACCCTGGACCCAAAGGAGTACGGAGACCACACCAAGCAAGATCACT 1494
Db 1201 TTCCCGCTAAAGCACCCTGGACCCAAAGGAGTACGGAGACCACACCAAGCAAGATCACT 1260
Qy 1495 GAAGCTCACATCCGGCATAAACATGGGAGGCTGTCTGGTGCAGAACCGACTGAGGAACAAG 1554
Db 1261 GAAGCTCACATCCGGCATAAACATGGGAGGCTGTCTGGTGCAGAACCGACTGAGGAACAAG 1320
Qy 1555 AGGCTCTTCATCTTAGACCAACCATGACCATTTCATGCCGTACCTCGACGAGATCAACGAG 1614
Db 1321 AGGCTCTTCATCTTAGACCAACCATGACCATTTCATGCCGTACCTCGACGAGATCAACGAG 1380

Qy 1615 CTGGAGGGGAACCTTCATCTACGCCACGAGGACCCCTACTGTTCTCTGAAGGACGATGGCACG 1674
Db 1381 CTGGAGGGGAACCTTCATCTACGCCACGAGGACCCCTACTGTTCTCTGAAGGACGATGGCACG 1440
Qy 1675 CTGAAGCCCCCTGGCCATCGAGCTGAGCCTGCCCCACCCCTGACGCGCAGCAGCGCGCGCG 1734
Db 1441 CTGAAGCCCCCTGGCCATCGAGCTGAGCCTGCCCCACCCCTGACGCGCAGCAGCGCGCGCG 1500
Qy 1735 GTCAGCAAGGTGTACACCCCGGCTCACACCGGCGTTCGAGGGGCCAGTCTGGCAGCTCGCC 1794
Db 1501 GTCAGCAAGGTGTACACCCCGGCTCACACCGGCGTTCGAGGGGCCAGTCTGGCAGCTCGCC 1560
Qy 1795 AAGGCTTATGCTCGCTGTAACGACTCTGCTGGCATCAGCTGATCAGCCACTGGCTGAAC 1854
Db 1561 AAGGCTTATGCTCGCTGTAACGACTCTGCTGGCATCAGCTGATCAGCCACTGGCTGAAC 1620
Qy 1855 ACGCACGCGGTGATCGAGCCGTTCTGTAATCGCGACAAACCGGCAGCTCAGCGTGGTGCAT 1914
Db 1621 ACGCACGCGGTGATCGAGCCGTTCTGTAATCGCGACAAACCGGCAGCTCAGCGTGGTGCAT 1680
Qy 1915 CCCGTGCACAAAGCTGCTGAGCCCGCATACCGTGACACGCTGAACATCAACGCCCTGGCA 1974
Db 1681 CCCGTGCACAAAGCTGCTGAGCCCGCATACCGTGACACGCTGAACATCAACGCCCTGGCA 1740
Qy 1975 CGCCAGACACTCATCAACGCCGGCGGCTTTCGAGCGCACCCGTGTCCTGCAAAAGTAC 2034
Db 1741 CGCCAGACACTCATCAACGCCGGCGGCTTTCGAGCGCACCCGTGTCCTGCAAAAGTAC 1800
Qy 2035 GCGCTGGGGATGTCGGGCAGACGCTGTACAAGAGCTGGAATTTCAACGAGCAGGCTCTCCCA 2094
Db 1801 GCGCTGGGGATGTCGGGCAGACGCTGTACAAGAGCTGGAATTTCAACGAGCAGGCTCTCCCA 1860
Qy 2095 GCAGATCTCGTCAAGAGAGGTGTGGCTGTGCGGGCTCGTCAATCGTGGTGGCGATCGAG 2214
Db 1861 GCAGATCTCGTCAAGAGAGGTGTGGCTGTGCGGGCTCGTCAATCGTGGTGGCGATCGAG 1920
Qy 2155 CTGCTGATCAAGGACTACCCCTATGCGGTTGACGGGCTCGTCAATCGTGGTGGCGATCGAG 2214
Db 1921 CTGCTGATCAAGGACTACCCCTATGCGGTTGACGGGCTCGTCAATCGTGGTGGCGATCGAG 1980
Qy 2215 CCGTGGGTCAAGGAGTACCTGGACATCTACTACCCCTAAACGACGGCGAGCTCCAGCGTGAC 2274
Db 1981 CCGTGGGTCAAGGAGTACCTGGACATCTACTACCCCTAAACGACGGCGAGCTCCAGCGTGAC 2040
Qy 2275 GTGAGCTGCAGGCGTGGTGAAGAGGTGCGTGAGGAGGCGCACCGGCGACCTCAAGGAC 2334
Db 2041 GTGAGCTGCAGGCGTGGTGAAGAGGTGCGTGAGGAGGCGCACCGGCGACCTCAAGGAC 2100
Qy 2335 CGAGACTGGTGGCCAGGATGGACACCCGTCAGCAGCTGGCTAGGGCGTGACGACCATC 2394
Db 2101 CGAGACTGGTGGCCAGGATGGACACCCGTCAGCAGCTGGCTAGGGCGTGACGACCATC 2160
Qy 2395 ATCTGGTGGCATCCGCGCTGCACGCGGCTGTCAACTTTGGGCAGTACCCATACGCCGGG 2454
Db 2161 ATCTGGTGGCATCCGCGCTGCACGCGGCTGTCAACTTTGGGCAGTACCCATACGCCGGG 2220
Qy 2455 TACCTCCGAAACCGGCCAGCGGCCAGCCGGCGCCCGATGCCGGAGCCAGGACCCACGAC 2514
Db 2221 TACCTCCGAAACCGGCCAGCGGCCAGCCGGCGCCCGATGCCGGAGCCAGGACCCACGAC 2280
Qy 2515 TACAAGAAGCTGGAGCGGGGCAGAAAGGAGCGGACATGGTGTTCATCCGACCATCACC 2574
Db 2281 TACAAGAAGCTGGAGCGGGGCAGAAAGGAGCGGACATGGTGTTCATCCGACCATCACC 2340
Qy 2575 AGCCAGTTCAGACCATCTCTGGGCATCTCGTGCATCGAGATCTCTCAAGCACTCTCTCC 2634
Db 2341 AGCCAGTTCAGACCATCTCTGGGCATCTCGTGCATCGAGATCTCTCAAGCACTCTCTCC 2400
Qy 2635 GACGAGGTGTACCTCGGCCAGCGTGACGAGCGTGATCGTGGACGTCGACGCCAAGGCG 2694
Db 2401 GACGAGGTGTACCTCGGCCAGCGTGACGAGCGTGATCGTGGACGTCGACGCCAAGGCG 2460

QY 2695 CTGGATCGGTTCAAAGATTCCGGAGCCGGCTGGTGCAGATTGAGAAATCGGATCAAGACG 2754
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Db 2461 CTGGATCGGTTCAAAGATTCCGGAGCCGGCTGGTGCAGATTGAGAAATCGGATCAAGACG 2520
|||
QY 2755 ATGAACGACAGTCCGGACTTGAAGAACCGGAAGGGCCCTGTGGAAATGCCGTACATGCTG 2814
|||
Db 2521 ATGAACGACAGTCCGGACTTGAAGAACCGGAAGGGCCCTGTGGAAATGCCGTACATGCTG 2580
|||
QY 2815 CTGTACCCCAACACGTCGGACGTTACCGGGCGAGAGGGCGAGGGGCTTACTGCCATGGGC 2874
|||
Db 2581 CTGTACCCCAACACGTCGGACGTTACCGGGCGAGAGGGCGAGGGGCTTACTGCCATGGGC 2640
|||
QY 2875 ATTCCCAACAGCATCTCCATATGA 2898
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Db 2641 ATTCCCAACAGCATCTCCATATGA 2664
|||

RESULT 5
US-10-132-350-27
; Sequence 27, Application US/10132350
; Publication No. US2003016855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Kolomiets, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxxygenase Polynucleotides and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286,889
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 2664
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)... (2664)
US-10-132-350-27

Query Match 85.0%; Score 2664; DB 14; Length 2664;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 235 ATGTTCTGGACACGGGTCGCGGACCGGCTGACGGGAAAGAACAAAGGAGCGGTGGAGCGAG 294
Db 1 ATGTTCTGGACACGGGTCGCGGACCGGCTGACGGGAAAGAACAAAGGAGCGGTGGAGCGAG 60
QY 295 GGCAAGATCCGGCGCACGGTGAGGCTGGTCAAGAAAGGAGGTGCTGGACGTCGGCGACTTC 354
Db 61 GGCAAGATCCGGCGCACGGTGAGGCTGGTCAAGAAAGGAGGTGCTGGACGTCGGCGACTTC 120
QY 355 AACGCCTCGCTCCTCGACGGCGTCCACAGGATCCTCGGCTGGGACGACGGCGTCCGCTTC 414
Db 121 AACGCCTCGCTCCTCGACGGCGTCCACAGGATCCTCGGCTGGGACGACGGCGTCCGCTTC 180
QY 415 CAGCTCGTCAGCGCCACCGCGGCCGACCCACGCAACCGGGGCCCTGGCAAGGTGGGGAAG 474
Db 181 CAGCTCGTCAGCGCCACCGCGGCCGACCCACGCAACCGGGGCCCTGGCAAGGTGGGGAAG 240
QY 475 GCGGCGCACTGGAGGAGCGGTGTGCTCAAGTCCACGGCGGACGGGGGACCGGTG 534
Db 241 GCGGCGCACTGGAGGAGCGGTGTGCTCAAGTCCACGGCGGACGGGGGACCGGTG 300
QY 535 TACCGGTGAGCTTCGAGTGGGACGAGTCCGGGATCCGGGGCGCGCTCCTGGTCAAG 594
Db 301 TACCGGTGAGCTTCGAGTGGGACGAGTCCGGGATCCGGGGCGCGCTCCTGGTCAAG 360

QY 595 AACCTGCAGCAGCGCGAGTTCTTCTCAAGACGCTACCCCTCGAGGGCGTCCACGCAAG 654
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Db 361 AACCTGCAGCAGCGCGAGTTCTTCTCAAGACGCTACCCCTCGAGGGCGTCCACGCAAG 420
|||
QY 655 GGCACCGTCTGTTCTGTCGCCAACTCGTGGGTCTACCCGCAACAGCTCTACTCCAGGAA 714
|||
Db 421 GGCACCGTCTGTTCTGTCGCCAACTCGTGGGTCTACCCGCAACAGCTCTACTCCAGGAA 480
|||
QY 715 CGCATCTTCTTCGCCAAACGACACCTATCTGCCGAGCAAAATGCCGGCGGCTTGGTGCCT 774
|||
Db 481 CGCATCTTCTTCGCCAAACGACACCTATCTGCCGAGCAAAATGCCGGCGGCTTGGTGCCT 540
|||
QY 775 TATCGCAAGATGAGCTCAAGATTCTCCGTGGCGAGATTAATCCTGGACCATACAGGAG 834
|||
Db 541 TATCGCAAGATGAGCTCAAGATTCTCCGTGGCGAGATTAATCCTGGACCATACAGGAG 600
|||
QY 835 CATGATCCGCTCTACCGTTACGACTACTACAATGACCTTGGTGATCCCGACAAAGGCGAA 894
|||
Db 601 CATGATCCGCTCTACCGTTACGACTACTACAATGACCTTGGTGATCCCGACAAAGGCGAA 660
|||
QY 895 GAGCACGCTCGGCCGATCCTCGTGGCAGCAAGAACACCCCGTATCCCGTCTGCTGCAG 954
|||
Db 661 GAGCACGCTCGGCCGATCCTCGTGGCAGCAAGAACACCCCGTATCCCGTCTGCTGCAG 720
|||
QY 955 ACTGGCGGCACCCAAACAAAGAAAGACCCAAATTCGGAGAGCAGGCTTTTCTGCTGAAC 1014
|||
Db 721 ACTGGCGGCACCCAAACAAAGAAAGACCCAAATTCGGAGAGCAGGCTTTTCTGCTGAAC 780
|||
QY 1015 CTGAACATCTACGTCGCCGCTGACGAACGCTTTGGGCACTCTCAAGATGTGCGACTTCCTT 1074
|||
Db 781 CTGAACATCTACGTCGCCGCTGACGAACGCTTTGGGCACTCTCAAGATGTGCGACTTCCTT 840
|||
QY 1075 GGGTACTCGCTGAAGACGATCATCGAGGCTGTTCTTCCAAACACTGGGACTTTTCGTCGAT 1134
|||
Db 841 GGGTACTCGCTGAAGACGATCATCGAGGCTGTTCTTCCAAACACTGGGACTTTTCGTCGAT 900
|||
QY 1135 GACACGCCCAAGGAGTTCGATTTCGTTGAGGATATCCTCGGGCTCTACGAGCTGGGCCA 1194
|||
Db 901 GACACGCCCAAGGAGTTCGATTTCGTTGAGGATATCCTCGGGCTCTACGAGCTGGGCCA 960
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QY 1195 GAGSCACCCAAACAAACCCACTGATAGCAGAGATCAGGAAGAAAGATCCCGAGGAGTTCCTT 1254
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Db 961 GAGSCACCCAAACAAACCCACTGATAGCAGAGATCAGGAAGAAAGATCCCGAGGAGTTCCTT 1020
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QY 1255 CGAAGCATTTCTCCGAAACGGTAGCCATGACCCCGCTAAAGATGCCCTTCCAAATGTC 1314
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Db 1021 CGAAGCATTTCTCCGAAACGGTAGCCATGACCCCGCTAAAGATGCCCTTCCAAATGTC 1080
|||
QY 1315 ATCAATCAGATGTGTTGAAAAAGGCTCCGGAGTTTAAAGTTTGGCTGGAGGACTGACGAA 1374
|||
Db 1081 ATCAATCAGATGTGTTGAAAAAGGCTCCGGAGTTTAAAGTTTGGCTGGAGGACTGACGAA 1140
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QY 1375 GAGTTCGCGAGAGACACATTGACGGCGTGAACCCAGTAATCATCAAACGTCGACGGAG 1434
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Db 1141 GAGTTCGCGAGAGACACATTGACGGCGTGAACCCAGTAATCATCAAACGTCGACGGAG 1200
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QY 1435 TTCCCCGCTAAAGCACCCCTGACCCCAAGGAGTACGGAGACCACACGCAAGATCACT 1494
|||
Db 1201 TTCCCCGCTAAAGCACCCCTGACCCCAAGGAGTACGGAGACCACACGCAAGATCACT 1260
|||
QY 1495 GAAGTCACTCCGGCATACATGGGAGGCTGTGCTGTCAGAACGCACTGAGGAACAAG 1554
|||
Db 1261 GAAGTCACTCCGGCATACATGGGAGGCTGTGCTGTCAGAACGCACTGAGGAACAAG 1320
|||
QY 1555 AGGCTCTTCATCCTAGACCACTGACCATTTTCATGCGGTACCTCGACGAGATCAACGAG 1614
|||
Db 1321 AGGCTCTTCATCCTAGACCACTGACCATTTTCATGCGGTACCTCGACGAGATCAACGAG 1380
|||
QY 1615 CTGAGGGGAACTTCATCTACGCCAGCAGGACCCCTACTGTTCTTGAAGGACGATGGCAG 1674
|||
Db 1381 CTGAGGGGAACTTCATCTACGCCAGCAGGACCCCTACTGTTCTTGAAGGACGATGGCAG 1440
|||

QY 1675 CTGAAGCCCTGGCCATCGAGCTGAGCTGCTGCCACCCCTGACGGCCAGCAGCGCGCGG 1734
Db |||||
Db 1441 CTGAAGCCCTGGCCATCGAGCTGAGCTGCTGCCACCCCTGACGGCCAGCAGCGCGCGG 1500
QY 1735 GTCAGCAAGGTGTACACCCCGGCTCACACCGGGCGTTCGAGGGCCACGTCTGGCAGCTCGCC 1794
Db |||||
Db 1501 GTCAGCAAGGTGTACACCCCGGCTCACACCGGGCGTTCGAGGGCCACGTCTGGCAGCTCGCC 1560
QY 1795 AAGGCTTATGCTGCGTAAACGACTCTGCTTGGCATCAGCTGATCAGCCACTGGCTGAAC 1854
Db |||||
Db 1561 AAGGCTTATGCTGCGTAAACGACTCTGCTTGGCATCAGCTGATCAGCCACTGGCTGAAC 1620
QY 1855 ACGCAGCGGTGATCGAGCCGTTCTGTAATCGCGACAAACCGGAGCTCAGCGTGTGCAT 1914
Db |||||
Db 1621 ACGCAGCGGTGATCGAGCCGTTCTGTAATCGCGACAAACCGGAGCTCAGCGTGTGCAT 1680
QY 1915 CCCGTGCACAAGCTGCTGAGCCCGCACTACCGTGACACGCTGAACATCAACGCCCTGGCA 1974
Db |||||
Db 1681 CCCGTGCACAAGCTGCTGAGCCCGCACTACCGTGACACGCTGAACATCAACGCCCTGGCA 1740
QY 1975 CGCCAGACTCATCAACCGCGGGCGTCTTCGAGCGCACCGTGTTCCTGCAAGTAC 2034
Db |||||
Db 1741 CGCCAGACTCATCAACCGCGGGCGTCTTCGAGCGCACCGTGTTCCTGCAAGTAC 1800
QY 2035 GCGCTGGGATGTGGCAGACGTGTACAAGAGCTGGAATTTCAACGAGCAGGCTTCCCCA 2094
Db |||||
Db 1801 GCGCTGGGATGTGGCAGACGTGTACAAGAGCTGGAATTTCAACGAGCAGGCTTCCCCA 1860
QY 2095 GCAGATCTCGTCAAGAGAGGTGTGGCTGTGCCGACCAAGTCAAGCCCATATGTTGTCGGA 2154
Db |||||
Db 1861 GCAGATCTCGTCAAGAGAGGTGTGGCTGTGCCGACCAAGTCAAGCCCATATGTTGTCGGA 1920
QY 2155 CTGCTGATCAAGGACTACCCCTATGCGGTGACGGGCTCGTCATCTGGTGGCGATCGAG 2214
Db |||||
Db 1921 CTGCTGATCAAGGACTACCCCTATGCGGTGACGGGCTCGTCATCTGGTGGCGATCGAG 1980
QY 2215 CGGTGGGTCAAGGAGTACCTGGACATCTACTACCCCTAACGACGGCGAGCTCCAGCGTGAC 2274
Db |||||
Db 1981 CGGTGGGTCAAGGAGTACCTGGACATCTACTACCCCTAACGACGGCGAGCTCCAGCGTGAC 2040
QY 2275 GTGGAGCTGAGCGCGTGGTGAAGGAGGTGCGTGAGGAGGCGCACGGCACCTCAAGGAC 2334
Db |||||
Db 2041 GTGGAGCTGAGCGCGTGGTGAAGGAGGTGCGTGAGGAGGCGCACGGCACCTCAAGGAC 2100
QY 2335 CGAGACTGTGGCCCGCAGGATGGACACCGTCCAGCAGCTGGTGGTGGCGGTGCACGACCATC 2394
Db |||||
Db 2101 CGAGACTGTGGCCCGCAGGATGGACACCGTCCAGCAGCTGGTGGTGGCGGTGCACGACCATC 2160
QY 2395 ATCTGGTGGCATCCGCGCTGCACCGCGCTGTCAAATTTGGCGAGTACCCATACGCGGG 2454
Db |||||
Db 2161 ATCTGGTGGCATCCGCGCTGCACCGCGCTGTCAAATTTGGCGAGTACCCATACGCGGG 2220
QY 2455 TACCTCCGAACCGGCGCAGCGGCCAGCGCGCGCGCGATGCCGAGCCAGGACCGAC 2514
Db |||||
Db 2221 TACCTCCGAACCGGCGCAGCGGCCAGCGCGCGCGCGATGCCGAGCCAGGACCGAC 2280
QY 2515 TACAAGAAGTGGGAGCGGGGCGAGAGGAGCGGACATGTTGTTTCATCCGCAACCATCAC 2574
Db |||||
Db 2281 TACAAGAAGTGGGAGCGGGGCGAGAGGAGCGGACATGTTGTTTCATCCGCAACCATCAC 2340
QY 2575 AGCCAGTTCAGACACCATCTCTGGGCACTCTCGCTCATCGAGATCTCTCCAAGCACTCTCC 2634
Db |||||
Db 2341 AGCCAGTTCAGACACCATCTCTGGGCACTCTCGCTCATCGAGATCTCTCCAAGCACTCTCC 2400
QY 2635 GACGAGGTGTACCTCGGCCAGCGTGACGAGCCTGATCGCTGACGCTCAGACGCCAAGCG 2694
Db |||||
Db 2401 GACGAGGTGTACCTCGGCCAGCGTGACGAGCCTGATCGCTGACGCTCAGACGCCAAGCG 2460
QY 2695 CTGGATCGCTTCAAAAGATTCCGGGAGCGGGCTGGTGCAGATTGAGAATCGGATCAAGACG 2754
Db |||||
Db 2461 CTGGATCGCTTCAAAAGATTCCGGGAGCGGGCTGGTGCAGATTGAGAATCGGATCAAGACG 2520
QY 2755 ATGAACGACAGTCCGGACTTGAAGAACCGGAAGGGGCGCTGTGGAATGCCGTACATGCTG 2814

Db 2521 ATGAACGACAGTCCGGACTTGAAGAACCGGAAGGGGCGCTGTGGAATGCCGTACATGCTG 2580
QY 2815 CTGTACCCCAACACGTGGACGTTACCGCGGAGAAAGGCCGAGGGGCTTACTGCCATGGGC 2874
Db |||||
Db 2581 CTGTACCCCAACACGTGGACGTTACCGCGGAGAAAGGCCGAGGGGCTTACTGCCATGGGC 2640
QY 2875 ATTCCCAACAGCATCTCCATATGA 2898
Db |||||
Db 2641 ATTCCCAACAGCATCTCCATATGA 2664

RESULT 6
US-10-132-350-17
; Sequence 17, Application US/10132350
; Publication No. US20030166855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Kolomietz, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxxygenase Polynucleotides and Methods
; TITLE OF INVENTION: Of Use
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286,889
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 3080
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (152)...(2815)
; OTHER INFORMATION: LOX4
US-10-132-350-17

Query Match 77.9%; Score 2440.4; DB 14; Length 3080;
Best Local Similarity 89.8%; Pred. No. 0;
Matches 2708; Conservative 0; Mismatches 279; Indels 27; Gaps 8;

QY 142 GGCAGGGCGGACGGAGCGGAGCAGGAGCGGCAAGAGCCCATCCACCCAGCCACCGCGTTCCTG 201
Db |||||
Db 55 GGCAGGGGAGCGAGCAGCAGGGCAAGGATCCACACCCACCCACCGGACAC-TCCCTG 113
QY 202 AGAAGCGAGGAGCGA-----GAAAGCGAAGAGCGGCGCATGTTTGGCACGGGGTCCGG 256
Db |||||
Db 114 AGAAGCGAAGCGAGAAAGCGAAGAGCGGCGGCCACCATGTTTGGCACGGGGTCCGG 173
QY 257 ACCGGTGCAGGAAAGAACAAAGAGCGGTGGAGCGGCAAGATCCGGCGCACCGGTGA 316
Db |||||
Db 174 ACCGGTGCAGGGAAGAACAAAGAGCGGTGGAACGAGGGAAGATCCGGCGCACCGGTGA 233
QY 317 GGCTGGTCAAGAAGGAGGTGCTGGAGCTCGGCGACTTCAAACGCTCGCTCCTCGACGGCG 376
Db |||||
Db 234 GGCTGGTCAAGAAGGAGGTGCTGGAGCTCGGCGACTTCAAACGCTCGCTCCTCGACGGCG 293
QY 377 TCCACAGGATCCTCGGTGGGACGAGCGCGTTCGCTTCCAGTCTGTCAGCGCCACCGCGG 436
Db |||||
Db 294 TACACAGGATCCTCGGTGGGACGAGCGCGTTCGCTTCCAGCTCGTCAGCGCCACCGCGG 353
QY 437 CCGACCCCAAGCAAGCGGCGCGTGGCAAGGTGGGGAAGCGGCGGCGCACCTGGAGGAGCGG 496
Db |||||
Db 354 CCGACCCCAAGCAAGCGGCGCGGCAAGGTTCGGGAAGCGGCGGCGCACCTGGAGGAGCGG 413
QY 497 TGGTGTGCTCAAGTCCACGCGCGGAGCGGAGACCGGTGTACCGGCTGAGCTTCGAGTGGG 556
Db |||||
Db 414 TGGTGTGCTCAAGTCCACGACGAGCGGAGACCGGTGTACCGGCTGAGCTTCGAGTGGG 473

Qy 557 ACGAGTCGACGGGCATCCCGGGCGCGTCTTGTCAGGAACCTGCGACGACCGCGAGTTCT 616
Db |||||
Qy 474 ACGGGTCGACGGGGCTCCCTGGCGCGCTCTTGTCAGGAACCTGCGACGCGCGAGTTCT 533
Db |||||
Qy 617 TCCTCAAGACGCTACCCCTCGAGGGCGTCCAGGCAAGGGCACCGTCTGTCGTCGCCA 676
Db |||||
Qy 534 TCCTCAAGTCGCTACCCCTCGAGGGCGTCCCGGACGGGGCACCGTCTGTCGTCGCCA 593
Db |||||
Qy 677 ACTCGTGGGTCTACCCGCACAAGCTCTACTCCAGGAACGCATCTTCTTCGCCAACGACA 736
Db |||||
Qy 594 ACTCGTGGATCTACCCGCACAATCTCTACTCCAGGAACGCGTCTTCTTCGCCAACGACA 653
Db |||||
Qy 737 CCTATCTGCCGAGCAAAATGCCGGCGCGTGTGGTGCCCTTATCGGCAAGATGAGCTCAAGA 796
Db |||||
Qy 654 CTTATCTGCCAAGCAAAATGCCCTGCGGCATTGGTGCCCTTACCGGCAGGACGAGCTCAAGA 713
Db |||||
Qy 797 TTCTCCGTGGCGACGATAATCTTGACCATACAGGAGCACGACCGCGTCTACCGTTACG 856
Db |||||
Qy 714 TTCTCCGCGCGACGATAATCTTGACCATACAGGAGCACGACCGCGTCTACCGTTACG 773
Db |||||
Qy 857 ACTACTACAANTGACCTTGGTGATCCCGACAAAGGCGAAGAGCACGCTCGGCCGATCCTCG 916
Db |||||
Qy 774 ACTACTACAACGACCTCGGTGAGCCAGACAAAGGTGAAGCCATGCCCGGCTGTCTCTCG 833
Db |||||
Qy 917 GTGGCAGCCAAGAACACCCGTATCCCGTCGCTGCAGAACTGGCCGSCACCCAAACAAGA 976
Db |||||
Qy 834 GGGCAGCCAAGAACACCCGTATCCCGTCGCTGCAGAACCGGCCGCGTCCAACAGAGA 893
Db |||||
Qy 977 AAGACCCAAATTCGGAGACGAGGCTTTCTCTGTGAACCTGAACATCTACGTCCCGCGTG 1036
Db |||||
Qy 894 CAGACCCCAACTCGGAGAGCAGGCTGTTCTGTGTGAACCTGAACATCTACGTCCCGCGG 953
Db |||||
Qy 1037 ACGAACGCTTTGGGCACTCAAGATGTCGGACTTCCTTGGGTACTCGTGAAGACGATCA 1096
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Qy 954 ACGACGGTTTGGGCATCTCAAGATGTCGGACTTCCTCGGTACTCTACTGAAGCGATCA 1013
Db |||||
Qy 1097 TCGAGGCTGTTCTTCCAAACACTGGGACTTTCTGTCGATGACACGCCCAAGGAGTTTCGATT 1156
Db |||||
Qy 1014 TCGAGGCTGTCTTCCGACGCTGGACGTTTCTGTCGACGATACGCCCAAGGAGTTTCGATT 1073
Db |||||
Qy 1157 CGTTTGAGGATATCCTTCGGGCTCTACGAGCTGGGCCAGAGGCCACCCAAACCCACTGA 1216
Db |||||
Qy 1074 CGTTCGAAGACATCCTTGGGCTCTACGAGCCGGGTCAGAGGCCGCCAAACCCACTGG 1133
Db |||||
Qy 1217 TAGCAGAGATCAGGAAGAAGATCCCGAGGAGTTCCTTGAAGCATCTGCGGAAACGGTA 1276
Db |||||
Qy 1134 TAGCAGAGGTCAGGAAGAGAATCCCGACGAGTTCCTCAGAAGCATCTGCCCCGATGGTA 1193
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Qy 1277 GCCATGACCAACCCGCTAAAGATGCCCTTCCAAATGTCTCAAAATCAGATGTGTGAAAA 1336
Db |||||
Qy 1194 GCCATGACCAACCCCTGAAGATGCCCTTCCAAATATCATCAGATCAGATGTGTGAAAA 1253
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Qy 1337 AGGCTCCGAGTTTAAAGTTTGGCTGGAGGACCGACGAAGAGTTTGGAGGGGAGACGCTTG 1396
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Qy 1254 AGGCTCCAGAGTTTAAAGTTTGGCTGGAGGACCGACGAAGAGTTTGGAGGGGAGACGCTTG 1313
Db |||||
Qy 1397 CAGGCGTGAAACCCAGTAATCATCAAAACGCTGACGGAGTTCCCGCTAAAAAGCACCCCTGG 1456
Db |||||
Qy 1314 CAGGCGTGAAACCCAGTGTCTCAAAACGCTGACGGAGTTTCCAGCTAAAAAGTACCCCTGG 1373
Db |||||
Qy 1457 ACCCAAGGCAGTACGGAGACCAACACAGCAAGATCACTGAAGCTCAGATCCGGCATAACA 1516
Db |||||
Qy 1374 ACCCAAGTCAATACGGAGACCATACGAGCAAGATCACCGAAGCTCAGATCCAGCATAACA 1433
Db |||||
Qy 1517 TGGGAGGCCTGTGCGTGAGAACCGCACTGAGGAACAAGAGGCTCTTTCATCCTTAGACCAAC 1576
Db |||||
Qy 1434 TGAAGGCCTGTGCGTGAGAAATGCACCTGAAGAAGAACAGGCTCTTTCATCCTTAGACCAATC 1493
Db |||||
Qy 1577 ATGACCATTTTCATGCCGTACCTCGACGAGATCAACGAGCTGGAGGGGAACCTTCATCTACG 1636
Db |||||
Qy 1494 ATGACCATTTTCATGCCGTACCTCAACAAGATCAACGAGTTTGGAGGGGAACCTTCATCTACG 1553
Db |||||

Qy 1637 CCAGCAGGACCCCTACTGTTCTGAAGGACGATGGCAGCGTGAAGCCCTGGCCATCGAGC 1696
Db |||||
Qy 1554 CCAGCAGGACCCCTACTGTTCTGAAGGACGATGGCAGCGTGAAGCCCTGGCCGTCGAGC 1613
Db |||||
Qy 1697 TGAGCCTGCCCCACCCCTGACGGCCAGCAGCGCGCGCGGTGAGCAAGGTGTACACCCCGG 1756
Db |||||
Qy 1614 TGAGCCTGCCCCACCCCGATGGCCAGCAGCAGCGCGCGGTGAGCAAGGTGTACACCCAG 1673
Db |||||
Qy 1757 CTCACACCGCGTCGAGGGCCACGCTCTGCGAGCTGCGCAAGGCTTATGCTGCGTAAACG 1816
Db |||||
Qy 1674 CTCACTCCGGCTGAGGGCCACGCTCTGGCAACTTGCCAAAGCTTATGCTGCGTGAACG 1733
Db |||||
Qy 1817 ACTTGCCTGGCATCAGCTGATCAGCCACTGCGTGAACACGACGCGCGGTGATCGAGCCGT 1876
Db |||||
Qy 1734 ACTTGCCTGGCATCAGCTGATCAGCCACTGCGTGAACACGACGCGCGGTGATCGAGCCGT 1793
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Qy 1877 TCGTAATCGCGACAAACCGGCAGCTCAGCGTGGTGCATCCCGTGCACAGCTGCTGAGCC 1936
Db |||||
Qy 1794 TCGTATCGCAACGAAACCGGCAGCTGAGCGTGGTGCATCCCGTGCACAGCTGCTGAGCC 1853
Db |||||
Qy 1937 CGCACTACCGTGACACGCTGAACATCAACGCGCTGGCACGCCAGACACTCATCAACGCCG 1996
Db |||||
Qy 1854 CACACTACCGTGACACGCTGAACATCAACGCGCTGGCACGCCAGACGCTCATCAACGCCG 1913
Db |||||
Qy 1997 GCGGCGTCTTCGAGCGCACCGTGTTCCTGTGAAAAGTACGCGCTGGGATGTGCGGCAGACG 2056
Db |||||
Qy 1914 ACGGCATCTTCGAGCGCACCGTGTTCCTGTGAAAAGTACGCGCTGGGATGTCTCTCGACG 1973
Db |||||
Qy 2057 TGTAACAAGAGCTGGAAATTTCAACGAGCAGGCTCTCCAGCAGATCTCTGTCGAAGAGAGGTG 2116
Db |||||
Qy 1974 TGTAACAAGAGCTGGAAATTTCAACGAGCAGGCTCTCCAGCAGACCTCTGTCGAAGAGAGGTG 2033
Db |||||
Qy 2117 TGGCTGTGCCGACCAAGTCAAGCCCATATGTTGTCTCCGACTGCTGATCAAGGACTACCCCT 2176
Db |||||
Qy 2034 TGGCTGTGCCGACCAAGTCAAGCCCATACGTTGTCTCCGCTGCTGATCAAGGACTACCCCT 2093
Db |||||
Qy 2177 ATGCCGTTGACGGGCTCGTCTATCTGTTGGCGCATCGAGCGGTGGGTCAAGGAGTACCTGG 2236
Db |||||
Qy 2094 ACGCCGTGGACGGGCTGGTCTATCTGTTGGCGCATCGAGCGGTGGGTCAAGGAGTACCTGG 2153
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Qy 2237 ACATCTACTACCTTAACGACGGCGAGTCCAGCGTGACGTGGAGCTGCGAGCGGTGGTGA 2296
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Qy 2154 ACGTCTACTACCCCAACGACGGCGAGTCCAGCGCGACGTGGAGCTGCGAGGCGGTGGTGA 2213
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Qy 2297 AGGAGGTGCTGAGGAGCGCACGGCGACTCCAGGACCTCAAGGACCGAGACTGGTGGCCAGGATGG 2356
Db |||||
Qy 2214 AGGAGGTGCGGAGGAGCGCACGGCGACTCCAGGACCTCAAGGACCGGAGACTGGTGGCCAGGATGG 2273
Db |||||
Qy 2357 ACACCGTCCAGCAGCTGGCTAGGGCTGACGACGACCATCATCTGGTGGCATCCGCGTGC 2416
Db |||||
Qy 2274 ACGCCGTCCAGCGGTGGCCAGGGCGTGCACGACCGTCTATCTGGGTAGCGTCCGCGTGC 2333
Db |||||
Qy 2417 ACGCGGCTGTCAACTTTGGGCAGTACCCATACGCGGGTACCTCCGAAACCGGCCGACGG 2476
Db |||||
Qy 2334 ACGCGGCGTCAACTTCGGGCAGTACCCGCTACGCGGGTACCTGCCGAACCGGCCGACCG 2393
Db |||||
Qy 2477 CCAGCCGGCCCGATCCCGGAGCCAGGACGACCCAGCTACAAGAAAGTGGGAGCGGGGC 2536
Db |||||
Qy 2394 TGAGCCGGCGCGGATGCCGGAGCCGGGACGCGACGACTACAAGAAAGTGGAGCGGGGC 2453
Db |||||
Qy 2537 AGAAGGAGGGGACATGGTGTTCATCCGACCATCACGAGCCAGTTCAGACCATCTCTGG 2596
Db |||||
Qy 2454 AGAAGGAGGGGACCGGGTGTTCATCCGACCATCACGAGCCAGTTCAGACCATCTCTGG 2513
Db |||||
Qy 2597 GCATCTCGTCTATCAGATCTCTCCAAGCACTCTCCGACGAGGTGTACCTCGGCCAGC 2656
Db |||||
Qy 2514 GCATCTCGTCTATCAGATCTCTCCAAGCACTCTCCGACGAGGTGTACCTCGGCCAGC 2573
Db |||||
Qy 2657 GTGACGAGCCTGATCGCTGGAGCTCAGACGCCAAGCGCTGGATGCGTTCAAAAGATTCC 2716
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Qy 2574 GCGACGAGCCTGAGCGCTGGACGTCCGACCCAGCGCGCTGGACGCGGTTCAGAAAGGTTCG 2633
Db |||||
Qy 2717 GGAGCCGGCTGGTGCAGATTGAGAAATCGGATCAAGACGATGAACGACAGTCCGACTTGA 2776
Db |||||

Db 2634 GAAGCCGCTGGTGGAGATCGAGAAAGCGGATCAGGACGATGAACGACAGCCCGACGTTGA 2693
Qy 2777 AGAACCGGAAGGGCCCTGTGGAAATGCGGTACATGCTGTGTATCCCAACACGTCGGACG 2836
Db 2694 AGAACCGGAAGGGCCCGTGGAGATGCCGTACATGCTGTGTATCCCAACACGTCGGATG 2753
Qy 2837 TTACCGGCGAGAAGGCCGAGGGCTTACTGCGCATGGGCAATCCCAACAGCATCTCCATAT 2896
Db 2754 TCACCGGCGAGAAGGGCGAGGGGCTCACTGCCATGGGCATTCCTCAACAGCATCTCCATAT 2813
Qy 2897 GAGCCTGGGCAGATTGT-----GTCTCGTAGTAAATTGTTGTGCTGCGCCGTGCGA 2947
Db 2814 GAGCCTCTCACTGCTGAGCGGATGGTTGTAGATGCTCTGTACGCTGTGTGTAATGT 2873
Qy 2948 TGTGTTCTTCATTTGTCAGTCTCAGGGTAGGGATGGAGATCATACCATGATC- 3006
Db 2874 GTCGTTTATTCGTTGTTTGTCACTCT--GGTAGGGAATGGAGATGTTGATTGGATCC 2930
Qy 3007 ---TTTGTAGGGTTGAGAGAGGAGTCCACGCTTGAATATTGTTGTCATGTATG--TAAT 3060
Db 2931 ATGATCTGTAGGGTTGAGAGAGGAG-CCACGCTCGATATGTTGTCATGTGTGTTCTT 2989
Qy 3061 TCTTGGTTAAATAAT-AAAGTTCGTGAGTTCATTCTTCTTAAATAAAAAACAATAAAAAA 3119
Db 2990 TCTTGGTTAAGATAATAAATTCTGCTGCTCAAAAAAATAAAAAAATAAAAAA 3049
Qy 3120 AAAAAAAAAAAAAA 3133
Db 3050 AAAAAAAAAAAAAA 3063

RESULT 7
US-10-425-114-34535
; Sequence 34535, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 34535
; LENGTH: 3003
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLM017282G11_FLI
US-10-425-114-34535

Query Match 77.6%; Score 2433.4; DB 12; Length 3003;
Best Local Similarity 89.4%; Pred. No. 0;
Matches 2652; Conservative 0; Mismatches 297; Indels 16; Gaps 3;
Qy 147 GCGAGGACCGAGCGAGCGAGGAGAGCCCATCCACGAGCCAGCCACCGCGTTCTCTGAGAAG 206
Db 32 GCGAGCAGCAGGCGAAGGCATCCACACCCACACCCACCGGACACTCCCTGAGAAAGCGAGA 91
Qy 207 CGAGGAGCGAGAAAGCGAAGAGCGGCGCATGTTCTGGCAAGGGGTGCGGACCGGCTGAC 266
Db 92 AGCGAGAGCGAAGAGCGGCGCGCCACCATGTTCTGGCAAGGGGTGCGGACCGGCTGAC 151
Qy 267 GGGAAAGAACAGGAGGCGGTGGAGCGAGGGCAAGATCCGCGGACCGGTGAGGCTGTCAA 326
Db 152 GGGGAAGAACAGGAGGCGGTGGAAACGAGGGAAGATCCGCGGACCGGTGAGGCTGTCAA 211

Qy 327 GAAGGAGGTGCTGGACGTGCGGCGACTTCAACGCCTCGCTCTCTGACGGCGTCCACAGGAT 386
Db 212 GAAGGAGGTGCTGGACGTGCGGCGACTTCAACGCCTCGCTCTCTGACGGCGTACACAGGAT 271
Qy 387 CCTCGGCTGGAGACGACGGCGTGCCTTCCAGCTCGTCAGCGCAACCGCGGCCGACCCAG 446
Db 272 CCTCGGCTGGAGACGACGGCGTGCCTTCCAGCTCGTCAGCGCAACCGCGGCCGACCCAG 331
Qy 447 CAACGGGGGCGGTGGCAAGGTGGGAAGCGGCGCACCTGAGGAGGCGGTGCTGCT 506
Db 332 CAACGGGAGCGCGCAAGGTGGGAAGCGGCGCACCTGAGGAGGCGGTGCTGCT 391
Qy 507 CAAGTCCACGGCGGACCGGGAGACCGTGTACCGGGTGAGCTTCGAGTGGACGAGTCGCA 566
Db 392 CAAGTCGACGACGACCGGGAGACCGTGTACCGGGTGAGCTTCGAGTGGACGAGTCGCA 451
Qy 567 GGGCATCCCGGCGCGCTCCTGCTCAGGAACCTGCAGCACGCGGAGTTCCTCTCAAGAC 626
Db 452 GGGCGTCCCGGCGCGCTCCTGCTCAGGAACCTGCAGCACGCGGAGTTCCTCTCAAGTC 511
Qy 627 GCTCACCTCGAGGGCGTCCCAGGCAAGGGCACCGTCTCTCTCGTCCCAACTCGTGGGT 686
Db 512 GCTCACCTCGAGGGCGTCCCAGGCAAGGGCACCGTCTCTCTCGTCCCAACTCGTGGGT 571
Qy 687 CTACCCGCAAGCTCTACTCCAGGAACGCTCTCTTCCGCAACGACACCTATCTGCC 746
Db 572 CTACCCGCAAGCTCTACTCCAGGAACGCGTCTCTTCCGCAACGACACTTATCTGCC 631
Qy 747 GAGCAAAATGCCGCGCGTGGTGGCTTATCGGCAAGATGAGTCAAGATTCTCCGTGG 806
Db 632 AAGCAAAATGCCGCGCATTTGGTGCTTACCGGACGAGTCGAGATTCTCCGCGG 691
Qy 807 CGACGATAATCTGGACCATACCGAGGACATGATCGCGTCTACCGTTACGACTACTACAA 866
Db 692 CGACGATAATCTGGACCATACAAAGGACGACCGCGTCTACCGTTACGACTACTACAA 751
Qy 867 TGACCTTGGTGATCCGACAAGGGGGAAGAGCAGCTCGGCGGATCTCTCGTGGCAGCCA 926
Db 752 CGACCTCGGTGAGCCAGACAAGGGTGAAGACCATGCCCGGCTCTCTCGGGGCGAGCCA 811
Qy 927 AGAACACCCGTATCCCGTCTGCAAGACTGGCGGCAACCCCAACAAAGAAAGACCCAAA 986
Db 812 AGAACACCCGTATCCCGTCTGAGGACCGCGGCGGCTCCAAACAGAGACAGACCCCAA 871
Qy 987 TTCGAGAGCAGGCTTTCTCTGCTGAACCTGAACATCTACGTCGCGGCTGACGAACGCTT 1046
Db 872 CTCGAGAGCAGGCTGTTCTGCTGAACCTGAACATCTACGTCGCGGCGGACGAGCGGTT 931
Qy 1047 TGGGCATCTCAAGATGTCGGACTTCTCTTGGGTACTCGCTGAAGACGATCATCGAGGCTGT 1106
Db 932 TGGGCATCTCAAGATGTCGGACTTCTCTGGGTACTCACTGAAGCGGATCATCGAGGCTGT 991
Qy 1107 TCTTCCAACTGGGGACTTTCGTTCGATGACACGCCCCAAGGAGTTCGATTCTGTTGAGGA 1166
Db 992 CTTCCGACGCTGGGACGTTTCGTTCGAGTACGCCCCAAGGAGTTCGATTCTGTTGGAAGA 1051
Qy 1167 TATCCTCGGGCTCTACGAGCTGGGCCAGAGGACCCCAACACCCACTGATAGCAGAGAT 1226
Db 1052 CATCCTTGGGCTCTACGAGCCGGTTCAGAGGCGGCCCAACACCCACTGTTAGCAGAGGT 1111
Qy 1227 CAGGAAGAGATCCCCAGCGAGTTCCTTCGAAGCATTTCTGCCAAGCGGTAGCCATGACCA 1286
Db 1112 CAGGAAGAGATCCCCAGCGAGTTCCTCAGAAGCATTTCTGCCAATGTTAGCCATGACCA 1171
Qy 1287 CCCGCTAAAGATGCCCTTCCAAATGTTCATCAATCAGATGTTGTTGAAAAAGGCTCCGGA 1346
Db 1172 CCCCTGAAGATGCCCTTCCAAATATCATCAGATCAGATGTTGTTGAAAAAGGCTCCAGA 1231
Qy 1347 GTTTAAGTTTGGCTGGAGGACTGACGAAGAGTTTCGCGAGAGAGACACTTTCAGGCGTGAA 1406
Db 1232 GTTTAAGTTTGGCTGGAGGACCCGACGAAGAGTTTCGAGGGGAGACGCTTGCAGGCGTGAA 1291
Qy 1407 CCCAGTAAATCATCAAAACGTCGTGACGGAGTTCCTCCGCTTAAAGCACCCTTGACCCCAAGGCA 1466

Db 1292 CCCAGTGTCTCATCAACGCTCTGACGGAGTTCCAGCTAAAAAGTACCCCTGGACCCAAAGTCA 1351
QY 1467 GTACGAGAGACCAACAGCAGCAAGATCACTGAAGCTCACTCCGGCATAACATGGGAGGCCT 1526
Db 1352 ATACGGAGACCATACGAGCAAGATCACCGAAGCTCACTCCAGCATAAACATGGAAGGCCT 1411
QY 1527 GTCGGTGCAGAAACGCACTGAGGAAACAAGAGGCTCTTTCATCTCTAGACCAACCATGACCAATTT 1586
Db 1412 GTCAGTGCAGAAATGCACCTGAAGAAGAAACAGGCTCTTTCATCTCTAGACCAACCATGACCAATTT 1471
QY 1587 CATGCCCTPACCTCGACGAGATCAACGAGCTGGAGGGGAACCTTTCATCTACGCCAGCAGGAC 1646
Db 1472 CATGCCCTPACCTCAACAAGATCAACGAGTTGGAGGGGAACCTTTCATCTACGCCAGCAGGAC 1531
QY 1647 CCTACTGTTCTGAAGGACGATGACACGCTGAAGCCCTGGCCATCGAGCTGAGCCTGCC 1706
Db 1532 CCTACTGTTCTGAAGGACGATGACACGCTGAAGCCCTGGCCATCGAGCTGAGCCTGCC 1591
QY 1707 CCACCCCTGACGGCCAGCAGCGCGCGGCTCAGCAAGGTGTACACCCCGGCTCACACCGG 1766
Db 1592 CCACCCCTGATGGCCAGCAGCACCGCGCGGCTCAGCAAGGTGTACACCCAGCTCACTCCGG 1651
QY 1767 CGTCGAGGGCCACGCTCTGGCAGCTCGCCAAAGCTTATGCTGCGTAAACGACTGTGCCTG 1826
Db 1652 CGCTGAGGGCCACGCTCTGGCAACTTGCCAAAGCTTATGCTGCGTGAACGACTCGGCCTG 1711
QY 1827 GCATCAGCTGATCAGCCACTGGCTGAACACGACGCGGCTGATCGAGCCGTTCTGTAATCGC 1886
Db 1712 GCATCAGCTGATCAGCCACTGGCTGAACACGACGCGGCTGATCGAGCCGTTCTGTCATCGC 1771
QY 1887 GACAAACCGGCAGCTCAGCGTGGTGCATCCCGTGCAACAAGCTGCTGAGCCCGCACTACCG 1946
Db 1772 AACGAACCGGCAGCTGAGCGTGGTGCATCCAGTGCAACAAGCTGCTGAGCCCACTACCG 1831
QY 1947 TGACACGCTGAACATCAACGCGCTGGCAGCGCAGACACTCATCAACGCGCGCGCTCTT 2006
Db 1832 TGACACGCTGAACATCAACGCGCTGGCAGCGCAGCGCTCATCAACGCGCGCGCTCTT 1891
QY 2007 CGAGCGCACCGTGTTCCTGTCAAAGTACGCGCTGGGATGTGCGGCAGACGCTGTACAAGAG 2066
Db 1892 CGAGCGCACCGTGTTCCTGTCAAAGTACGCGCTGGGATGTCTCTCCGACGCTGTACAAGAG 1951
QY 2067 CTGGAATTTCAACGAGCAGGCTCTCCAGCAGATCTCGTCAAGAGAGGTGTGGCTGTGCC 2126
Db 1952 CTGGAATTTCAACGAGCAGGCTCTCCAGCAGACCTCGTCAAGAGAGGTGTGGCTGTGCC 2011
QY 2127 GGACCACTCAAGCCCATATGGTGTCCGACTGCTGATCAAGACTACCCCTATGCCGTGA 2186
Db 2012 GGACCACTCAAGCCCATATGGTGTCCGACTGCTGATCAAGACTACCCCTTACGCCGTGA 2071
QY 2187 CGGGCTCGTCACTGTGGTGGCGATCGAGCGGTGGTCAAGAGTACCTGGACATCTACTA 2246
Db 2072 CGGGCTGGTCACTGTGGTGGCGATCGAGCGGTGGTCAAGAGTACCTGGACATCTACTA 2131
QY 2247 CCCTAACGACGCGGAGCTCCAGCGTGAAGCTGAGCTGAGCGGTGGTGAAGGAGGTGCG 2306
Db 2132 CCCCACGACGCGGAGCTCCAGCGGAGCTGAGCTGAGCGGTGGTGAAGGAGGTGCG 2191
QY 2307 TGAGGAGGCGCAGCGGACCTCAAGGACCGGAGACTGGTGGCCAGGATGGACACCGTCCA 2366
Db 2192 CGAGGAGGCGCAGCGGACCTCAAGGACCGGAGACTGGTGGCCAGGATGGACGCGCTCCA 2251
QY 2367 GCAGCTGGCTAGGGCGTGCACGACCATCATCTGGTGGCATCTGGGCTGCACGCGGCTGT 2426
Db 2252 GCGGCTGGCCAGGGCGTGCACGACCGTCACTGGGTAGCGTCCGCGTGCACGCGGCGT 2311
QY 2427 CAACCTTTGGGAGTACCCATACGCGCGGTACCTCCCGAACCGGCGGACGCGCGGCG 2486
Db 2312 CAACCTTCGGGAGTACCCGTACGCGCGGTACCTCCCGAACCGGCGGACGCGCGGCG 2371
QY 2487 CCCGATGCCGAGCCAGGCGCACCGACTCAAGAAGCTGGGAGCGGGGCAGAAGGAGGC 2546

Db 2372 GCCGATGCCGAGCCCGGCGAGCGAGCACTACAAGAAGCTGGAGCGGGCGAGAGGAGGC 2431
QY 2547 GGACATGGTGTTCATCCGCAACCATCACCAGCCAGTTCAGAGCCATCCTGGGCACTCTCGCT 2606
Db 2432 GGACGCGGTGTTCATCCGCAACCATCACCAGCCAGTTCAGAGCCATCCTGGGCACTCTCGCT 2491
QY 2607 CATCGAGATCCTCTCCAAGCACTCCTCCGACGAGGTGTACCTCGGCCAGCGTGACGAGCC 2666
Db 2492 CATCGAGATCCTCTCCAAGCACTCCTCCGACGAGGTGTACCTCGGCCAGCGGAGAGCC 2551
QY 2667 TGATCGCTGGACGTCAGACGSCCAAGGCGCTGGATGCGTTCAAAAGATTTCGGGAGCGGCT 2726
Db 2552 TGAGCGCTGGACGTCGGACGCGGCGCTGGACGCGTTCAGAAGGTTTCGGAAGCGGCT 2611
QY 2727 GGTGAGATTGAGAAATGCCGTACATGCTGCTGTACCCCAACACAGCTCGGACGTTACCGCGA 2786
Db 2612 GGTGAGATCGAGAAAGCGGATCAGGACGATGAACGACAGCCCGACGTTGAAGAACCGGAA 2671
QY 2787 GGGGCTGTGGAATGCCGTACATGCTGCTGTACCCCAACACAGCTCGGACGTTACCGCGA 2846
Db 2672 GGGGCGGTGGAGATGCCGTACATGCTGTACCCCAACACAGCTCGGATGTACCGGCGA 2731
QY 2847 GAAGCCGAGGGGCTTACTGCCATGGGCATTCCTCAACAGCATCTCCATATGAGCCTGGC 2906
Db 2732 GAAGGCCAGGGGCTCACTGCCATGGGCATTCCTCAACAGCATCTCCATATGAGCCTCCTC 2791
QY 2907 AGATTGT-----GTCTCGTAGTAAATTTGTTGTTGCTGCGCCGTCGATGTGTTCTT 2957
Db 2792 ACTGCTCAGCGGATGGTTTGTAGATGTTCTGTTACGCTGTGTAAATGTGTCGTTATT 2851
QY 2958 CATTGTTTGTGTCAGTCTCAGGTAGGGATGGAGATGAGATCATACCATGATC-----TTTGT 3012
Db 2852 CGTTGTTTGTGTCAGTCTCAGGTAGGGAATGTTGTCATGTTGTTCTTTCTTTGTTAAG 2911
QY 3013 GGGTTGAGAGAGGAGTCCACGCT--TGAATATTGTTGTCATGTATGTAATCTTGGTTAA 3070
Db 2912 GGGTTGAGAGAGGAGTCACTGCTGGAGAATGTTGTCATGTTGTTCTTTCTTTGTTAAG 2971
QY 3071 TAATAAAGTTCGTCACTTCATTCT 3095
Db 2972 AATAAAGTTCGTCACTTCATTAT 2996

RESULT 8

US-10-132-350-19
; Sequence 19, Application US/10132350
; Publication No. US20030166855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Kolomietz, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxigenase Polynucleotides and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286,889
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 2664
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2664)
US-10-132-350-19

Query Match 75.6%; Score 2368; DB 14; Length 2664;

Best Local Similarity 93.1%; Pred. No. 0;				
Matches 2479; Conservative 0; Mismatches 185; Indels 0; Gaps 0;				
QY	235	ATGTTCTGGCACGGGGTCGCGGACCGGCTGACGGGAAGAAACAAGAGCGCTGGAGCGAG	294	
Db	1	ATGTTCTGGCACGGGGTCGCGGACCGGCTGACGGGAAGAAACAAGAGCGCTGGAAACGAG	60	
QY	295	GGCAAGATCCGCGGCACGGTGAGGCTGGTCAAGAAGGAGGTGCTGGACGTGGCGGACATTC	354	
Db	61	GGAAAGATCCGCGGCACGGTGAGGCTGGTCAAGAAGGAGGTGCTGGACGTGGCGGACATTC	120	
QY	355	AACGCCTCGCTCCTCGACGGCGTCCACAGGATCCTCGGCTGGGACGACGGCGTCGCCCTTC	414	
Db	121	AACGCCTCGCTCCTCGACGGCGTACACAGGATCCTCGGCTGGGACGACGGCGTCGCCCTTC	180	
QY	415	CAGCTCGTCAGCGCACCGCGGCCGACCCAGCAACCGGGGCCCTGGCAAGGTGGGGAAG	474	
Db	181	CAGCTCGTCAGCGCACCGCGGCCGACCCAGCAACCGGAGCCCGCGCAAGGTCCGGGAAG	240	
QY	475	GCGGCGCACCTGGAGGAGCGGTGGTGTCTCGCTCAAGTCCACGGCGGACGGGGAGACCGTG	534	
Db	241	GCGGCGCACCTGGAGGAGCGGTGGTGTCTCGCTCAAGTTCGACGACGGGGAGACCGTG	300	
QY	535	TACCGGGTGAGCTTCGAGTGGGACGAGTGGCAGGGCATCCCGGGCCCGTCTCTGGTCAAG	594	
Db	301	TACCGGGTGAGCTTCGAGTGGGACGAGTGGCAGGGCGTCCCTGGCGCCCGTCTCTGGTCAAG	360	
QY	595	AACCTGCAGCACGCGGAGTTCTTCTCTAAGACGCTCACCTCGAGGGCGTCCAGGCAAG	654	
Db	361	AACCTGCAGCACGCGGAGTTCTTCTCTAAGTGGCTCACCTCGAGGGCGTCCCGGCGAG	420	
QY	655	GGCACCGTCGTCTTCTGCGCAACTCGTGGGTCTACCCGACACAGCTCTACTCCAGGAA	714	
Db	421	GGCACCGTCGTCTTCTGCGCAACTCGTGGATCTACCCGCAATCTCTACTCCAGGAA	480	
QY	715	CGCATCTTCTTCGCCAACGACACCTATCTGCGGAGCAAAATGCCGGCGCGTGGTGCCT	774	
Db	481	CGCGTCTTCTTCGCCAACGACACTTATCTGCCAAGCAAAATGCTGCGGCATTGGTGCCT	540	
QY	775	TATCGGCAAGATGAGCTCAAGATTCTCCGTGGCGACGATAATCCTGGACCATACCAGGAG	834	
Db	541	TACCGGCAGGACGAGCTCAAGATTCTCCGGGCGACGATAATCCTGGACCATACAAGGAG	600	
QY	835	CATGATCGCGTCTACCGTTACGACTACTACAAATGACCTTGGTGATCCCGACAAGGGCGAA	894	
Db	601	CACGACCGGCTTACCGTTACGACTACTACAAAGACCTCGGTGAGCCAGACAAGGGTGAA	660	
QY	895	GAGCACGCTCGGCCGATCTCTCGGTGGCAGCAAGAACACCCGATCCCGCTCGCTGCAGA	954	
Db	661	GACCATGCCCGCGCTCTCTCGGGGCGAGCAAGAACACCCGATCCCGCTCGCTGCAGG	720	
QY	955	ACTGGCCGGCACCCAAACAAAGAAAGACCCAAATTCGAGAGCAGGCTTTCTGCTGAAC	1014	
Db	721	ACCGGCCGGGCTCCAAACAGAGACAGACCCCAACTCGGAGAGCAGGCTTTCTGCTGAAC	780	
QY	1015	CTGAACATCTACGTCCCGCGTGACGAAACGCTTTGGGCATCTCAAGATGTCGGACTTCCTT	1074	
Db	781	CTGAACATCTACGTCCCGCGCGACGAGCGGTTTGGGCATCTCAAGATGTCGGACTTCCTC	840	
QY	1075	GGGTACTCGCTGAAGACGATCATCGAGGCTGTCTTCCAAACACTCGGGACTTTCTGTCGAT	1134	
Db	841	GGGTACTCACTGAAGCGGATCATCGAGGCTGTCTTCCGACGCTGGGACGTTTCGTCGAC	900	
QY	1135	GACACGCCCAAGGAGTTCGATTCTGTTTGGGATATCTCTCGGGCTCTACGAGCTGGGCCCA	1194	
Db	901	GATACGCCCAAGGAGTTCGATTCTGTTTGAAGACATCTTGGGGCTCTACGAGCCGGGTCCA	960	
QY	1195	GAGGCACCCCAACCCACTGATAGCAGAGATCAGGAAGAAGATCCCCAGCGAGTTCCIT	1254	
Db	961	GAGGCGCCCAACACCCACTGGTAGCAGAGGTGAGGAAGAGATCCCCAGCGAGTTCCITC	1020	
QY	1255	CGAAGCATCTGCGGAACGGTAGCCATGACCAACCCGCTAAAGATGCCCCCTTCCAAATGTC	1314	

Db	1021	AGAAGCATTTCTGCCGATGGTAGCCATGACCACCCCTGAAGATGCCCTTCCAATATC	1080	
QY	1315	ATCAAATCAGATGTGTTGAAAAAGGCTCCGAGGTTTAAAGTTTGGTGGAGGACTGACGAA	1374	
Db	1081	ATCAGATCAGATGTGTTGAAAAAGGCTCCAGAGTTTAAAGTTTGGTGGAGGACCGACGAA	1140	
QY	1375	GAGTTCGCGAGAGAGACACTTGCAGGCGTGAAACCCAGTAATCATCAAACGTCTGACGGAG	1434	
Db	1141	GAGTTCGCGAGGAGACGCTTGCAGGCGTGAAACCCAGTGCTCATCAAACGTCTGACGGAG	1200	
QY	1435	TTCCCGCTAAAAGCACCTTGGACCCCAAGGAGTACGGAGACCACACAGCAAGATCACT	1494	
Db	1201	TTCCAGCTAAAAGTACCTTGGACCCCAAGTCAATACGGAGACCATAACAGCAAGATCAAC	1260	
QY	1495	GAAGCTCACATCCGGCATAAACATGGGAGGCGCTGTCCGTGCAGAACGCACTGAGGAACAAG	1554	
Db	1261	GAAGCTCACATCCAGCATAAACATGGAAGGCGTGTCCGTGCAGAAATGCATGAAGAAGAC	1320	
QY	1555	AGGCTCTTTCATCCTAGACCAACCATGACCAATTTTCATGCCGTACCTCGACGAGATCAACGAG	1614	
Db	1321	AGGCTCTTTCATCCTAGACCATCATGACCAATTTTCATGCCGTACCTCAACAAGATCAACGAG	1380	
QY	1615	CTGGAGGGGAACCTTCATCTACGCCAGCAGGACCCTACTGTTCTCTGAAGACGATGGCAG	1674	
Db	1381	TTGGAGGGGAACCTTCATCTACGCCAGCAGGACCCTACTGTTCTCTGAAGACGATGGCACC	1440	
QY	1675	CTGAAGCCCTTGGCCATCGAGCTGAGCCTTGCCTCCCAACCTTGACGGCCAGCAGCGCGCG	1734	
Db	1441	CTGAAGCCCTTGGCGTCTGAGCTGAGCCTTGCCTCCCAACCTTGAGGGCCACGTTGGCAACTTGC	1500	
QY	1735	GTCAGCAAGGTGTACACCCCGGCTCACACCGGGCGTCAGGGGCCACGTTGGCAGCTCGCC	1794	
Db	1501	GTCAAGCAAGGTGTACACCCAGCTCACTCCGGCGCTGAGGGCCACGTTGGCAACTTGC	1560	
QY	1795	AAGGCTTATGCTGCGTAAACGACTCTGCTGGGCATCAGCTGATCAGCCACTGGCTGAAC	1854	
Db	1561	AAGGCTTATGCTGCGTAAACGACTCTGCTGGGCATCAGCTGATCAGCCACTGGCTGAAC	1620	
QY	1855	ACGCACGCGGTGATCGAGCCCGTTCGTAATTCGCGCAAAACCGGCAGCTCAGCGTGGTGCAT	1914	
Db	1621	ACGCACGCGGTGATCGAGCCCGTTCGTCATTCGCAACGAAACCGGCAGCTGAGCGTGGTGCAT	1680	
QY	1915	CCCGTGACAAAGCTGCTGAGCCCGCGCTTTCGAGCGCACCGTGTTCCTTGCAAAATAC	2034	
Db	1681	CCCGTGACAAAGCTGCTGAGCCCGCACACTACCGTGACACGCTGAACATCAACGCCCTTGCA	1740	
QY	1975	CGCCAGACACTCATCAACCGCGCGGCTTTCGAGCGCACCGTGTTCCTTGCAAAATAC	2094	
Db	1741	CGCCAGACGCTCATCAACCGCGCGGCTTTCGAGCGCACCGTGTTCCTTGCAAAATAC	1800	
QY	2035	CGCTGGGGATGTCGGCAGACGCTGTACAAAGAGCTGGAATTTCAACGAGCAGGCTCTCCCA	2094	
Db	1801	CGCTGGGGATGTCCTCCGACGCTGTACAAAGAGCTGGAATTTCAACGAGCAGGCTCTCCCA	1860	
QY	2095	GCAGATCTCGTCAAGAGAGGTGTGGCTGTGCTGCGGACCCAGTCAAGCCCATATGTTGTCGA	2154	
Db	1861	GCAGACCTCGTCAAGAGAGGTGTGGCTGTGCTGCGGACCCAGTCAAGCCCATACGTTGTCGA	1920	
QY	2155	CTGCTGATCAAGGACTACCCCTATGCGGTTGACGGGCTCGTTCATCTGTTGGGCGATCGAG	2214	
Db	1921	CTGCTGATCAAGGACTACCCCTTACGCGCTGACGGGCTGGTTCATCTGTTGGGCGATCGAG	1980	
QY	2215	CGGTGGGTCAAGGAGTACCTGGACATCTACTACCTAACGACGGCGAGCTCCAGCGTGAC	2274	
Db	1981	CGGTGGGTCAAGGAGTACCTGGACGCTCTACTACCCCAACGACGGCGAGCTCCAGCGGAC	2040	
QY	2275	GTGAGCTGCAGGCGTGGTGAAGGAGTCCGTGAGGAGCGGCAACGCGACCTCAAGGAC	2334	
Db	2041	GTGAGCTGCAGGCGTGGTGAAGGAGTCCGCGAGGAGGCGCACCGGACCTCAAGGAC	2100	
QY	2335	CGAGACTGGTGGCCAGGATGGACACCGTCCAGCAGCTGGCTAGGCGTGACACGACCATC	2394	
Db	2101	CGAGACTGGTGGCCAGGATGGACACCGCTCCAGCGGCTGGCCAGGCGTGACGACCGGTC	2160	

QY	2395	ATCTGGGTGGCATCCGGCTGACGCGGTGTCAACTTTGGGCAGTACCCATACGCCGGG	2454
DB	2161	ATCTGGGTAGCGTCCGGCTGACGCGCGGTCAACTTCGGGCAGTACCCGTACGCCGGG	2220
QY	2455	TACCTCCCGAAACCGGCGGACGGCCAGCCGGCGCCCGATGCCGAGCCAGGCAGCACACGAC	2514
DB	2221	TACCTGCCGAACCGGCGGACCGGTAGCCCGCGGCCGATGCCGAGCCGGGCAGGCAGCAC	2280
QY	2515	TACAAGAAGCTGGAGCGGGGCAGAAAGGAGGCGGACATGGTGTTCATCCGCAACCATCACC	2574
DB	2281	TACAAGAAGCTGGAGCGGGGCAGAAAGGAGGCGGACGCGGTGTTCATCCGCAACCATCACC	2340
QY	2575	AGCCAGTTCAGACACCATCCTGGGCATCTCGCTCATTCGAGATCCTCTCCAAGCACTCCTCC	2634
DB	2341	AGCCAGTTCAGACACCATCCTGGGCATCTCGCTCATTCGAGATCCTCTCCAAGCACTCCTCC	2400
QY	2635	GACGAGGTGTACCTCGGCCAGCGTGACGAGCCCTGATCGCTGGACGTGACAGCCCAAGGCG	2694
DB	2401	GACGAGGTGTACCTCGGCCAGCGCGACGAGCCCTGAGCGCTGGACGTGCGACGCCAGGGCG	2460
QY	2695	CTGGATCGGTTCAAAAGATTCTGGGAGCCGGCTGGTGCAGATTGAGAAATCGGATCAAGACG	2754
DB	2461	CTGGACGCGTTTCAGAAAGGTTTCGGAAGCCGGCTGGTGGAGATCGAGAAACGGGATCAGGACG	2520
QY	2755	ATGAACGACAGTCCGGACTTGAAGAAACCGAAGGGGCCCTGTGGAAATGCCGTACATGCTG	2814
DB	2521	ATGAACGACAGCCCGACGTTTGAAGAAACCGAAGGGGCCCGGTGGAGATGCCGTACATGCTG	2580
QY	2815	CTGTACCCCAACACGTCCGACGTTTACCGGCGAAGGCCCGAGGGGCTTACTGCCATGGGC	2874
DB	2581	CTGTACCCCAACACGTCCGATGTACCGGCGAAGGGCGAGGGGCTCACTGCCATGGGC	2640
QY	2875	ATTCCCAACAGCATCTCCATATGA	2898
DB	2641	ATTCCCAACAGCATCTCCATATGA	2664

RESULT 9

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US-10-132-350-53
; Sequence 53, Application US/10132350
; Publication No. US20030166855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Kolomiets, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxigenase Polynucleotides and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286,889
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 7492
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)...(2086)
; FEATURE:
; NAME/KEY: TATA_signal
; LOCATION: (1548)...(1555)
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1864)...(2086)
; FEATURE:
; NAME/KEY: misc feature

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; LOCATION: (28)...(31)
; OTHER INFORMATION: W box
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (86)...(89)
; OTHER INFORMATION: W box
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (345)...(348)
; OTHER INFORMATION: W box
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (414)...(417)
; OTHER INFORMATION: W box
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (733)...(736)
; OTHER INFORMATION: W box
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (928)...(931)
; OTHER INFORMATION: W box
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1023)...(1025)
; OTHER INFORMATION: W box
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (260)...(266)
; OTHER INFORMATION: MRE-like element
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (167)...(172)
; OTHER INFORMATION: H box
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1446)...(1552)
; OTHER INFORMATION: C2H2 response element
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (6569)...(6767)
;
; US-10-132-350-53

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	Query Match	54.2%;	Score 1698.4;	DB 14;	Length 7492;
	Best Local Similarity	79.4%;	Pred. No. 0;		
	Matches 2369;	Conservative	0;	Mismatches 11;	Indels 604; Gaps 6;
QY	718	ATCTTCTTCGCAACGACACACCTATCTGCCGAGCAAAATCCGGCGCGTGGTGCCTTAT	777		
DB	3785	ATCCTGTGTGCTTGCAGACCTATCTGCCGAGCAAAATCCGGCGCGTGGTGCCTTAT	3844		
QY	778	CGGCAAGATGAGCTCAAGATTCTCCGTGGCAGCGATAATCCTGGACCATACCAGGAGCAT	837		
DB	3845	CGGCAAGATGAGCTCAAGATTCTCCGTGGCAGCGATAATCCTGGACCATACCAGGAGCAT	3904		
QY	838	GATCGGCTTACCGTTACGACTACTACAATGACCTTGGTGATCCCGACAAGGCGAAGAG	897		
DB	3905	GATCGGCTTACCGTTACGACTACTACAATGACCTTGGTGATCCCGACAAGGCGAAGAG	3964		
QY	898	CACGCTCGGCGGATCCTCGGTGGCAGCCAAAGAACACCCGTATCCCGTCGTCGAGAACT	957		
DB	3965	CACGCTCGGCGGATCCTCGGTGGCAGCCAAAGAACACCCGTATCCCGTCGTCGAGAACT	4024		
QY	958	GGCGGCGACCCCAACAAGAA-----	977		
DB	4025	GGCGGCGACCCCAACAAGAAAGGTACTAGCTCAAGTCAGCTAGTGCTAGTCCATACCATA	4084		
QY	978	-----AGACCCCAA	986		
DB	4085	CAGGATGCCAGAAATTGGCTGAAATCCTTGCTGAGTTAACTTTTACGCAGACCCCAA	4144		
QY	987	TTCCGAGAGCAGGCTTTTCCTGCTGAACCTGAACATCTACGTCCCGCGTGACGAACGCTT	1046		

Db 4145 TTCGGAGAGCAGGCTTTTCCTGCTGAACCTGAACATCTACGTCGCGGTGACGAACGCTT 4204
QY 1047 TGGGCATCTCAAGATGTCGGACTTCCTTGGTACTCGCTGAAGACGATCATCGAGGCTGT 1106
Db 4205 TGGGCATCTCAAGATGTCGGACTTCCTTGGTACTCGCTGAAGACGATCATCGAGGCTGT 4264
QY 1107 TCTTCCAACACTGGGACTTTTCGTCGATGACACGCCCAAGGAGTTCGATTCTGTTGAGGA 1166
Db 4265 TCTTCCAACACTGGGACTTTTCGTCGATGACACGCCCAAGGAGTTCGATTCTGTTGAGGA 4324
QY 1167 TATCCTCGGGCTTACGAGCTGGGCCAGAGGCCACCCCAACACCACTGATAGCAGAGAT 1226
Db 4325 TATCCTCGGGCTTACGAGCTGGGCCAGAGGCCACCCCAACACCACTGATAGCAGAGAT 4384
QY 1227 CAGGAAGAAGATCCCCAGCGAGTTTCCTTCGAAGCATTCCTGCCGAACGGTAGCCATGACCA 1286
Db 4385 CAGGAAGAAGATCCCCAGCGAGTTTCCTTCGAAGCATTCCTGCCGAACGGTAGCCATGACCA 4444
QY 1287 CCCGCTAAAGATGCCCTTCCAAATGTCAATAAT----- 1321
Db 4445 CCCGCTAAAGATGCCCTTCCAAATGTCAATAATCAGGTAACCCCAAAATTTCTTTT 4504
QY 1322 ----- 1321
Db 4505 TTTGGAATCTTCTATGTTTAAACGGCCGGTGCCTGAACTAGAAAAAAATTTACATGGCT 4564
QY 1322 -----CAGATGTGTGAAAAAGGCTCCGGAGTTTAAAT 1354
Db 4565 AAGGCTGAATCTTGGTGGTATAAAACAGATGTGTGAAAAAGGCTCCGGAGTTTAAAT 4624
QY 1415 TCATCAAAACGTCTGAC----- 1430
Db 4685 TCATCAAAACGTCTGACGGTTAGCGTTCTTGCATCATTTTGGATCGGCAAAAATACACCTTG 4744
QY 1431 ----- 1430
Db 4745 CCCCATATATTAATGAGTACAGAGCCCTTAAAGGCCCTTTTATATATATATTTTCGTAT 4804
QY 1431 ---GGAGTTCCCGCTAAAGACACCCCTGACCCCAAGGCAGTACGGAGACCACACCCAGCA 1486
Db 4805 CTCAGGAGTTCCCGCTAAAGACACCCCTGACCCCAAGGCAGTACGGAGACCACACCCAGCA 4864
QY 1487 AGATCACTGAAGTCACATCCGGCATAAATGGGAGGCCCTGTCGGTGCAGAAC----- 1539
Db 4865 AGATCACTGAAGTCACATCCGGCATAAATGGGAGGCCCTGTCGGTGCAGAACGTATGCT 4924
QY 1540 ----- 1539
Db 4925 GGACTGCATGAACCGACGCAGTACAACCGAAAGCCGCTTAAACCATCGACTGATCTGA 4984
QY 1540 -----GCAGTGAGGAACAAGAGGCTCTTCATCCTAGACCA 1574
Db 4985 TTTCCGCGTAACGAACCCCTGTGCAAGGCACTGAGGAACAAGAGGCTCTTCATCCTAGACCA 5044
QY 1575 CCATGACCATTTTCATGCCGTACCTCGACGAGATCAACGAGTGGAGGGGAACCTTCATCTA 1634
Db 5045 CCATGACCATTTTCATGCCGTACCTCGACGAGATCAACGAGTGGAGGGGAACCTTCATCTA 5104
QY 1635 CGCCAGCAGGACCCCTACTGTTCTGAAAGACGATGGCACGCTGAAGCCCTCGGCCATCGA 1694
Db 5105 CGCCAGCAGGACCCCTACTGTTCTGAAAGACGATGGCACGCTGAAGCCCTCGGCCATCGA 5164
QY 1695 GCTGAGCCTGCCACCCCTGACGGCCAGCAGCGCGCGGTGACCAAGGTTGACACCCC 1754
Db 5165 GCTGAGCCTGCCACCCCTGACGGCCAGCAGCGCGCGGTGACCAAGGTTGACACCCC 5224
QY 1755 GGCTCACACCGCGGTGAGGGCCACGTTGCGCAGCTCGCCAAAGGCTTATGCCCTGCGGTAAA 1814
Db 5225 GGCTCACACCGCGGTGAGGGCCACGTTGCGCAGCTCGCCAAAGGCTTATGCCCTGCGGTAAA 5284

QY 1815 CGACTCTGCCCTGGCATCAGCTGATCAGCCACT----- 1846
Db 5285 CGACTCTGCCCTGGCATCAGCTGATCAGCCACTGGTATAAGAAATGTTTCTGGTGCCTTTT 5344
QY 1847 ----- 1846
Db 5345 TCTCTTTTTCCTTTTAAATTAATTAATGATACATAGATAACTGAAGCACTAATCTTAA 5404
QY 1847 -----GGCTGAACACGCACGCGGTGATCGAGCCGTTCTGTAA 1882
Db 5405 TTGTGTGGCTTGCAATTGCATTGCAAGGCTGAACACGCACGCGGTGATCGAGCCGTTCTGTAA 5464
QY 1883 TCGCGACAAACCGGCAGCTCAGCGTGTGTCATCCCGTGACAAAGCTGTGAGCCCGCACT 1942
Db 5465 TCGCGACAAACCGGCAGCTCAGCGTGTGTCATCCCGTGACAAAGCTGTGAGCCCGCACT 5524
QY 1943 ACCGTGACACGCTGAACATCAACGCCCTGGCACGCCAGACACTCATCAACGCCGCGCGG 2002
Db 5525 ACCGTGACACGCTGAACATCAACGCCCTGGCACGCCAGACACTCATCAACGCCGCGCGG 5584
QY 2003 TCTTCGAGCGCACCGTGTTCCTTGCAAAGTACGCGTGGGATGTGCGCAGACGTTGATA 2062
Db 5585 TCTTCGAGCGCACCGTGTTCCTTGCAAAGTACGCGTGGGATGTGCGCAGACGTTGATA 5644
QY 2063 AGAGCTGGAATTTCAACGAGCAGGCTCTCCAGCAGATCTCGTCAAG----- 2109
Db 5645 AGAGCTGGAATTTCAACGAGCAGGCTCTCCAGCAGATCTCGTCAAGAGGTACGTAGACA 5704
QY 2110 ----- 2109
Db 5705 ATACACTGAGGTGAGCAGCACTAAACGCCTATAGAAAACCTGTTTCGGTCTTTGACGTGTT 5764
QY 2110 -----AGAGGTGTGGCTGTGCGGACCCAGTCAAGCCCATATGTTGTCG 2153
Db 5765 GTGGTTGCGTGGCTTTCAGAGGTGTGGCTGTGCGGACCCAGTCAAGCCCATATGTTGTCG 5824
QY 2154 ACTGCTGATCAAGGACTACCCCTATGCCGTTGACGGGCTCGTCACTGTTGGTGGCGATCGA 2213
Db 5825 ACTGCTGATCAAGGACTACCCCTATGCCGTTGACGGGCTCGTCACTGTTGGTGGCGATCGA 5884
QY 2214 GCGGTGGTCAAGGACTACCTGGACATCTACTACCTTAAACGCGGAGCTCCAGCGTGA 2273
Db 5885 GCGGTGGTCAAGGACTACCTGGACATCTACTACCTTAAACGCGGAGCTCCAGCGTGA 5944
QY 2274 CGTGAGCTGCAAGCGTGGTGAAGGAGTGTGCTGAGGAGCGCACGCGGACCTCAAGGA 2333
Db 5945 CGTGAGCTGCAAGCGTGGTGAAGGAGTGTGCTGAGGAGCGCACGCGGACCTCAAGGA 6004
QY 2334 CCGGAGCTGGTGGCCAGGATGGACACCGTCCAGCAGCTGGCTAGGCGTGCACGACCAT 2393
Db 6005 CCGGAGCTGGTGGCCAGGATGGACACCGTCCAGCAGCTGGCTAGGCGTGCACGACCAT 6064
QY 2394 CATCTGGTGGCATCCGCGCTGCACGCGGCTGTCAAATTTGGGCACTACCCATACGCGG 2453
Db 6065 CATCTGGTGGCATCCGCGCTGCACGCGGCTGTCAAATTTGGGCACTACCCATACGCGG 6124
QY 2454 GTACCTCCGAAACCGCCGACGCGCCAGCGCGCCCGATGCCGAGCCAGGACCCACGA 2513
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QY 2514 CTACAAGAAGCTGGGAGCGGGGCAAGGAGGCGGACATGTTGTTTCATCCGACCATCAC 2573
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QY 2634 CGACGAGGTGTACCTGGCCAGCGTGAAGGCGCTGATCGCTGGAAGCTGAGAGCCCAAGGC 2693
Db 6305 CGACGAGGTGTACCTGGCCAGCGTGAAGGCGCTGATCGCTGGAAGCTGAGAGCCCAAGGC 6364

QY 2694 GCTGGATCGTTCAAAAGATTCCGGAGCGCGCTGGTGCAGATTGAGAATCGGATCAAGAC 2753
Db |||||
QY 6365 GCTGGATCGTTCAAAAGATTCCGGAGCGCGCTGGTGCAGATTGAGAATCGGATCAAGAC 6424
Db |||||
QY 2754 GATGAACGACAGTCCGGACTTGAAGAACCGGAAGGGCCCTGTGAAAATGCCGTACATGCT 2813
Db |||||
QY 6425 GATGAACGACAGTCCGGACTTGAAGAACCGGAAGGGCCCTGTGAAAATGCCGTACATGCT 6484
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QY 2814 GCTGTACCCCAACACAGTCGGACGTTACCGGCGAGAAAGGCCGAGGGGCTTACTGCCATGGG 2873
Db |||||
QY 6485 GCTGTACCCCAACACAGTCGGACGTTACCGGCGAGAAAGGCCGAGGGGCTTACTGCCATGGG 6544
Db |||||
QY 2874 CATTCCCAACAGCATCTCCATATGAGCCTGGGCAGATTGTGCTCGTAGTAAATTGTTGT 2933
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QY 6545 CATTCCCAACAGCATCTCCATATGAGCCTGGGCAGATTGTGCTCGTAGTAAATTGTTGT 6604
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QY 2934 GCTGCGCCGTCGATGTTTCTTCAATGGTTTGTCACTCTCAGGGTAGGGGATGGAGA 2993
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QY 6605 GCTGCGCCGTCGATGTTTCTTCAATGGTTTGTCACTCTCAGGGTAGGGGATGGAGA 6664
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QY 2994 TCATACCATGATCTTTGTAGGGTTGAGAGAGGAGTCCACGCTTGAATATTGTTGTGATGT 3053
Db |||||
QY 6665 TCATACCATGATCTTTGTAGGGTTGAGAGAGGAGTCCACGCTTGAATATTGTTGTGATGT 6724
Db |||||
QY 3054 ATGTAATCTTGGTTAATAATAAGTTCTGTCAGTTTCATTTCTTA 3097
Db |||||
QY 6725 ATGTAATCTTGGTTAATAATAAGTTCTGTCAGTTTCATTTCTTA 6768
Db |||||

RESULT 10

US-10-132-350-56
; Sequence 56, Application US/10132350
; Publication No. US20030166855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Kolomiets, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxigenase Polynucleotides and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286,889
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 4483
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)...(211)
; OTHER INFORMATION: LOXS
; FEATURE:
; NAME/KEY: intron
; LOCATION: (212)...(915)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (916)...(1205)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1206)...(1716)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1717)...(1960)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1961)...(2051)
; FEATURE:

; NAME/KEY: exon
; LOCATION: (2052)...(2396)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (2397)...(2508)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (2509)...(2615)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (2616)...(2723)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (2724)...(2831)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (2832)...(2923)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (2924)...(3231)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (3232)...(3343)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (3344)...(3608)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (3609)...(3696)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (3697)...(4483)
US-10-132-350-56
Query Match 47.8%; Score 1499.4; DB 14; Length 4483;
Best Local Similarity 77.9%; Pred. No. 0;
Matches 2170; Conservative 0; Mismatches 11; Indels 604; Gaps 6;
QY 718 ATCTTCTTCGCCAACGACACCTATCTGCCGAGCAAAATGCCGGCGCGTGGTGCCTTAT 777
Db |||||
QY 1699 ATCCTGTGTGCTTGCAGACCTATCTGCCGAGCAAAATGCCGGCGCGTGGTGCCTTAT 1758
Db |||||
QY 778 CGGCAAGATGAGCTCAAGATTCTCCGTGGCGACGATAATCCTGGACCATACCAGGAGCAT 837
Db |||||
QY 1759 CGGCAAGATGAGCTCAAGATTCTCCGTGGCGACGATAATCCTGGACCATACCAGGAGCAT 1818
Db |||||
QY 838 GATCGCGTCTACCGTTACGACTACTACAATGACCTTGGTATCCCGCAAGGGCGAAGAG 897
Db |||||
QY 1819 GATCGCGTCTACCGTTACGACTACTACAATGACCTTGGTATCCCGCAAGGGCGAAGAG 1878
Db |||||
QY 898 CACGCTCGGCGGATCCTCGGTGGCGCAAGAACACCCCGTATCCCGTGCAGAACT 957
Db |||||
QY 1879 CACGCTCGGCGGATCCTCGGTGGCGCAAGAACACCCCGTATCCCGTGCAGAACT 1938
Db |||||
QY 958 GGCCGGCACCCCAAAAGAA----- 977
Db |||||
QY 1939 GGCCGGCACCCCAAAAGAAAGGTACTAGCTCAAGTCAGCTAGTGTAGTCCATACCATA 1998
Db |||||
QY 978 -----AGACCCAAA 986
Db |||||
QY 1999 CAGGATGCCAGAAATTGGCTGAATCCTTGTGAGTTAACCTTTTACGCAGACCCAAA 2058
Db |||||
QY 987 TTCGGAGAGCAGCGCTTTTCTCTGCTGAACCTGAACATCTACGTCCCGCGTGACGAACGCTT 1046
Db |||||
QY 2059 TTCGGAGAGCAGCGCTTTTCTCTGCTGAACCTGAACATCTACGTCCCGCGTGACGAACGCTT 2118
Db |||||
QY 1047 TGGGCATCTCAAGATGTCGGACTTCTTGGGTACTCGCTGAAGACGATCATCGAGGCTGT 1106
Db |||||
QY 2119 TGGGCATCTCAAGATGTCGGACTTCTTGGGTACTCGCTGAAGACGATCATCGAGGCTGT 2178
Db |||||
QY 1107 TCTTCCAACACTGGGAGCTTTCTGTCGATGACACGCCCAAGGAGTTCGATTCTTTGAGGA 1166
Db |||||
QY 2179 TCTTCCAACACTGGGAGCTTTCTGTCGATGACACGCCCAAGGAGTTCGATTCTTTGAGGA 2238
Db |||||

QY 1167 TATCCTCGGGCTCTACGAGCTGGGCCAGAGGACCCAAACAAACCACTGATAGCAGAGAT 1226
Db 2239 TATCCTCGGGCTCTACGAGCTGGGCCAGAGGACCCAAACAAACCACTGATAGCAGAGAT 2298
QY 1227 CAGGAAGAAGATCCCGACGAGATTCTTGAAGCATTTCTGCCGAACGGTAGCCATGACCA 1286
Db 2299 CAGGAAGAAGATCCCGACGAGATTCTTGAAGCATTTCTGCCGAACGGTAGCCATGACCA 2358
QY 1287 CCCGCTAAAGATGCCCTTCCAAATGTCTCAAAAT 1321
Db 2359 CCCGCTAAAGATGCCCTTCCAAATGTCTCAAAATCAGGTAAACCCAAATTTCTTTT 2418
QY 1322 1321
Db 2419 TTTGGAATCTTTCTATGTTAAACGGCGGCTGAACTAGAAAAAAATTTACCATGGCT 2478
QY 1322 -----CAGATGTGTTGAAAAAGGCTCCGGAGTTTAAGT 1354
Db 2479 AAGGCTGAATCTTGGTTGTTAAACACAGATGTGTTGAAAAAGGCTCCGGAGTTTAAGT 2538
QY 1355 TTGGCTGGAGGACTGACGAAGAGTTTCGCGAGAGAGACACTTGCAGGCGTGAACCCAGTAA 1414
Db 2539 TTGGCTGGAGGACTGACGAAGAGTTTCGCGAGAGAGACACTTGCAGGCGTGAACCCAGTAA 2598
QY 1415 TCATCAAAACGTCGTAC----- 1430
Db 2599 TCATCAAAACGTCGTACGCTTAGCGTTCTTTCATCATTTTGGATCGGCAAAATACACCTTG 2658
QY 1431 ----- 1430
Db 2659 CCCCATATATTAAGTACTGAGTACAGAGCCTTAAAGGCTTTTATATATATATTTTCGTAT 2718
QY 1431 -----GGAGTTCCCGCTAAAGCAACCTTGGACCCAAAGGAGTACGGAGACCAACACAGCA 1486
Db 2719 CTCAGGAGTTCCCGCTAAAGCAACCTTGGACCCAAAGGAGTACGGAGACCAACACAGCA 2778
QY 1487 AGATCACTGAAGCTCACATCCGGCATAAACATGGGAGGCTGTCGGTGCAGAAC----- 1539
Db 2779 AGATCACTGAAGCTCACATCCGGCATAAACATGGGAGGCTGTCGGTGCAGAACGTATGCT 2838
QY 1540 ----- 1539
Db 2839 GGACTGATGAACGCACGCACGTACAAACCGAAAGCCGTTTAAACCATCGACTGATCTGA 2898
QY 1540 -----GCACTGAGGAACAAGAGCTCTTTCATCCTAGACCA 1574
Db 2899 TTTCCGCTGAACGAACCTGTGACGCACTGAGGAACAAGAGCTCTTTCATCCTAGACCA 2958
QY 1575 CCATGACCAATTCATGCCGTACCTCGACGAGATCAACGAGCTGGAGGGGAACCTTCATCTA 1634
Db 2959 CCATGACCAATTCATGCCGTACCTCGACGAGATCAACGAGCTGGAGGGGAACCTTCATCTA 3018
QY 1635 CGCCAGCAGGACCCCTACTGTTCTGAAAGGACGATGGCACGCTGAAGCCCTGGCCATCGA 1694
Db 3019 CGCCAGCAGGACCCCTACTGTTCTGAAAGGACGATGGCACGCTGAAGCCCTGGCCATCGA 3078
QY 1695 GCTGAGCCTGCCACCCCTGACGGCCAGCAGCGCGGCGGCTGAGCAAGGTGTACACCCC 1754
Db 3079 GCTGAGCCTGCCACCCCTGACGGCCAGCAGCGCGGCGGCTGAGCAAGGTGTACACCCC 3138
QY 1755 GGCTCACACCGGCGTGCAGGGCCACGCTCTGGCAGCTCGCCAAAGGCTTATGCCTGCTAAA 1814
Db 3139 GGCTCACACCGGCGTGCAGGGCCACGCTCTGGCAGCTCGCCAAAGGCTTATGCCTGCTAAA 3198
QY 1815 CGACTCTGCCTGGCATCAGCTGATCAGCCACT----- 1846
Db 3199 CGACTCTGCCTGGCATCAGCTGATCAGCCACTGGTATAAGAAATGTTTCTGTGCTTTT 3258
QY 1847 ----- 1846
Db 3259 TCTCTTTTCTTTTCTTTTAAATTAATTAATGATACATAGATAAAGTGAAGCACTAATCTTAA 3318

QY 1847 -----GGCTGAACACGCACCGCGGTGATCGAGCCGTTCTGTAA 1882
Db 3319 TTGTGTGGCTTGCATTCAGGCTGAACACGCACCGCGGTGATCGAGCCGTTCTGTAA 3378
QY 1883 TCGCGACAAAACCGCAGCTCAGCGTGGTGCATCCCGTGCACAAGCTGTGAGCCCGCACT 1942
Db 3379 TCGCGACAAAACCGCAGCTCAGCGTGGTGCATCCCGTGCACAAGCTGTGAGCCCGCACT 3438
QY 1943 ACCGTGACACGCTGAACATCAACGCCCTGGCAGCCAGACACTCATCAACCGCCGGCGG 2002
Db 3439 ACCGTGACACGCTGAACATCAACGCCCTGGCAGCCAGACACTCATCAACCGCCGGCGG 3498
QY 2003 TCTTCGAGCGCACCGTGTTCCTGCAAAAGTACCGCTGGGGATGTTCGGCAGACGTGTACA 2062
Db 3499 TCTTCGAGCGCACCGTGTTCCTGCAAAAGTACCGCTGGGGATGTTCGGCAGACGTGTACA 3558
QY 2063 AGAGCTGGAATTTCAACGAGCAGGCTCTCCAGCAGATCTCGTCAAG----- 2109
Db 3559 AGAGCTGGAATTTCAACGAGCAGGCTCTCCAGCAGATCTCGTCAAGAGGTACGTAGACA 3618
QY 2110 ----- 2109
Db 3619 ATACACTGAGTGAGCAGCACTAAACGCCCTATAGAAAAACTGTTTCGGTCTTGTACGTGGTT 3678
QY 2110 -----AGAGGTGTGGTGTGTGCGGACCAAGTCAAGCCCATATGTTGTCG 2153
Db 3679 GTGGTTGCGTGGCTCAGAGGTGTGGCTGTGCGGACCAAGTCAAGCCCATATGTTGTCG 3738
QY 2154 ACTGCTGATCAAGGACTACCCCTATGCCCTGACGGGCTCGTCTATCTGGTGGCGATCGA 2213
Db 3739 ACTGCTGATCAAGGACTACCCCTATGCCCTGACGGGCTCGTCTATCTGGTGGCGATCGA 3798
QY 2214 GCGGTGGTCAAGGAGTACCTGGACATCTACTACCTAAACGCGGAGCTCCAGCGTGA 2273
Db 3799 GCGGTGGTCAAGGAGTACCTGGACATCTACTACCTAAACGCGGAGCTCCAGCGTGA 3858
QY 2274 CGTGAGCTGCAAGGCTGTGGTGAAGGAGTGTGAGGAGCGCGCAGCTCAAGGA 2333
Db 3859 CGTGAGCTGCAAGGCTGTGGTGAAGGAGTGTGAGGAGCGCGCAGCTCAAGGA 3918
QY 2334 CCGAGACTGTGGCCCCAGGATGGACACCGTCCAGCAGCTGGCTAGGGCGTGCACGACCAT 2393
Db 3919 CCGAGACTGTGGCCCCAGGATGGACACCGTCCAGCAGCTGGCTAGGGCGTGCACGACCAT 3978
QY 2394 CATCTGGGTGGCATCCGCGCTGCACGCGGCTGTCAAATTTGGGAGTACCCATACGCGCG 2453
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QY 2454 GTACCTCCCGAACCGGCCCGACCGCCAGCGCGCGCGCGATGCCGAGCCAGGACGCCA 2513
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Db 4159 CAGCCAGTTCAGACCATCTCTGGCATCTCGCTCATCGAGATCTCTCCAAGCACTCCTC 4218
QY 2634 CGACGAGGTGTACCTCGGCCAGCGTGACGAGCCTGATCGCTGGACGTGAGCGCCAAAGG 2693
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QY 2694 GCTGGATGGTTCAAAAGATTTCGGGAGCGCGCTGGTGCAGATTGAGAAATCGGATCAAGAC 2753
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QY 2754 GATGAACGACAGTCCGGACTTGAAGAACCGGAAGGGGCTGTGGAAATGCCGTACATGCT 2813
Db 4339 GATGAACGACAGTCCGGACTTGAAGAACCGGAAGGGGCTGTGGAAATGCCGTACATGCT 4398
QY 2814 GCTGTACCCCAACACGTCGGACGTTACCGGGGAGAAAGGCCGAGGGGCTTACTGCCATGGG 2873

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Db 4399 GCTGTACCCCAACACAGCTCGGACGTTACCGCGGAGAAAGCCGAGGGGCTTACTGCCATGGG 4458
QY 2874 CATTCCCAACAGCATCTCCATATGA 2898
Db 4459 CATTCCCAACAGCATCTCCATATGA 4483

RESULT 11
US-10-132-350-9
; Sequence 9, Application US/10132350
; Publication No. US20030166855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Kolomiets, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxxygenase Polynucleotides and Methods
; TITLE OF INVENTION: Of Use
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286,889
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 3007
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (65)...(2659)
; OTHER INFORMATION: LOX2b
US-10-132-350-9
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Best Local Similarity 71.7%; Pred. No. 0;
Matches 1907; Conservative 0; Mismatches 679; Indels 72; Gaps 10;

QY 246 CGGGGTCCGCGACCGGCTGACCGGAAAGAACAGAGGCGTGGAGCGAGGGCAAGATCCG 305
Db 73 CGGGATCATCGACGGGCTGACCGGGCGAACAGCATGCGCGCTCAAG----- 121

QY 306 CGGCACGGTGAGGCTGGTCAAGAGAGGAGTGTCTGGACGTGGCGGACTTCAACGCTCGCT 365
Db 122 -GGCACGGTGGTGTCTCATCGCAAGAACGTGTGGACCTCAACGACTTCCGGCGCCACCGT 180

QY 366 CCTCGACGGCGTCCACAGGATCCTCGGCTGGGACGACGGCGTCCCTTCCAGCTCGTCAG 425
Db 181 CGTTGACAGCATCAGCGAGTTCTTCGGCA-----AGGGGTACCTGCCAGCTCATCAG 234

QY 426 CGCCACCGCGCGCACCCAGCAACGGGGCGCGTGGCAAGGTGGGAAGGCGGCGCACCT 485
Db 235 CTCACCTCGTCGACGCCCAACACGGCAACCGCGGCGGGTCCGGGCGGAGCGCAACCT 294

QY 486 GGAGAGCGCGTGGTGTCTCAAGTCCACGGCGGACCGGGGAGACCGGTGTACCGGGTGAG 545
Db 295 GGAGCAGTGGCTGACGAGCCTGCCGTGCTGACGACCGGCGAGTCCAAGTTCCGGCGTCAC 354

QY 546 CTTGAGTGGGA---CGAGTCGAGGGGCATCCCGGGCGCGTCTCTGGTCAAGAACCTGCA 602
Db 355 GTTCGACTGGGAGGTGGAGAGTGGGAGTCCCGGGGCGGTCTCGTCAAGAACCAACCA 414

QY 603 GCACGGCGAGTTCTTCTCAAGACGCTCACCTCGAGGGCGTCCAGGCAAGGGCACCGT 662
Db 415 CGCCGCGGAGTTCTTCTCAAGACAAATCACCTCGACGAGTCCCGGGCGCGCGCGT 474

QY 663 CGTCTTGTGCGCAACTCGTGGTCTACCCGACAAAGTCTACTCCAGGAACGATCTT 722
Db 475 CACCTTGTGCGCAACTCTGGTCTACCCCGGGGCAAGTACCGCTACAACCGGCTCTT 534
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QY 723 CTTCCGCAACGACACCTATCTGCGAGCAAAATCCCGGCGGTGGTGCCTTATCGGCA 782
Db 535 CTTCTCCAAGCATACGTACCTGCCAAGCCAGATCCCGGCGGCGTGAAGCCGTACCGCA 594

QY 783 AGATGAGCTCAAGATTCTCCGTGGGACGATAATCTCTGGACATACAGGAGCATGATCG 842
Db 595 CGACGAGCTCCGCAACCTCCGCGGCGACGACGAGGCGCCCTACAGGAGCACGACCG 654

QY 843 CGTCTACGTTACGACTACTACATGACCTTGGTGATCCCGACAAGGCGGAAGACAGC 902
Db 655 CGTGTACCGCTACGACGTCTACAAGACCTCGGCGAGCCCGACGGCGGC-----AACCC 708

QY 903 TCGGCCGATCTCGGTGGCAGCCCAAAATTCGGAGAGCAGGCTTTCTCTGCTGAACCTGAACAT 1022
Db 709 GCGCCCCATCTCGGCGGCTCCGCGGACCAACCCGTACCCGCGCGCTGCCGACCGGCGG 768

QY 963 GCACCCCAAAAGAAAGACCCCAATTCGGAGAGCAGGCTTTCTCTGCTGAACCTGAACAT 1022
Db 769 CAAGCCCCCAAAACCGACCCCACTCGGATAGCCGACTGCTGCTGCTGGA---GCAGAT 825

QY 1023 CTACGTCGCGGTGACGAACGCTTTGGGCATCTCAAGATGTCGGACTTCTTGGGTACTC 1082
Db 826 CTACGTCGCGGGGACGAGCGCTTCGGCCACCTCAAGATGTCGACTTCTTGGGTACTC 885

QY 1083 GCTGAAGACGATCATCGAGGCTGTTCTTCCAAACACTGGGACTTTCTGTCGATGACAGCC 1142
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QY 1143 CAAGGAGTTCGATTCTGTTGAGGATATCTCGGGCTCTACGAGCTGGGCCCCAGAGGCAC 1202
Db 946 GGGCGAGTTCGACTCTCTCCAGGACATCATCAACCTGTACAGGGCGGGATCAAGCTGCC 1005

QY 1203 CAACACCCACTGATAGCAGAGATCAGGAAGAAGATCCCAGCGAGTTCTTCTCGAAGCAT 1262
Db 1006 CAAGATCCAGGCGCTCGAGGACATGCGCAAGCTCTTCCGCTCCAGCTCGTCAAGACCT 1065

QY 1263 TCTGCCGAACGGTAGCCATGACACCCGCTAAAGATGCCCTTCCAAATGTATCAATAATC 1322
Db 1066 CTTCCC---CGCCGGCGGGGACTACCTGTCTCAAGCTCCCATCCACAGATCATCAA-- 1120

QY 1323 AGATGTGTTGAAAAGGCTCCGAGTCTTAAGTTTGGTGGAGGAGTACGAGAGAGTTCCG 1382
Db 1121 -----GAGGACAAGAACGCGTGGAGGACCGACGAGGAGTTCCG 1158

QY 1383 GAGAGAGACATTGACGGCGTGAACCCAGTAATCATCAAACTGTCTGACGGAGTTCCCGCG 1442
Db 1159 GCGGAGGTGCTCGCCGCGGTCAACCCGATGGTGATCACGCGCTCACGAGGTTCGCGCC 1218

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Db 1219 CAAGAGCACGCTGGACCCCAAGTACGGCGACCAACACAGCATCACGCGGAGCA 1278

QY 1503 CATCCGCAATAACATGGGAGGCTGTGCGTGCAGAACGCACTGAGGAACAAGAGGCTCTT 1562
Db 1279 CATCGAGAAGAACCTCGAGGCTCACGGTGCAGAGGCGCTGGAACGCAACAGGCTCTA 1338

QY 1563 CATCTAGACCAACCATGACCATTTTCATGCCGTACCTCGACGAGATCAACGAGCTGGAGGG 1622
Db 1339 CATCTGGACCAACCAACGAGCTTTCATGCCGTCTCTCATCGACGTCAACAACTGGAGGG 1398

QY 1623 GAACCTCATCTACGCCAGCAGGACCCCTACTGTTCTCTGAAGGACGATGGCACGCTGAAGCC 1682
Db 1399 TAACTTCATCTACGCCACAGGACCCCTCTTCTCTCGCGGCGAGCGGAGGCTCGCGCC 1458

QY 1683 CTTGCCCATCGAGCTGAGCCTGCCCAACCCCTGAGCGGCGAGCGGCGGCGGTGAGCA 1742
Db 1459 CTTGCTATCGAGCTCAGGAGCCGTACATCGACGGGACCTTACCGTGGCCCAAGAGCAA 1518

QY 1743 GGTGTACACCCCGGCTCACACGGCGCTCGAGGGCCACGCTCTGGCAGCTCGCCAGGCTTA 1802
Db 1519 GGTGTACACCGCGGCTCCAGCGGCGTTCGAGGCTTGGGTGTGGCAGCTCGCCAGGCTTA 1578
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QY 1803 TGCCTGCGTAAACGACTCTGCCTGGCATCAGCTGATCAGCCACTGGCTGAACACGCACGC 1862
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1579 TGTCCCGCTCAACGACTCTGGCTGGCACCAACTCGTCAGCCACTGGCTGAACACGCACGC 1638
QY 1863 GGTGATCGAGCCGCTTCGTAATCGCGACAAACCGGCAGCTCAGCGTGGTGCATCCCGTGCA 1922
Db |||||
1639 GGTGATGGAGCCGCTTCGTGATCGCGACGACCGGCAGCTGAGCGTGACGCACCCCGTGCA 1698
QY 1923 CAAGCTGCTGAGCCGCACTACCGTGACACGCTGAACATCAACGCGCTTGGCAGCCAGAC 1982
Db |||||
1699 CAAGCTCCTGAGCTCGCACTTCGCGACACCATGACCATCAACGCGCTGGCGGCAGAC 1758
QY 1983 ACTCATCAACGCGCGCGCTCTTCGAGCGCACCGTGTTCCTGCAAAAGTACGCGCTGG 2042
Db |||||
1759 GCTCATCAACGCGCGCGCATCTTCGAGATGACCGTCTTCGCGGCAAGTACGCGCTGG 1818
QY 2043 GATGTCGGCAGACGTGTACAAGAGCTGGAATTTCAACGAGCAGGCTCTCCAGCAGATCT 2102
Db |||||
1819 CATGTCCTCCGTGCTGTACAAGAGCTGGAATTTCAACGAGCAGGCTCTCCCGCGACCT 1878
QY 2103 CGTCAAGAGAGGTGTGGCTGTGCCGACAGTCAAGCCCATATGCTGTCCGACTGCTGAT 2162
Db |||||
1879 CGTCAAGAGGGCGTGGCGGTGGCGGACCGCTCCAGCCTGTACAAGGTGCGGTGCTGAT 1938
QY 2163 CAAGGACTACCCCTATGCCGTTGACGGGCTCGTCACTGTGGTGGGATCGAGCGGTGGGT 2222
Db |||||
1939 CGAGGACTACCCGTACGCGAGCGACGGGCTGGCCATCTGGCACGCGCATCGAGCAGTGGGT 1998
QY 2223 CAAGGAGTACCTGGACATCTACTACCTTAACGACGGCGAGCTCCAGCGTGACGTGGAGCT 2282
Db |||||
1999 GGGCGAGTACCTGGCCATCTACTACCCCGACGACGGCGCTGCGGGGCGACGAGGAGCT 2058
QY 2283 GCAGGCGTGTGGAAGGAGGTGCGTGAGGAGCGCACGGCGACCTCAAGGACCGAGACTG 2342
Db |||||
2059 GCAGGCGTGTGGAAGGAGGTGCGCGAGGTGCGGACGGCGACCCACCAAGGACGGCCCTG 2118
QY 2343 GTGGCCCGAGGATGACACCGTCCAGCAGCTGGCTAGGGCGTGACGACCATCATCTGSGT 2402
Db |||||
2119 GTGGCCCAAGATGACGGCCGTGTGCGAGCTGCGCAGCGCTGCACCATCATCTGAT 2178
QY 2403 GGCATCCGCGCTGACCGCGCTGTCAACTTTGGGCAGTACCCATACGCCCGGTACCTCCC 2462
Db |||||
2179 CGCGTCGGCGCTCACGCCCGCTCAACTTCGGCCAGTACCCGTACCGGGGTACCTCCC 2238
QY 2463 GAACGCGCCGACGCGCAGCGCGCGCCGATGCCGGAGCCAGGACGCCACGACTACAAGAA 2522
Db |||||
2239 GAACAGGCCCAAGTGAGCCCGCGCGGATGCCGGAGCCCGGACGCAAGGAGTACGAGGA 2298
QY 2523 GCTGGAGCGGGGAGAGGAGCGGACATGCTGTTTCATCCGACCATCACCAGCCAGTT 2582
Db |||||
2299 GCTGG-----AGCGCGACCCCGAGCGCGGCTTCATCCACACCATCAGAGCCAGAT 2349
QY 2583 CCAGACCATCTGGGCATCTCGCTCATCGAGATCCTCTCCAAGCATCTCTCCGACGAGGT 2642
Db |||||
2350 CCAGACCATCATCGGCATCTCGCTCATCGAGATCCTCTCCAAGCATCTCTCCGACGAGGT 2409
QY 2643 GTACCTCGGCCAGGTGACGAGCCTGATCGCTGGAGCTCAGACGCGCAAGCGCTGGATGC 2702
Db |||||
2410 GTACCTCGGCCAGCGCACACCCCGCA---GTGGACCTCCGACCGCGCGCGCTGGCGGC 2466
QY 2703 GTTCAAAAGATTCCGGAGCCGGCTGTTGAGATGAGAAATCGGATCAAGACGATGAACGA 2762
Db |||||
2467 GTTCAAGAGGTTACGCGACGCGCTGTTCAAGATCGAGGGCAAGGTGGTGGCGGAGAACCG 2526
QY 2763 CAGTCCGGACTTTGAAGAACCGGAAGGGGCTGTGGAATGCGGTATCATGCTGTGTACCC 2822
Db |||||
2527 CGACCCGACGCTGAGGAACAGGAACGGCCCGCGGAGTTCCCTTCATGCTGTCTACCC 2586
QY 2823 CAACACGTCGGACGTTACCGGCGGAGAGGTCGAGGGGCTTACTGTCATGGGCATTTCCCAA 2882
Db |||||
2587 CAACACCTCTGACACAGTGGCG---CCGCGGAGGGGCTCACTGCAAGGGCATCCCCAA 2643
QY 2883 CAGCATCTCCATATGAGC 2900

Db 2644 CAGCATCTCCATCTGAGC 2661
RESULT 12
US-10-132-350-11
; Sequence 11, Application US/10132350
; Publication No. US20030166855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Kolomiets, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxigenase Polynucleotides and Methods
; TITLE OF INVENTION: Of Use
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286,889
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2595
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2595)
US-10-132-350-11
Query Match 42.3%; Score 1325.6; DB 14; Length 2595;
Best Local Similarity 71.7%; Pred. No. 0;
Matches 1905; Conservative 0; Mismatches 679; Indels 72; Gaps 10;
QY 246 CCGGGTCCGGACCGGCTGACGGGAAAGAACAAAGGAGGCGTGGAGCGAGGGCAAGATCCG 305
Db |||||
9 CCGGATCATCGACGGCTGACGGGGCGGAACAGCATGCGGGCTCAAG-----57
QY 306 CGGCACGGTGAGGTGGTCAAGAAGGAGTCTGGACGTGGCGACTTCAACGCCCTCGCT 365
Db |||||
58 -GGCACGGTGGTGTCTCATGCGCAAGAACGTGTGGACCTCAACGACTTCGGCGCCACCGT 116
QY 366 CCTCGACGGGTCACAGGATCCTCGGCTGGGACGACGGCGTGCCTTCCAGCTCGTCA 425
Db |||||
117 CGTTGACAGCATCAGCGAGTTCTTCGGCA-----AGGGGGTCACTGCCAGTCTATCAG 170
QY 426 CGCCACCGCGGCCACCCAGCAACCGGGGCGCTGGCAAGTGGGAAGCGCGCACCT 485
Db |||||
171 CTCACCCCTCGTCCAGCGCAACCAACCGGCAACCGGGGCGGTTCGGGGGAGGGCACT 230
QY 486 GGAGGAGCGGTGGTGTCTCAAGTCCAGCGCGGACCGGGGAGACCGGTACCGGTGAG 545
Db |||||
231 GGAGCAGTGGTGCAGGACCTGCCGTGCTGACGACCGCGGAGTCCAAAGTTCGGCGTCA 290
QY 546 CTTTCAGTGGGA---CGAGTCGACGGGATCCCGGGCGCGTCTCTGTCAGGAACCTGCA 602
Db |||||
291 GTTCGACTGGGAGTGGAGAAGCTGGGAGTCCCGGGGCGCTGCTGCTCAAGAACCA 350
QY 603 GCACGCCGAGTTCTTCTCAAGACGCTCAACCTCGAGGGCGTCCAGGCAAGGGCACCGT 662
Db |||||
351 GCAGCGCGAGTTCTTCTCAAGACATCACTTCGACGACGTGCGCGCGCGCGCGCT 410
QY 663 CGTCTTCGTCGCCAACTCGTGGTCTACCCGCAAGCTCTACTCCAGGAACGATCTT 722
Db |||||
411 CACCTTCGTCGCCAACTCTGGGTCTACCCCGGGGCAAGTACCGGTACAAACCGGTCTT 470
QY 723 CTTTCGCCAACGACACCTATCTGCCGAGCAAAATGCCGGCGGCTTGGTGCCTTATCGCA 782
Db |||||
471 CTTTCCAAACGATACGTACCTGCCAAAGCCAGATGCCGGCGGCTGAAGCCGTACCGCGA 530

Db 1831 CCACCGTCTTCCCGCGCCAGTACGCGTTCGAGATGTCCTCCGTCACTACAAGGACTGGA 1890
QY 2072 ATTTAAACGAGCAGGCTCTCCAGCAGATCTCGTCAAGAGAGGTGTGGCTGTCCGGACC 2131
Db 1891 ACTTCACAGAGCAGGCTCTCCCTGACGACCTAATCAAGAGAGGCATGGCGGTGCGAGACC 1950
QY 2132 AGTCAAGCCCATATGGTGTCCGACTGCTGATCAAGGACTACCCCTATGCGGTTGACGGGC 2191
Db 1951 CGTCGAGCCCGTACAAAGGTACGGTGTGTTGGAGGACTACCCGTACCGCTCGGACGGGC 2010
QY 2192 TCGTCATCTGGTGGGATCGAGCGGTGGGTCAAGGAGTACCTGGACATCTACTACCCTA 2251
Db 2011 TGGCCATCTGGCACGCCATCGAGCAGTGGGTGACGGAGTACCTCGCGTCTACTACCCCA 2070
QY 2252 ACGACGGCGAGCTCCAGCGTGACGTGGAGCTGCAGGCGTGGTGGAAAGAGGTGCGTGAGG 2311
Db 2071 ACGACGGCGTGTGCGGCGGACGTGGAGCTGCAGGCGTGGTGGAAAGAGGCGCGGAGG 2130
QY 2312 AGGCGCACGGCGACCTCAAGGACCGAGACTGTGGTGGCCAGGATGGACACCGTCCAGCAGC 2371
Db 2131 TCGGGCACGCCGACCTCAAGGACCGCGCCCTGTGGCCCCAAGATGCAGACGTTGGCCGAGC 2190
QY 2372 TGGCTAGGGCGTGCAGACCATCATCTGGGTGGCATCCGCGCTGCAGCGGCTGTCAACT 2431
Db 2191 TGGTCAAGGCTGCACACCATCATCTGGATCGGTGCGGCTCAACGCGGCGCTCAACT 2250
QY 2432 TTGGGCAGTACCCATACGCCCGGTACCTCCCGAACCGCGCGACGCGCGCGCCCGA 2491
Db 2251 TCGGGCAGTACCCGTACGCCGGGTACCTCCCGAACCGCGCGTCCGTGAGCCGGAAGCCGA 2310
QY 2492 TGCCGGAGCCAGGCAGCCACGACTACAAGAGTGGAGCGGGGAGAGGAGGCGGACA 2551
Db 2311 TGCCGGCGCCGGGACGAGCAGTACGCGGAGCTGG-----AGCGAAGCCGGAGA 2361
QY 2552 TGGTGTTCATCCGCAACCATCACAGCCAGTTCAGACCATCTCTGGGCATCTCGCTCATCG 2611
Db 2362 AGGTGTTGTTGCGCAACCATCACAGCCAGTTCAGGCGCTCGTGGCATCTCGCTGCTGG 2421
QY 2612 AGATCCTCTCCAAGCACTCTCCGACGAGGTGTACCTCGGCGAGCGGTGACGCGCTGATC 2671
Db 2422 AGATCCTGTCCAGCCACTCTCTCCGACGAGGTGTACCTCGGCGAGCG-----CGACACCAAGG 2478
QY 2672 GCTGGACGTGACAGCCCAAGGCGCTGGATGGTTCAAAAGATTTCGGGAGCGCGTGGTGC 2731
Db 2479 AGTGGACGTGCGACGCCCAAGGCGCAGGAGCGGTTCAAGCGGTTTCGGCGCGCGGTGACCG 2538
QY 2732 AGATTGAGAATCGGATCAAGACGATGAACACAGTCCGGAATTGAAGAACCGGAAGGGGC 2791
Db 2539 AGATCGAGAAACGCGTGTCTACCATGAACGCGGACCCCTCGCCTCAAGAACCGCAACGGCC 2598
QY 2792 CTGTGGAAATGCGTACATGCTGTGTATCCCAACACGTCGGAAGTACCGGCGAGAGG 2851
Db 2599 CGGCGAGTTCCCTTACACGCTGCTCTACCCCAACACCTCCGACACGAAGGGCG---ACG 2655
QY 2852 CCGAGGGGCTTACTGCCATGGGCATTCCCAACAGCATCTCCATATGAGCCTGGGCAGATT 2911
Db 2656 CCGCGGCATCACCGCCAAGGGCATTCCAACACAGCATCTCCATTGAGTTCTGTCTGTCT 2715
QY 2912 GTG 2914
Db 2716 GAG 2718

RESULT 14
US-10-425-114-17199
; Sequence 17199, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 17199
; LENGTH: 2874
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3068-041-P8_FLI
US-10-425-114-17199

Query Match 40.5%; Score 1268.8; DB 12; Length 2874;
Best Local Similarity 71.0%; Pred. No. 0;
Matches 1831; Conservative 0; Mismatches 687; Indels 60; Gaps 9;

QY 338 TGGACGTGGCGGACTTCAACGCCCTCGTCTCGACGGCGTCCACAGGATCCTCGGCTGGG 397
Db 166 TGGACGTCAACAGCATGCGCGGCTCCCTCTCGACGGCATCGGGGAGTTCTCGGCCG-- 223
QY 398 ACGACGGCGTGCCTTCCAGCTGTCTAGCGCCACCGCGCGACCCCGAGCAACGGGGCC 457
Db 224 ----CGGCGTCACTGCCAGCTTATCAGTCCACCGTCTCGTCCGACCTAACCAACGGCAACC 279
QY 458 GTGGCAAGGTGGGAAAGCGGCGCACCTGGAGGAGGCGGTGGTGTGCTCAAGTCCACGG 517
Db 280 GCGGGAAGTTGGGCGCGGAGGCGAGCCTGGAGCAGTGGTGTGTAACCCCGCCGCTTC 339
QY 518 CGGACGGGAGACCGTGTACCGGTGAGTTCGAGTGGGA---CGAGTCGAGGGGCATCC 574
Db 340 TGTCCAGCGAGAACCAAGTTCCGCGTCACTTCGACTGGGAGTGGAGAACGAGGCGATCC 399
QY 575 CGGGCGCGTCTCTGGTCAAGAACCTTGACGACCGCGAGTTCCTTCAAGACGCTCACCC 634
Db 400 CGGGCGCCATCATGTCAGGAACAACCAACGCGCTCCGAGTTCCTTCAAGACCATCACCC 459
QY 635 TCGAGGGCGTCCAGGCAAGGCGCACCGTCTCTCGTCCGCAACTCGTGGGTCTACCCGC 694
Db 460 TCAACGACGTCCCGGCGCACGCGCACCATGCTCTTCGTCGCAACTCATGGATCTACCCGC 519
QY 695 ACAAGCTCTACTCCAGGAACGCACTCTTCTCGCAACGACACCATCTTCCGAGCAAAA 754
Db 520 AGTCCAAGTACCGTACAACCGCGTCTTCTTCTCAACGACGCTACCTCCCGAGCCAGA 579
QY 755 TGCCGGCGGCTGGTGCCCTTATCGGCAAGATGAGTCAAGATTCTCCGTGGCGACGATA 814
Db 580 TGCCGGCGGCTGAAGCCCTTACCGCGACGACGAGTCCGGAACCTGAGGGCGACGACC 639
QY 815 ATCCTGGACCATACAGGAGCATGATCGGCTTACCGTTACGACTACTACAATGACCTTG 874
Db 640 AGCAGGGCCCGTACCAGGAGCACGACCGCGTCTACCGCTACGACGCTTACAACGACCTGG 699
QY 875 GTGATCCCGACAAAGGCGAAGAGCACGCTCGGCCGATCCTCGGTGGCAGCCCAAGAACACC 934
Db 700 GCCTGCCTGACAGCGG-----GAACCGCGCCCCCTCTCTCGGCGGCACCAAGGAGCTCC 753
QY 935 CGTATCCCGCTCGTGCAGAACTGGCGGCGACCCCAACAAAGAAAGACCCAAATTCGGAGA 994
Db 754 CCTACCGCGCGCTGCCGCACCCGCGGGAAGCCCAACAGAGGACCCCAACAGCGAGA 813
QY 995 GCAGGCTTTCTCTGCTGAACCTGAACATCTACGTCCTCCGCGTACGAAACGCTTTGGGCATC 1054
Db 814 GCAGGCTCACGCTGGTCGACGGCGGACGCTCTACGTGCGCGCGGACGAGCGCTTCGGCCACA 873
QY 1055 TCAAGATGTCGACTTCCTTTGGGTACTCGCTGAAGACGATCATCGAGGCTGTTCTTCCAA 1114
Db 874 TCAAGAAAGTCGACTTCTACGGGTACGCCATCAAGGGGCTGGTGAACGCGCTCATCCCGG 933
QY 1115 CACTGGGGACTTTCGTCGATGACACGCCCCAAGGAGTTCGATTTCGTTGAGGATATCCTCG 1174

Db 934 CAATCCGCACCTACGTCGACCTGTGCGCCGCGGAGTTCGACTCCTTCAGGACATCATGA 993
QY 1175 GGCTCTACGAGCTGGGCCAGAGGACCCCAACACCCCACTGATAGCAGAGATCAGGAAGA 1234
Db 994 AGCTGTACGAGGGCGGATCCAGCTGCCCAAAATACAGCCCTCGAGACCTCGGAAGC 1053
QY 1235 AGATCCCGAGCGAGTTCCTTCGAAGCATTCCTCGCAACGGTAGCCATGACCAACCCGCTAA 1294
Db 1054 AGTCCCACTCGAGCTCGTCAAGGATGTCTCCCGGTGCGCGC--GACTACCTCCTCA 1110
QY 1295 AGATGCCCTTCCAAATGTTCATCAAAATCAGATGTGTGAAAAGGCTCCGGAGTTAAAGT 1354
Db 1111 AGCTCCCATGCCGCGAGATCATCAA-----GAGGACAAGA 1146
QY 1355 TTGGCTGGAGGACTACGAAGAGTTTCGCGAGAGAGACACTTTCAGGCGGTGAACCCAGTAA 1414
Db 1147 CAGGTTGATGACAGATGAGGAGTTTGGACGGGAGATTCTCGCCGCGGTGAACCCCATGC 1206
QY 1415 TCATCAAAACGTCGCGGAGTTCCTCCGCTAAAGACACCTGGACCCCAAGGAGTACGGAG 1474
Db 1207 TCGTCAAGCGTCTCAGGAGTTCCCTCCGAGGAGCAGTCTTGACCCGAGCAAGTACGGCG 1266
QY 1475 ACCACACGAGCAAGATCACTGAAGCTCACATCCGGCATAACATGGGAGGCTGTGCGGTGC 1534
Db 1267 ACCACACGAGCAACATCAGGAGGCGGACCTCGAGAAACAAGCTCGAGGCGCTGACGGTGC 1326
QY 1535 AGAACGCACTGAGGAACAAGAGGCTCTTATCTCTAGACCAACATGACCAATTTATGCCGT 1594
Db 1327 AGCAGGCGCTGACGGCAACCGGCTCTACATCTGAGGCAACTTCATCGCAAACTTCATGCCGT 1386
QY 1595 ACCTCGACGAGATCAAGAGCTGGAGGGGAATTCATCTACGCCAGAGGACCCCTACTGT 1654
Db 1387 TCCTGGTCAGGGTGAACAGCTGGAGGGCAACTTCATCTACGCCACCAAGGACCGTGTGT 1446
QY 1655 TCCTGAAGGACGATGGCAGCTGAAGCCCTTGCCCATCGAGCTGAGCTGAGCTGCCACCCCTG 1714
Db 1447 TCCTGCGGCGACGCGACGCTGGTCCCGGTGGCCATCGAGCTGAGCTGAGCTGCCGAGCTCC 1506
QY 1715 ACGGCCAGCAGCGCGCGCGGTTCAGCAAGGTGTACACCC--GGTCAACACCGCGCTGC 1771
Db 1507 GGGACGGCTGACCAACCGCCAAAGAGCACCGGTGTACACGCCCAAGTGCACCGCGCGG 1566
QY 1772 AGGCCACGCTTGCGAGCTGCCAAGGCTTATGCTCGTAAACGACTCTGCTTGGCATC 1831
Db 1567 AGCGTGGGTGTGGCACTTGGCCAAAGGCTTACGCCCAACGTAACGACTACTGCTGGCAAC 1626
QY 1832 AGCTGATCAGCCACTGGCTGAACACGACGCGGTGATCGAGCCGTTCGTAATCGGACAA 1891
Db 1627 AGCTCATCAGCCACTGGCTCAACACCCACGCGGTGATGGAGCCGTTCGTATCGCCACCA 1686
QY 1892 ACCGGCAGCTCAGCGTGGTGCATCCCGTGCACAAGCTGCTGAGCCCGCACTACCGTGACA 1951
Db 1687 ACCGGCAGCTCAGCGTGAAGCACCCCGTGCACAAGCTCCTCCTGCGCACTACCGTGACA 1746
QY 1952 CGCTGAACATCAACGCCCTGGCACGCCAGACACTCATCAACGCCGCGCGCTCTTCGAGC 2011
Db 1747 CCATGAACATCAACTCAACGCGCGCCAGATGCTCGTCAACGCCGCGGCACTCTTCGAGA 1806
QY 2012 GCACCGTGTTCCTGCAAAAGTACGCGCTGSSGATGTCGGCAGACGCTGTACAAGAGCTGGA 2071
Db 1807 CCACCGTCTTCCCGCGCCAGTACGCGTTCGAGATGTCCTCCGTATCTACAAGGACTGGA 1866
QY 2072 ATTTCAACGAGCAGGCTCTCCAGCAGATCTCGTCAAGAGAGGTGTGGCTGTGCCGGACC 2131
Db 1867 ACTTCACAGAGCAGGCTCTCCCTGACGACCTAATCAAGAGAGGATGGCGGTGCGAGACC 1926
QY 2132 AGTCAAGCCCATATGTTGTCGAGCTGCTGATCAAGGACTACCCCTATGCCGTTGACGGGC 2191
Db 1927 CGTCGAGCCCTGACAAGGTACGGCTGCTGGTGGAGGACTACCCGTACGCGTCGGACGGGC 1986
QY 2192 TCGTCATCTGTGGCGGATCGAGCGGTGGTCAAGGAGTACCTGGACATCTACTACCCCTA 2251

Db 1987 TGGCCATCTGGCACGCCCATCGAGCAGTGGGTGACGGAGTACCTCGCCGCTCTACTACCCCA 2046
QY 2252 ACACCGGCGAGCTCCAGCGTGACGTGGAGCTGCAGGCGTGGTGAAGGAGGTGGTGGAGG 2311
Db 2047 ACACCGGCGTGTGCGGCGGACGCTGGAGCTGCAGGCGTGGTGAAGGAGGCGCGGAGG 2106
QY 2312 AGCGCACGCGGACCTCAAGGACCGAGACTTGGTGGCCAGGATGGACACCGTCCAGCAGC 2371
Db 2107 TCGGCACGCGGACCTCAAGGACCGGCCCTGTTGGTCCCAAGATGCAGACGCTGGCGGAGC 2166
QY 2372 TGGTAGGGCGTGCACGACCATCATCTGGGTGGCATCCGCGTGCACGCGGCTGTCAACT 2431
Db 2167 TGGTCAAGGCGCTGCACACCATCATCTGGATCGCGTCCGCGCTCCACGCGCGCTCAACT 2226
QY 2432 TTGGGCGTACCCATACCGCGGCTACCTCCCGAACCGGCGGACCGCGCGCGCCCGA 2491
Db 2227 TCGGCGAGTACCCGTACCGCGGTACCTCCCGAACCGCGCTCCGTCCGCGGAGCCGA 2286
QY 2492 TCGCGGAGCGGAGCGACGACGACTACAAGAGCTGGGAGCGGGGAGGAGGCGGAGCA 2551
Db 2287 TCGCGGCGCGGCGAGCGAGTACGCGGAGTGG-----AGCGCAAGCGGAGA 2337
QY 2552 TGGTGTTCATCCGCAACCATCACGACGAGTTCAGACCATCTCTGGCATCTCGCTCATCG 2611
Db 2338 AGGTGTTCTGTCGCGACCATCACGACGAGTTCAGGCGCTCGTCGCGCATCTCGTGTGG 2397
QY 2612 AGATCCTCTCCAAGCACTCTCCGACGAGGTGTACCTCGGCCAGCGTGCAGGCGCTGATC 2671
Db 2398 AGATCCTGTCCAGCCACTCTCCGACGAGGTGTACCTCGGCCAGCG--CGACACCAAG 2454
QY 2672 GCTGGACGTCAGACGCCAAGCGCTGGATGGTTCGTTCAAGATTTCGGGAGCGCGCTGGTGC 2731
Db 2455 AGTGGACGTCGGACGCCAAGCGCGAGGAGGCGTTCAGCGGTTCCGCGCGCGCTGACCG 2514
QY 2732 AGATTGAGAAATCGGATCAAGACGATGAACGACAGTCCGACCTTGAAGAACCGGAAGGGC 2791
Db 2515 AGATCGAGAAACGCGTCTGTCACCATGAACGCGGACCTCGCTCAAGAACCGCAACGCGC 2574
QY 2792 CTGTGGAATGCCGTACATGCTGCTGTATACCCCAACACGTCGGACGTTACCGCGGAGAGG 2851
Db 2575 CGGCCGAGTTCCTCTACGCTGCTCTACCCCAACACCTCCGACACGAGGCG--ACG 2631
QY 2852 CCGAGGGGCTTACTGCCATGGGCTTCCCAACAGCATCTCCATATGAGCTGGGCGAGA 2909
Db 2632 CCGCCGCGCATCACCGCAAGGGCATTCCAAACAGCATCTCCATTTGAGTTCTGTCTGA 2689

RESULT 15
US-10-132-350-3
; Sequence 3, Application US/10132350
; Publication No. US20030166855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Kolomiets, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxigenase Polynucleotides and Methods
; TITLE OF INVENTION: Of Use
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286,889
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2622
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS

; LOCATION: (1)...(2622)									
US-10-132-350-3									
Query Match 40.4%; Score 1267.4; DB 14; Length 2622;									
Best Local Similarity 71.1%; Pred. No. 0;									
Matches 1826; Conservative 0; Mismatches 681; Indels 60; Gaps 9;									
QY	338	TGGACGTCGGCGACTTCAACGCCTCGCTCCCTCGACGGCGTCCACAGGATCCTCGS	397						
Db	110	TGGACGTCACAGCATGCGCGGCTCCCTCCTCGACGGCATCGGCGAGTTCCTCGGCGG--	167						
QY	398	ACGACGGCGTCGCCCTTCCAGCTCGTCAGCGCCACCGCGGCCGACCCCGAGCAACGSGGGCC	457						
Db	168	----CGGCGTCACTGCCAGCTTATCAGCTCCACCGTCTGTCGACCCCTAACACAACGSCAAC	223						
QY	458	GTGGCAAGGTGGGAAAGGCGCGCACCTGGAGGAGGCGGTGGTGTGCGTCAAGTCCACGG	517						
Db	224	GCGGGAAGTTGGGCGGAGGCGAGCCCTGGAGCAGTGGCTGCTGAACCCCGCCGCTTC	283						
QY	518	CGGACGGGGAGACCGTGTACCGGGTGAGCTTCGAGTGGGA--CGAGTCGCAGGGCATCC	574						
Db	284	TGTCCAGCGAGAACCAAGTTCGCGGTCACTTCGACTGGGAGGTGGAGAAAGCAGGGCATCC	343						
QY	575	CGGGCGCGTCTCTGGTCAAGAAACCTGCAGCACGCGCGAGTTCCTTCTCAAGACGCTCACCC	634						
Db	344	CGGGCGCATCATCTGTCGAAGAACCAACACGCTCCGAGTTCCTTCTCAAGACCATCACCC	403						
QY	635	TCGAGGGCGTCCCAGGCAAGGGCACCGTCTGTTCTGTCGCCCAACTCGTGGGTCTACCCGC	694						
Db	404	TCAACGACGTCCCGCCCGCCACGGCACCATCGTCTTCGTCGCCAACTCATGGATCTACCCGC	463						
QY	695	ACAAGCTCTACTCCAGGAACGCACTTCTTCGCCAAACGACACCTATCTGCGGAGCAAAA	754						
Db	464	AGTCCAAGTACCGCTACAACCGCGTCTTCTTCTCCAACGACACGTACCTCCCCAGCCAGA	523						
QY	755	TGCCGGCGGCTTGGTGCCTTATCGGCAAGATGAGCTCAAGATTCTCCGTGGCGACGATA	814						
Db	524	TGCCGGCGGCTGAAGCCCTACCGGACGACGAGCTCCGGAACCTGAGGGCGGACGACC	583						
QY	815	ATCCTGGACCATACGAGGACATGATCGCGTCTACCGTTACGACTACTACAATGACCTTG	874						
Db	584	AGCAGGGCCCGTACCAGGAGCAGACCGCGTCTACCGTACGACGTCTACAACGACCTGG	643						
QY	875	GTGATCCCGACAAGGGCGAAGAGCACGCTCGSGCGATCCTCGTGGCGAGCCCAAGAACACC	934						
Db	644	GCCTGCTGACAGCGG-----GAAACCGCGCCCGTCTCTCGGCGGACCAAGGAGCTCC	697						
QY	935	CGTATCCCGCTCGCTGCAGAACTGGCCCGCACCCCAACAAAGAAAGACCCCAATTCGGAGA	994						
Db	698	CCTACCCGCGCGCTGCGCACACGGGCGGAAGCCCAACCAAGAGCGACCCCAACAGCGAGA	757						
QY	995	GCAGGCTTTCTGCTGAACCTGAACATCTACGTCCCGGTGACGAACGCTTTGGGCGATC	1054						
Db	758	GCAGGCTCAAGTGGTCGACGGCGACGCTTACGTGCGCGCGGACGAGCGCTTCGGCCACA	817						
QY	1055	TCAAGATGTCGGACTTCTCTGGGTACTCGCTGAAGACGATCATCGAGGGCTGTTCTTCCAA	1114						
Db	818	TCAAGAAGTCGGAATTCCTACGGCTACGCCATCAAGGCGCTGGTGAACGCCGCTCATCCCGG	877						
QY	1115	CACCTGGGACTTTCGTGATGACACGCCCAAGGAGTTCGATTGTTGAGGATATCCTCG	1174						
Db	878	CAATCCGCACCTACGTCGACCTGTGCGCCCGCGAGTTCGACTCCTTCAAGGACATCATGA	937						
QY	1175	GGCTCTACGAGCTGGGCCACAGAGGCACCCCAACACCCACTGATAGCAGAGATCAGGAAGA	1234						
Db	938	AGCTGTACGAGGGCGGGATCCAGCTGCCCAAAAATACAGCCCTCGAGGACCTGCGGAAGC	997						
QY	1235	AGATCCCAGCGAGTTCCTTCGAAGCATTTCTGCGCAACCGGTAGCCATGACCAACCCGCTAA	1294						
Db	998	AGTTCCTCACTCGAGCTCGTCAAGGATGTCCTCCCGGTGCGGCGC--GACTACCTCCTCA	1054						
QY	1295	AGATGCCCTTCCAAATGTTCATCAAAATCAGATGTGTTGAAAAGGCTCCGGAGTTTAAGT	1354						

Db	1055	AGCTCCCATGCGCAGATCATCAA-----GAGGACAAGA	1090
QY	1355	TTGGCTGGAGGACTGACGAAGAGTTTCGCGAGAGAGACACTTGCAGGGCGTGAACCCAGTAA	1414
Db	1091	CAGGTTGGATGACAGATGAGGAGTTTGGACGGAGATTCTCGCCGGCGTGAACCCCATGC	1150
QY	1415	TCATCAAAACGTCTGACGGAGTTCCCGCTAAAGCACCTTGAACCCAGGAGTACGGAG	1474
Db	1151	TCGTCAAGCGTCTACGGAGTTCCCTCCGAGGAGCAGTCTTGAACCCGAGCAAGTACGGCG	1210
QY	1475	ACCACACGAGCAAGATCACTGAAGCTCAATCCGGCATAAACATGGAGGCTGTCCGTGC	1534
Db	1211	ACCACACGAGCAACCATCAGGGAGGCGGACCTCGAGAAACAAGCTCGAGGCTGACGGTGC	1270
QY	1535	AGAACGCACTGAGGAACAAGAGGCTCTTCACTCTAGACCAACCATGACCATTTTCATGCCGT	1594
Db	1271	AGCAGGCGCTGCAACGCAACCGGCTCTACATCTCTGGACCAACCAACGACAACTTCATGCCGT	1330
QY	1595	ACCTCGACGAGATCAACGAGCTGGAGGGGAACTTCACTACCTAGACCAACCATGACCATTTTCATGCCGT	1654
Db	1331	TCCTGGTCAAGGTGAACAGCTGGAGGGGAACTTCACTACCTAGACCAACCATGACCATTTTCATGCCGT	1390
QY	1655	TCCTGAAGGACGATGGCACCGTGAAGCCCTGGCCCATCGAGCTGAGCTGCCCCACCCCTG	1714
Db	1391	TCCTGCGGCGACGSCACGCTGGTGGCCGGTGGCCCATCGAGCTGAGCTGCCCGAGCTCC	1450
QY	1715	ACGGCCAGCAGCGCGGCGCGGTGAGCAAGGTGTACACCCC---GGCTCACACCGGCGTGC	1771
Db	1451	GGGACGGCTGACACCGCAAGAGCACCGGTGTACACGCCCAAGTGCACCAACCGGCGGG	1510
QY	1772	AGGGCCACGCTCTGGCAGCTCGCCAAAGGCTTATGCTGCTGCTAAACGACTGCTGCTGGCATC	1831
Db	1511	AGGCGTGGTGTGGCACCTTGGCCAAAGGCTACGCCAACCGTGAACGACTACTGCTGGCAC	1570
QY	1832	AGCTGATCAGCCACTGGCTGAACACGACGCGGCTGATCGAGCCGTTCGTAATCGGACAA	1891
Db	1571	AGCTCATCAGCCACTGGCTCAACACCCACGCGCTGATGGAGCCGTTCGTGATCGCCACCA	1630
QY	1892	ACGGCAGCTCAGGCTGTGTCATCCCGTGCACAAGCTGCTGAGCCGCACTACCGTGACA	1951
Db	1631	ACGGCAGCTCAGGCTGACGACCCCGTGCACAAGCTCCTCCTGCGGCACTACCGTGACA	1690
QY	1952	CGCTGAACATCAAGCCCTGGCACGCCACACACTCATCAACGCCGCGGCGTCTTCGAGC	2011
Db	1691	CCATGAACATCAACTCAACGCGCGCCAGATGCTCGTCAACGCCGCGGCGCATCTTCGAGA	1750
QY	2012	GCACCGTGTTCCTGCAAAAGTACGCGCTGGGATGTGGGAGAGGTGTGGCTGTCCGGACC	2071
Db	1751	CCACCGTCTTCCCGCGCCAGTACGCGTTCGAGATGTCTCCGTCTATCAAGGACTGGA	1810
QY	2072	ATTTCAACGAGCAGGCTCTCCCGACAGATCTCGTCAAGAGAGGTGTGGCTGTCCGGACC	2131
Db	1811	ACTTCAAGAGCAGGCTCTCCCTGACGACCTAATCAAGAGAGGCTGGCGTTCGAGACC	1870
QY	2132	AGTCAAGCCCATATGGTGTCCGACTGCTGATCAAGGACTACCCCTATGCGGTGACGGGC	2191
Db	1871	CGTCGAGCCCGTACAAGGTACGGCTGCTGGTGGAGGACTACCCGTCGCGTTCGAGCGGC	1930
QY	2192	TCGTCTCTGGTGGCGCATCGAGCGGTGGGTCAAGGAGTACCTGGACATCTACTACCCCTA	2251
Db	1931	TGGCCATCTGGCACGCCCATCGAGCAGTGGGTGACGGAGTACCTCGCGCTCTACTACCCCA	1990
QY	2252	ACGACGGCGAGCTCCAGCGTGAACGCTGAGCGGTGGTGGAGGAGGTGCGTGAGG	2311
Db	1991	ACGACGGCGTGTGCGGGCGGACGCTGGAGCTGACGGCTGGTGGAGGAGGCGCGGAGG	2050
QY	2312	AGGCGCACGGCGACCTCAAGGACCGGACTGGTGGCCCCAGGATGGACACCGTCCAGCAGC	2371
Db	2051	TCGGGCACGCGACCTCAAGGACCGGCCCTGGTGGCCCCAAGATGACAGCGGTGGCCGAGC	2110
QY	2372	TGGTAGGGGTGCACGACCATCATCTGGGTGGCATCCGCGTGCACGCGGCTGTCAACT	2431
Db	2111	TGGTCAAGGCGCTGCACCAACCATCATCTGGATCGCGTCCGCGCTCCACGCGGCGTCAACT	2170

QY	2432	TTGGGCAGTACCCATACGCCGGGTACCTCCCGAACCGGCCGAGCGGCCAGCCGGCGCCCGA	2491
Db	2171	TCGGGCAGTACCCGTACGCCGGGTACCTCCCGAACCGGCCGTCGGTCAGCCGGAAGCCGA	2230
QY	2492	TGCCGGAGCCAGGCAGCCACGACTACAAGAAAGCTGGAGCCGGGCAGAAAGGAGCGGACA	2551
Db	2231	TGCCGGCGCCGGGCAGCGAGTACCGGGAGCTGG-----AGCGCAAGCCCGAGA	2281
QY	2552	TGGTGTTCATCCGCACCATCACCGAGGTCCAGACCATCCTGGGGCATCTCGCTCATCG	2611
Db	2282	AGGTGTTTCGTGCGCACCATCACCGAGGTCCAGGCCCTCGTCGGCATCTCGCTGCTGG	2341
QY	2612	AGATCCTCTCCAAGCACTCCTCCGACGAGGTGTACCTCGGCAGCGTGACGAGCCTGATC	2671
Db	2342	AGATCCTGTCCAGCCACTCCTCCGACGAGGTGTACCTCGGCAGCG---CGACACCAAGG	2398
QY	2672	GCTGGACGTCAAGCGCCAAAGCGCTGGATGCGTTCAAAAGATTGGGAGCCGGCTGGTGC	2731
Db	2399	AGTGGACGTGGACGCGCAAGGCGCAGGAGCGGTTCAAGCGGTTTCGGCGCGGCTGACCG	2458
QY	2732	AGATTGAGATCGGATCAAGACGATGAACGACAGTCCGGACTTTGAAGAACCGGAAGGGGC	2791
Db	2459	AGATCGAGAAACGCGTCGTCAACCATGAACGGGACCCCTCGCCTCAAGAACCGCAACGCC	2518
QY	2792	CTGTGGAATGCGGTACATGCTGCTGTACCCCAACACACGTCGACGTTACCGGCGAGAAGG	2851
Db	2519	CGGCCGAGTCCCTTACACGCTGCTCTACCCCAACACCTCCGACACGAAGGGCG---ACG	2575
QY	2852	CCGAGGGGCTTACTGCCATGGGCATTCCCAACAGCATCTCCATATGA	2898
Db	2576	CCGCCGGCATCACCGCCAAGGGCAATCCAAACAGCATCTCCATTGA	2622

Search completed: March 23, 2004, 06:57:47
Job time : 1290 secs

Db 625 TCTGGTGGCATCCGCGTGCACGCGCTGTCAACTTTGGCAGTACCCTACATACGCGGGT 566
QY 2456 ACCTCCGAAACCGCGCGACGGCCAGCGCGCGCCCGATGCCGAGCCAGGACGCCAGACT 2515
Db 565 ACCTCCGAAACCGCGCGACGGCCAGCGCGCGCCCGATGCCGAGCCAGGACGCCAGACT 506
QY 2516 ACAAGAAGCTGGGAGCGGGGCAGAGGAGCGGACATGGTGTTCATCCGCACCATCACCA 2575
Db 505 ACAAGAAGCTGGGAGCGGGGCAGAGGAGCGGACATGGTGTTCATCCGCACCATCACCA 446
QY 2576 GCCAGTTCCAGACCATCCTGGGCAATCTCGCTCATCGAGATCCTCTCCAAGCACTCTCCG 2635
Db 445 GCCAGTTCCAGACCATCCTGGGCAATCTCGCTCATCGAGATCCTCTCCAAGCACTCTCCG 386
QY 2636 ACGAGGTGTACCTCGGCCAGCGGTGACGAGCCCTGATCGCTGACGCTCAGACGCCAAGGCGC 2695
Db 385 ACGAGGTGTACCTCGGCCAGCGGTGACGAGCCCTGATCGCTGACGCTCAGACGCCAAGGCGC 326
QY 2696 TGGATGCGTTCAAAAGATTTCGGGAGCGCGCTGGTGACGATTGAGAAATCGGATCAAGACGA 2755
Db 325 TGGATGCGTTCAAAAGATTTCGGGAGCGCGCTGGTGACGATTGAGAAATCGGATCAAGACGA 266
QY 2756 TGAACGACAGTCCGGAATTTGAAGAACCGGAAGGGCGCTGTGAAAATGCCGTACATGCTGC 2815
Db 265 TGAACGACAGTCCGGAATTTGAAGAACCGGAAGGGCGCTGTGAAAATGCCGTACATGCTGC 206
QY 2816 TGTACCCCAACACGTCGGACGTTACCGGCGAGAGGCCGAGGGGCTTACTGCCATGGGCA 2875
Db 205 TGTACCCCAACACGTCGGACGTTACCGGCGAGAGGCCGAGGGGCTTACTGCCATGGGCA 146
QY 2876 TTCCCAACAGCATCTCCATATGAGCCTGGGCGAGATTGTGTCTCGTAGTAAATTTGTGTC 2935
Db 145 TTCCCAACAGCATCTCCATATGAGCCTGGGCGAGATTGTGTCTCGTAGTAAATTTGTGTC 86
QY 2936 TGCGCGCTGCGATGTTTCTTCATTGGTTTGTGTCAGTCTCAGGGTAGGGGATGAGATC 2995
Db 85 TGCGCGCTGCGATGTTTCTTCATTGGTTTGTGTCAGTCTCAGGGTAGGGGATGAGATC 26
QY 2996 ATACCATGATCTTTGTAGGGTTGAG 3020
Db 25 ATACCATGATCTTTGTAGGGTTGAG 1

RESULT 3
CG157905
LOCUS CG157905 944 bp DNA linear GSS 21-AUG-2003
DEFINITION PUFQD69TB_ZM_0.6_1.0_KB_Zea_mays_genomic_clone_ZMMBTA0707L18,
genomic survey sequence.
ACCESSION CG157905
VERSION CG157905.1 GI:34048706
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 944)
REFERENCE Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
AUTHORS Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
Maize Genomics Consortium
JOURNAL Unpublished (2003)
COMMENT Other_GSSs: PUFQD69TD
Contact: Cathy Whitelaw
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers

source 1. .944
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTA0707L18"
/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
Cot selected genomic DNA library"
ORIGIN
Query Match 22.8%; Score 715; DB 29; Length 944;
Best Local Similarity 88.8%; Pred. No. 3.4e-63;
Matches 788; Conservative 0; Mismatches 90; Indels 9; Gaps 1;
QY 2110 AGAGGTGGCTGTGCCGAGCCAGTCAAGCCCATATGTTGTCGACTGCTGATCAAGGAC 2169
Db 58 AGAGGTGGCTGTGCCGAGCCAGTCAAGCCCATACGGTGTCCGGTGTGCTGATCAAGGAC 117
QY 2170 TACCCCTATGCGGTTGACGGGCTCGTCACTGTGGTGGCGATCGAGCGGTGGTCAAGGAG 2229
Db 118 TACCCCTATGCGGTTGACGGGCTCGTCACTGTGGTGGCGATCGAGCGGTGGTCAAGGAG 177
QY 2230 TACCTGGACATCTACTACCCCTAACGACGGCGAGCTCCAGCGTGAAGTGGAGCTGCAGGGG 2289
Db 178 TACCTGGACATCTACTACCCCTAACGACGGCGAGCTCCAGCGCGAGCTGGAGCTGCAGGGG 237
QY 2290 TGGTGAAGAGGTGCGTGAGGAGCGGACGCGGCGACCTCAAGAGCCGAGACTGGTGGGCC 2349
Db 238 TGGTGAAGAGGTGCGTGAGGAGCGGACGCGGCGACCTCAAGAGCCGAGACTGATGGGCC 297
QY 2350 AGGATGGACACCGTCCAGCAGCTGGCTAGGGCGTGACAGACCATCATCTGGTGGCATCC 2409
Db 298 AGGATGGACACCGTCCAGCAGCTGGCTAGGGCGTGACAGACCATCATCTGGTGGCATCC 357
QY 2410 GCGCTGCACCGCGCTGTCAACTTTGGGCGAGTACCCATACGCGGGTACCTCCCGAACCGG 2469
Db 358 GCGCTGCACCGCGCGTCAACTTTGGGCGAGTACCCGTAAGCGGGTACCTGCCGAACCGG 417
QY 2470 CCGACGCGCAGCGCGCGCGCGATGCCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 2529
Db 418 CCGACGCGTACCGCGCGCGCGCGATGCCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 477
QY 2530 GCGGGGCGAAGGAGCGCGCGCGCGATGGTGTTCATCCGCGACCATCACCGAGCTTCAGACC 2589
Db 478 GCGGGGCGAAGGAGCGCGCGCGCGATGGTGTTCATCCGCGACCATCACCGAGCTTCAGACC 537
QY 2590 ATCTTGGGCATCTCGCTCATCGAGATCCTCTCCAAGCACTCTCCGACGAGGTGACCTC 2649
Db 538 ATCTTGGGCATCTCGCTCATCGAGATCCTCTCCAAGCACTCTCCGACGAGGTGACCTC 597
QY 2650 GGCACGCTGACGAGCGCTGATCGCTGGACGCTCAGACGCGGAGCGGAGCGGAGCGGAG 2709
Db 598 GGCACGCGCAGCGAGCGCTGAGCGCTGGACGCTCGGAGCGGAGCGGAGCGGAGCGGAGCG 657
QY 2710 AGATTGGGAGCGCGCTGGTGCAGATTGAGAAATCGGATCAAGACGATGAACGACAGTCCG 2769
Db 658 AGTTTCGGAAGCGCGCTGGTGGAGATCGAGAAGCGGATCAGGACGATGAACGACAGCGCG 717
QY 2770 GACTTGAAGAACCGGAAGGGCGCTGTGAAATGCCGTACATGCTGTGATACCCCAACACG 2829
Db 718 ACGTTGAAGAACCGGAAGGGCGCTGGAGATGCCGTACATGCTGTGATACCCCAACACG 777
QY 2830 TCGGACGTTACCGGCGAGAGCGCGGCTTACTGCCATGGGCAATCCCAACAGCATC 2889
Db 778 TCGGATGTACCGGCGAGAGCGGCGGCTCACTGCCATGGGCAATCCCAACAGCATC 837
QY 2890 TCCATATGAGCCTGGGCGAGATTGT-----GTCTCGTAGTAAATTTGTTGCTGCGC 2940
Db 838 TCCATATGAGCCTCGTCACTGCGCTGAGCGGATGGTTGTAGATGTTCTGTACGCTGTGT 897
QY 2941 CGTGGCATGTGTTTCTTCAATGGTTTGTTCAGTCTCAGGGTAGGGGA 2987

Db	898	GTATGTGTCGTTTATTTCGTTGGTTTGTGAGTCTCAGGCTCAGGGTAGGGAA	944
RESULT 4			
CG238091			
LOCUS	CG238091	992 bp	DNA linear GSS 22-AUG-2003
DEFINITION	OGWHX42TV ZM_0.7_1.5_KB Zea mays genomic clone ZM582G12, genomic survey sequence.		
ACCESSION	CG238091		
VERSION	CG238091.1	GI:34137977	
KEYWORDS	GSS.		
SOURCE	Zea mays		
ORGANISM	Zea mays		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.		
AUTHORS	Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.		
TITLE	Consortium for Maize Genomics		
JOURNAL	Unpublished (2002)		
COMMENT	Other GSSs: OGWHX42TH Contact: Cathy Whitelaw		
FEATURES	TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 301-838-0208 Email: whitelaw@tigr.org Seq primer: TF Class: sheared ends. Location/Qualifiers 1..992 /organism="Zea mays" /mol_type="genomic DNA" /strain="B73" /db_xref="taxon:4577" /clone="ZM582G12" /clone_lib="ZM_0.7_1.5_KB" /note="vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"		
ORIGIN	Query Match 22.3%; Score 698.8; DB 29; Length 992; Best Local Similarity 89.8%; Pred. No. 1.4e-61; Matches 799; Conservative 0; Mismatches 2; Indels 89; Gaps 1;		
Qy	1845	CTGGCTGAACACGACGCGGTGATCGAGCCGTTCTGTAATCGGACAAACCGGAGCTCAG	1904
Db	103	CAGGCTGAACACGACGCGGTGATCGAGCCGTTCTGTAATCGGACAAACCGGAGCTCAG	162
Qy	1905	CGTGGTGCATCCCGTGCAAGCTGCTGAGCCGCACTACCGTGACACGCTGAACATCAA	1964
Db	163	CGTGGTGCATCCCGTGCAAGCTGCTGAGCCGCACTACCGTGACACGCTGAACATCAA	222
Qy	1965	CGCCTGGCACGCCAGACACTCATCAACGCCGGCGGCTCTTCGAGCGCACCGTGTCCC	2024
Db	223	CGCCTGGCACGCCAGACACTCATCAACGCCGGCGGCTCTTCGAGCGCACCGTGTCCC	282
Qy	2025	TGCAAAAGTACGCGCTGGGATGTCCGCGAGACGCTGTACAAGAGCTGGAATTTCAACGAGCA	2084
Db	283	TGCAAAAGTACGCGCTGGGATGTCCGCGAGACGCTGTACAAGAGCTGGAATTTCAACGAGCA	342
Qy	2085	GGCTCTCCAGCAGATCTCGTCAAG-----AGAGGT	2109
Db	343	GGCTCTCCAGCAGATCTCGTCAAGAGGTACGTAGACAATACACTGAGGTGAGCAGCACT	402
Qy	2110	-----AGAGGT	2115
Db	403	AAAGCCTATAGAAAACCTGTTGGTTCTTACGCTGGTTGTTGGTTGCGTTCAGAGGT	462
Qy	2116	GTGGCTGTCCGGACCAAGTCAAGCCCATATGGTGTCCGACTGTGATCAAGGACTACCCC	2175
Db	463	GTGGCTGTCCGGACCAAGTCAAGCCCATATGGTGTCCGACTGTGATCAAGGACTACCCC	522
Qy	2176	TATGCGTTGACGGGCTCGTCACTCTGGTGGCGGATCGAGCGGTGGTCAAGGAGTACCTG	2235
Db	523	TATGCGTTGACGGGCTCGTCACTCTGGTGGCGGATCGAGCGGTGGTCAAGGAGTACCTG	582
Qy	2236	GACATCTACTACCTAAACGACGCGAGCTCCAGCGTGAAGTGAAGTGAAGTGAAGTGAAGT	2295
Db	583	GACATCTACTACCTAAACGACGCGAGCTCCAGCGTGAAGTGAAGTGAAGTGAAGTGAAGT	642
Qy	2296	AAGGAGTGTGAGGAGGCGGACGCGGACCTCAAGGACCGAGACTGGTGGCCAGGATG	2355
Db	643	AAGGAGTGTGAGGAGGCGGACGCGGACCTCAAGGACCGAGACTGGTGGCCAGGATG	702
Qy	2356	GACACGCTCCAGCAGCTGGCTAGGGCGTGCACGACCACTATCTGGTGGCATCCGCGCTG	2415
Db	703	GACACGCTCCAGCAGCTGGCTAGGGCGTGCACGACCACTATCTGGTGGCATCCGCGCTG	762
Qy	2416	CACGCGGCTGTCAACTTTGGGCGAGTACCCATACGCGGGTACCTCCCGAACCGGCGGACG	2475
Db	763	CACGCGGCTGTCAACTTTGGGCGAGTACCCATACGCGGGTACCTCCCGAACCGGCGGACG	822
Qy	2476	GCCAGCGGCGCCGATGCGGAGCGGAGCCAGCCAGCCAGCTACAAGAGCTGGGAGCGGG	2535
Db	823	GCCAGCGGCGCCGATGCGGAGCGGAGCCAGCCAGCCAGCTACAAGAGCTGGGAGCGGG	882
Qy	2536	CAGAGGAGCGGAGCATGGTGTTCATCCGCGACCATCAAGGAGCTCCAGACCATCCTG	2595
Db	883	CAGAGGAGCGGAGCATGGTGTTCATCCGCGACCATCAAGGAGCTCCAGACCATCCTG	942
Qy	2596	GGCATCTCGCTCATCGAGACTCTTCCAGCACTCTCCGAGGAGGTGTA	2645
Db	943	GGCATCTCGCTCATCGAGACTCTTCCAGCACTCTCCGAGGAGGTGTA	992
RESULT 5			
CB669925			
LOCUS	CB669925	848 bp	mRNA linear EST 09-APR-2003
DEFINITION	OSJNE02L22.f OSJNE Oryza sativa (japonica cultivar-group) cDNA clone OSJNE02L22 5', mRNA sequence.		
ACCESSION	CB669925		
VERSION	CB669925.1	GI:29673650	
KEYWORDS	EST.		
SOURCE	Oryza sativa (japonica cultivar-group)		
ORGANISM	Oryza sativa (japonica cultivar-group)		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartioideae; Oryzeae; Oryza.		
AUTHORS	Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E., Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.		
TITLE	Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Rod Wing Arizona Genomics Institute University of Arizona Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ 85721-0088, USA Tel: 520 626 3967 Fax: 520 621 9288 Email: http://genome.arizona.edu PCR Primers FORWARD: gta aaa cga cgg cca gtc BACKWARD: gga aac agc tat gac cat g Plate: 02 row: L column: 22 Seq primer: gta aaa cga cgg cca gtc.		
FEATURES	Location/Qualifiers 1..848 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="mRNA" /cultivar="Nipponbare" /db_xref="taxon:39947"		

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		/clone_lib="OSJNEe"	
		/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2: XhoI; 24 hrs after inoculation with Rice Blast (70-15)"	
ORIGIN			
Query Match		21.1%; Score 660.8; DB 14; Length 848;	
Best Local Similarity		86.2%; Pred. No. 1e-57;	
Matches 731; Conservative		0; Mismatches 117; Indels 0; Gaps 0;	
Qy	1600	GACGAGATCAACGAGCTGGAGGGAACTTCATCTACGCCAGCAGGACCCCTACTGTTCTCTG	1659
Db	1	GACAAGATCAACAAGTTCCTTGGTAACTTCATATATCGGAGCAGGACCACTTCTGCTCCTG	60
Qy	1660	AAGACGATGGCACGCTGAAGCCCTGGCCATCGAGCTGAGCCTGCCCCACCCCTGACGGC	1719
Db	61	AAGACGATGGCACCCCTGAAGCCCTGGCGATCGAGCTGAGCCTGCCGACCCCGATGGC	120
Qy	1720	CAGACGCGCGCGGTGAGCAAGGTGTACACCCCGGCTCACACCGCGCTCGAGGGCCAC	1779
Db	121	CAGCAGCACGGCGCGCTGAGCAAGGTGTACACTCCAGCCAAACACCGCGCTCGAGAGCCAA	180
Qy	1780	GTCGGCAGCTCGCAAGGCTTATGCTGCGTAAACGACTCTGCTGGCATCAGCTGATC	1839
Db	181	ATCTGGCAGCTCGCCAAAGTTTACGCTCCGCTCCGTCACGACTCTGTTGGCACGAGTGATC	240
Qy	1840	AGCCACTGGCTGAACACGACGCGGTGATCGAGCCGTTCTGTAATCGCGACAAACCCGGCAG	1899
Db	241	AGCCACTGGCTGAACACTCAGCCCGTGTATCGAGCCGTTCTGATCGCGACGAACCCGGCAG	300
Qy	1900	CTCAGCGTGGTGATCCCGTGACAAAGCTGCTGAGCCCGCACTACCCGTGACACGCTGAAC	1959
Db	301	CTCAGCGTGGTGACCCCGTGACAAAGCTGCTGAGCCCGCACTACCCGCGACGATGAAC	360
Qy	1960	ATCAACGCCCTGGCACGCGGACACTCATCAACCGCGCGGCTTCTTCGAGCGCACCCGTG	2019
Db	361	ATCAACGCTCTGGCACGCGGACACTCATCAACCGCGGATGGCATCTTCGAGAACCCGTC	420
Qy	2020	TTCCTGTCAAAGTACGCGCTGGGATGTGCGGACAGCTGTACAAGAGCTGGAATTTCAAC	2079
Db	421	TTCGAGGCAAGTACGCGCTCGAGATGTCTCCGTCTGTACAAGAACTGGAAGTTCAAC	480
Qy	2080	GAGCAGGCTCTCCAGCAGATCTCTGTCAAGAGAGGCTGTGCTGTGCCGACCACTCAAGC	2139
Db	481	GAGCAGGCTCTCCCGTCTGATCTGTCAAGAGAGGCTGTGCTGTGCCGACCCGACGAGC	540
Qy	2140	CCATATGGTGTCCGACTGCTGATCAAGGACTACCCCTATGCCGTGACGGGCTCGTCATC	2199
Db	541	CCGTACAACGTCGCGCTGTGATCAAGGACTACCCGTACGCGCTGGACGGGCTGGTGATC	600
Qy	2200	TGGTGGCGATCGAGCGGTGGTCAAGGAGTACCTGGACATCTACTACCCCTAACGACGGC	2259
Db	601	TGGTGGCGATCGAGCGGTGGTGGGCGAGTACCTGGCCATCTACTACCCCAACGACGGC	660
Qy	2260	GAGCTCCAGGTGACGCTGGAGCTGCAGGCGTGGTGAAGGAGGTGCGTGAGGAGCGCAC	2319
Db	661	GTGCTCCGCGGACGAGGAGCTGCAGGCGTGGTGAAGGAGGTGCGGAGGTCGGCCAT	720
Qy	2320	GGCGACCTCAAGGACCGAGACTGGTGGCCCGGATGGACACCGTCCAGCAGCTGGCTAGG	2379
Db	721	GGCGACCTCAAGGACCGAGACTGGTGGCCCGAAGATGGACACCGTCCAGGAGCTACCCGG	780
Qy	2380	GCGTGCACGACCATCATCTGGTGGCATCCGCGGTGACGCGGCTGTCACTTTGGGCGAG	2439
Db	781	GCGTGCACCATCATCATCTGGATCGCGTGGCGCTGCGCGGCTGACGCGGCTCACTTCGGCCAG	840
Qy	2440	TACCCATA	2447
Db	841	TACCCGTA	848

RESULT 6	CK161284	1158 bp	mrna	linear	EST 05-DEC-2003
LOCUS	FGAS013850	Triticum aestivum FGAS: Library 4 Gate 8	Triticum		
DEFINITION	aestivum cDNA, mRNA sequence.				
ACCESSION	CK161284				
VERSION	CK161284.1	GI:38989328			
KEYWORDS	EST.				
SOURCE	Triticum aestivum (bread wheat)				
ORGANISM	Triticum aestivum				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
	Poideae; Triticeae; Triticum.				
REFERENCE	1 (bases 1 to 1158)				
AUTHORS	Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,D., Genswein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A., Links,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilson,D., Penniket,C., Roach,J.L. and Sarhan,F.				
TITLE	Functional Genomics of Abiotic Stress In Wheat and Canola Crops				
JOURNAL	Unpublished (2003)				
COMMENT	Contact: Wm L Crosby Bioinformatics University of Saskatchewan, Department of Computer Science 1C101 Engineering Building, 57 Campus Drive, Saskatoon, Saskatchewan, S7N 5A9, Canada Tel: 306 966 1769 Fax: 306 966 2033 Email: fgas_est@cs.usask.ca This sequence is the direct result of the Base calling software Phred (default parameters). It is the raw base calls. To aid in the identification of the high quality insert the software Lucy (default parameters) has been run on this sequence. Lucy identified the region [58,840]. Plate: L4B001 row: E column: 21. Location/Qualifiers 1..1158 /organism="Triticum aestivum" /mol_type="mrna" /db_xref="taxon:4565" /clone_lib="Triticum aestivum FGAS: Library 4 Gate 8" /note="Organ: Crown and leaf; Vector: pCMV.SPORT6; Aerial parts (crown and leaf) of wheat cultivar Norstar during dehydration stress. 8 mRNA populations were combined before constructing the library. The first four come from removing plants from vermiculite (7 day old plants) and incubating them at 20C on the bench without water for 1, 2, 3 and 4 days. The last four come from plants grown in soil in a growth chamber after watering is terminated. Four samplings were taken in a two week period; the first after wilting was observed and the last, two weeks later, consisted of live crown and stem tissue (leaf tissue was yellow and dead). First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NotI."				
FEATURES	source				
ORIGIN					
Query Match	20.6%;	Score 647;	DB 14;	Length 1158;	
Best Local Similarity	82.0%;	Pred. No. 2.2e-56;			
Matches 756; Conservative	0;	Mismatches 160;	Indels 6;	Gaps 1;	
Qy	1555	AGGCTCTTCATCCTAGACCACTGACCATTTTCATGCGGTACCTCGACGAGATCAACGAG	1614		
Db	5	AGGTCTTCTTNCNAGAACACCAAGAACTTCATGCCATCCCTTGACCCGTATCAACAAG	64		
Qy	1615	CTGAGGGGAACCTTCATCTACGCCAGCAGGACCCCTACTGTTCTCTGAAGGACGATGGCAG	1674		
Db	65	CTGGAAGGCGGACTACATCTACGCTTCGAGGACCCCTGCTGTTCTCTGAAGGCCGACGCGCAG	124		
Qy	1675	CTGAAGCCCTTGGCCATCGAGCTGAGCCTGCCCCACCCCTGACGGCCAGCAGCGCGCGCG	1734		
Db	125	CTGAAGCCCTTGGCCATCGAGCTGAGCCTGCCACACCCCTGACCGAATACAGCAGCGCGCG	184		

QY	1735	GT	CAGCAAGGTGTACACCCCGGC-----TCACACCGGCGTTCGAGGGCCACGCTCTGGCAG	1789
Db	185	AAGAGCACGGTGTACCTTCCGGCTGATATTGACTCTGGTTGATGGCCAGATCTGGCAG	244	
QY	1789	CT	CGCCAAGGCTTATGCGTGCCTAAACGACTCTGCCCTGGCATCAGCTGATCAGCCACTGG	1848
Db	245	CT	TGCCAAGGCTTACGCGCTCGTTCGACGACTCTGCGTGGCATCAGCTTATCAGCCACTGG	304
QY	1849	CT	GAACACGACGCGGTGATCGAGCCGTTTCGTAATCGGACAAACCGGCAGCTCAGCGTG	1908
Db	305	CT	GAACACACACGCGGTGATCGAGCCGTTTCGTGATTGGGACGAACCGGCAACTCAGTG	364
QY	1909	GT	GATCCCGTGCACAAGCTGTCTGAGCCCGCACTACCGTGACACGCTGAACATCAACGCC	1968
Db	365	GT	GACCCCGGTGCACAAGCTGTCTGAGCCCAACATTACCGGACACGTTGAACATCAATGCC	424
QY	1969	CT	GCACGCCAGACACTCATCAACGCCGGCGGCTCTTCGAGCGCACCGTGTTCCTGCA	2028
Db	425	CT	GGCGGAACCACTCTCATCAACGCCGGTGGCGCTTTTGAGATGACCGCTCTTCCCGGAG	484
QY	2029	AAG	TACGCGTGGGATGTCTCGGCAGACGTGTACAAGAGCTGGAATTTCAACGAGCAGGCT	2088
Db	485	AA	TATGCGCTTGAGATGTCTTCATCGTCTACAAGAACTGGAAGCTCACCGAGCAGGGC	544
QY	2089	CT	CCAGCAGATCTCGTCAAGAGAGGTGTGGCTGTGCCGACCAGTCAAGCCCCATATGGT	2148
Db	545	CT	CCCGACGATCTCGTCAAGAGAGGCATGGCTGTGCCGATTTCATCGAGCCCCATACGGT	604
QY	2149	GT	CCGACTGCTGATCAAGGACTACCCCTATGCCGTTGACGGGCTCGTCATCTGGTGGCG	2208
Db	605	GT	CCGGCTGCTGATCAAGGACTACCCGTACCGCGTGGACGGGCTGGTGATCTGGTGGCG	664
QY	2209	AT	CGACGGTGGGTCAAGGAGTACCTGGACATCTACTACCTAACGACGGCGAGTCCAG	2268
Db	665	AT	CGACGGTGGGTGAACGAGTACCTGGCCATCTACTACCCCAACGACGGCGTGTCCGG	724
QY	2269	CG	TGACGTGGAGCTGCAGGCGTGGTGGAAAGGAGGTGCGTGAGGAGGCGCACGGCGACCTC	2328
Db	725	GCC	GACAAGGAGCTGGAGGAGTGGTGGAAAGGAGGTGCGCGAGGTGCGGACCGCGACCTC	784
QY	2329	AAG	ACCGAGACTGTTGGCCCCAGGATGGACACCGTTCAGACAGCTGGCTAGGGCGTGACG	2388
Db	785	AAG	GACGCCGACTGGTGGCCCCAAGATGGTGACCCGTGCAGGAGCTGGCCACGCTGCACC	844
QY	2389	ACC	ATCATCTGGTGGCATCCGCGCTGCACCGCGGTCTCAACTTTGGGCACTACCCATAC	2448
Db	845	ACC	ATCATCTGGTGGCATCGGCGCTACACGCGGCGGTNCACCTTCGGGCAGTACCCGTAC	904
QY	2449	GCC	GGTACCTCCCGAACCGGC	2470
Db	905	GCT	GGTACTCCCGAACCGGC	926

RESULT	7
CAL139868	
LOCUS	758 bp mRNA linear EST 24-SEP-2003
DEFINITION	SCEZRT2017B11.g RT2 Saccharum officinarum cDNA clone SCEZRT2017B11 5', mRNA sequence.
ACCESSION	CAL139868
VERSION	CAL139868.1 GI:35032284
KEYWORDS	EST.
SOURCE	Saccharum officinarum
ORGANISM	Saccharum officinarum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum. 1 (bases 1 to 758)
REFERENCE	Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P. The libraries that made SUCEST
AUTHORS	Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
TITLE	Contact: Arruda P
JOURNAL	Centro de Biologia Molecular e Engenharia Genetica
COMMENT	Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
<http://www.bcccenter.fcav.unesp.br>
Plate: 017 row: B column: 11
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Vector: pSport1; Site 1: SalI; Site 2: NotI; An
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tips(0.3cm-long) from adult plants]. cDNA was prepared
from polyA+ mRNA using SuperScript Plasmid System Kit
(Invitrogen). The double-strand cDNAs were fractionated
in a sepharose CL-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 Kb were directionally cloned into the
vector. Details of each source of RNA and library
construction can be obtained at
<http://sucest.lad.ic.unicamp.br/public>"

Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br


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VERSION
KEYWORDS
SOURCE
ORGANISM
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Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.
1 (bases 1 to 709)
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 073 row: G column: 08
Seq primer: T7 Promoter Primer.
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Vector: pSport1; Site1: SalI; Site2: NotI; An
unidirectional cDNA library generated from [Root
tips(0.3cm-long) from adult plants]. cDNA was prepared
from polyA+ mRNA using Superscript Plasmid System Kit
(Invitrogen). The double-strand cDNAs were fractionated
in a sepharose CL-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 Kb were directionally cloned into the
vector. Details of each source of RNA and library
construction can be obtained at
http://sucust.lad.ic.unicamp.br/public"
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ORIGIN

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Query Match 19.9%; Score 622.6; DB 13; Length 709;
Best Local Similarity 94.8%; Pred. No. 7.7e-54;
Matches 643; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
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QY 2360 CCGTCCAGCAGCTGGCTAGGCGTGCACGACCATCATCTGGGTGGCATCCGCGCTGCACG 2419
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QY 2420 CGGTGTCAACTTTGGGCACTPACCCATACCGCGGTACCTCCGACCGCGGCGGCGCA 2479
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Db 602 CCGGCGAGAAGGGCGGCGGCTTACTGCCATGGGCGATTCCCAACAGCATCTCCATATGAG 661
QY 2900 CTTGGCGAGATTGTGCT 2917
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LOCUS
DEFINITION
SCBFR3094B01.g RT3 Saccharum officinarum cDNA clone SCBFR3094B01
5', mRNA sequence.
CA279071
ACCESSION
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CA279071
772 bp mRNA linear EST 26-SEP-2003
SCBFR3094B01.g RT3 Saccharum officinarum cDNA clone SCBFR3094B01
5', mRNA sequence.
CA279071
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VERSION	CA279071.1	GI:36004162	
KEYWORDS	EST.		
SOURCE	Saccharum officinarum		
ORGANISM	Saccharum officinarum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum.		
AUTHORS	1 (bases 1 to 772)		
TITLE	Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.		
JOURNAL	The libraries that made SUCEST		
COMMENT	Genet. Mol. Biol. 24 (1-4), 1-7 (2001) Contact: Arruda P Centro de Biologia Molecular e Engenharia Genetica Universidade Estadual de Campinas Caixa Postal 6010, 13083-970, Campinas SP, Brazil Tel: 55 19 3788 1137 Fax: 55 19 3788 1089 Email: parruda@unicamp.br Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br Plate: 094 row: B column: 01 Seq primer: T7 Promoter Primer. Location/Qualifiers 1..772 /organism="Saccharum officinarum" /mol_type="mRNA" /db_xref="taxon:4547" /clone="SCBRT3094B01" /lab_host="DH10B" /clone_lib="RT3" /note="Organ: Root apex from adult plants; Vector: pSport1; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from [Root apex from adult plants]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public "		
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ORIGIN			
Query Match	19.7%;	Score 617.6;	DB 14; Length 772;
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Db	3	GACACATTGACCATCATTTGCCCTGACACGCCAGACACTCATCAACGCTGGTGCATCTTC	62
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QY	2128	GACCAGTCAAGCCCCATATGTTGTCGACTGCTGATCAAGGACTACCCCTATGCCGTTGAC	2187
Db	183	GACCAATCAAGCCCCATATGTTGTCGACTGCTGATCAAGGACTACCCATATGCCGTTGAT	242
QY	2188	GGGCTCGTCACTCTGTGGCGGATCGAGCGGTGGTCAAGGAGTACCTGGACATCTACTAC	2247
Db	243	GGGCTCGTCACTCTGTGGCGGATTGAGCAGTGGTCAAGGAGTACTTGGACGTCTACTAC	302
QY	2248	CCTAACGACGGCGAGTCCAGCGTGACGTGGAGCTGCAGCGGTGTGGAAGGAGGTGCGT	2307
Db	303	TCTAACGACGGTGAGTCCAGCGTGATGTGGAGCTGCAGGCATGTTGGAAGAGGTGCGT	362
QY	2308	GAGGAGCGCACGGCGACCTCAAGGACCGAGACTGGTGGCCCCAGGATGGACACCGTCCAG	2367
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Db	1845	CTGGCTGAACACGACCGCGGTGATCGAGCGTTCGTAATCGCGACAAACCGGACGCTCAG	1904
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Db	363	GAGGAGCGCACGGCGACCTTAAGGATCGAGACTGTTGGCCCCAGGATGAACACCGTCCAG	422
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ACCESSION	CG325032		
VERSION	CG325032.1	GI:34242298	
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ORGANISM	Zea mays		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.		
REFERENCE	1 (bases 1 to 892)		
AUTHORS	Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.		
TITLE	Consortium for Maize Genomics		
JOURNAL	Unpublished (2002)		
COMMENT	Contact: Cathy Whitelaw TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 301-838-0208 Email: whitelaw@tigr.org Seq primer: TF Class: sheared ends.		
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Db |||||
QY 160 CGTGGTGCATCCCGTGCACAAGCTGCTGAGCCCGCACTACCGTGACACGCTGAACATCAA 219
Db |||||
QY 1965 CGCCTTGCACGCCAGACACTCATCAACGCCGGCGGCTTCGAGCGCACCGTGTCCC 2024
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VERSION CA298585.1 GI:36069249
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE 1 (bases 1 to 679)
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica

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Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 044 row: A column: 07
Seq primer: T7 Promoter Primer.
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/lab_host="DH10B"
/clone_lib="FL8"
/note="Organ: Developing inflorescence and rachis
(10cm-long); Vector: pSport1; Site_1: SalI; Site_2: NotI;
An unidirectional cDNA library generated from [Developing
inflorescence and rachis (10cm-long)]. cDNA was prepared
from polyA+ mRNA using SuperScript Plasmid System Kit
(Invitrogen). The double-strand cDNAs were fractionated
in a sepharose CL-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 Kb were directionally cloned into the
vector. Details of each source of RNA and library
construction can be obtained at
http://sucest.fad.ic.unicamp.br/public"

ORIGIN

Query Match 19.0%; Score 594.2; DB 14; Length 679;
Best Local Similarity 92.2%; Pred. No. 5.6e-51;
Matches 626; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
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QY 1790 TCGCCAAGGCTTATGCCCTGCGTAAACGACTCTGCCCTGGCATCAGCTGATCAGCCACTGGC 1849
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QY 301 TGGCAGCCAGACACTCATCAACGCTGGTGGCATCTTCGAGCGCACTGTGTTCCCTGGAA 360
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QY 421 TCCCGCAGATCTCGTCAAGAGAGGTGTGGCTGTACAGACCAATCAAGCCCATATGGTG 480
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QY 2330 AGGACCGAGACTGGTGGCC 2348
Db 661 AGGATCGAGACTGGTGGCC 679

RESULT 13
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DEFINITION
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SCJLRT1021H02.g RT1 Saccharum officinarum cDNA clone SCJLRT1021H02

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
CA135806
CA135806.1 GI:35024177
EST.
Saccharum officinarum
Saccharum officinarum

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.

1 (bases 1 to 707)
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089

Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 021 row: H column: 02
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1..707

FEATURES
source
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCJLRT1021H02"
/lab_host="DH10B"
/clone_lib="RT1"
/note="Organ: Root tips (0.3cm-long) from adult plants;
Vector: pSport1; Site_1: SalI; Site_2: NotI; An
unidirectional cDNA library generated from [Root tips
(0.3cm-long) from adult plants]. cDNA was prepared from
polyA+ mRNA using SuperScript Plasmid System Kit
(Invitrogen). The double-strand cDNAs were fractionated
in a sepharose CL-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 Kb were directionally cloned into the
vector. Details of each source of RNA and library
construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"

ORIGIN
Query Match 18.9%; Score 592.6; DB 13; Length 707;
Best Local Similarity 90.7%; Pred. No. 8e-51;
Matches 631; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1612 GAGCTGAGGGGAACCTCATCTACGCCAGCAGGACCCCTACTGTTCTCTGAAGGACGATGGC 1671
Db 11 GGGTTGAGGGGAACCTCATCTATGCAAGCAGGACCCCTACTGTTCTTGAAGGACGATGGC 70

QY 1672 ACCTGAAGCCCTCGGCCATCGAGCTGAGCCTGCCACCCTGTACGGCCAGCAGCGCGC 1731
Db 71 ACCCTGAAGCCCTCGGCCATTGAGCTGAGCCTGCCACCCTGTACGGTGAGCAGCAGCGC 130

QY 1732 GCGGTCAACAAGGTGTACACCCGGCTCACACCGGGCTCAGGGGCCACGTCTGGCAGCTC 1791
Db 131 GCAGTCACAAGGTGTACACCCGGCTCACACTGGCGTGAGGGTCAATCTGGCAACTT 190
QY 1792 GCCAAGGCTTATGCCTGCGTAAACGACTCTGCCTGGCATCAGCTGATCAGCCACTGGCTG 1851
Db 191 GCCAAGGCTTACGCTGCGTAAACGACTCTGCTTGGCATCAGCTGATCAGCCACTGGTTG 250
QY 1852 AACACGACCGCGGTGATCGAGCCGCTCGTAATCGCGACAAACCGGCAGCTCAGCGTGGTG 1911
Db 251 AACACGACCGCGGTGATTGAGCCGCTTGCATCTCAACAACCGGCAGCTCAGCGTGGTG 310
QY 1912 CATCCCGTCACAAGCTGCTGAGCCGCGCACTACCGTGACACGCTGAACATCAACGCCCTG 1971
Db 311 CATCCCGTCATAAGTCTGAGCCCACTACCGTGACACATTAACATCAATGCCCTG 370
QY 1972 GCACGCCACAGACTCATCAACCGCGCGCGGTCTTCGAGCGCACCGTGTTCCTTGCAAG 2031
Db 371 GCACGCCACAGACTCATCAACCGCTGGTGCACTCTTCGAGCGCACTGTGTTCCCTGGAAAA 430
QY 2032 TACGCGCTGGGATGTCCGCGACAGCTGTACAAGAGCTGGAATTTCAACGAGCAGGCTCTC 2091
Db 431 TACGCGCTGGGATGTCTCCGAGCTGTACAAGAGCTGGAATTTCAACGAGCAGGCTCTC 490
QY 2092 CCAGCAGATCTCGTCAAGAGAGGTGTGGTGTGCCGACAGTCAAGCCCCATATGGTGTG 2151
Db 491 CCCGCGATCTCGTCAAGAGAGGTGTGGTGTGTACAGACCAATCAAGCCCCATATGGTGTG 550
QY 2152 CGACTGCTGATCAAGGACTACCCCTATGCCGTGTGACGGGCTCGTCATCTGGTGGCGGATC 2211
Db 551 CGACTGCTGATCAAGGACTACCCATATGNCCTGTATGGGCTCGTGATCTGGTGGCGGAT 610
QY 2212 GAGCGTGGGTCAAGGAGTACCTGGACATCTACTACCTAACGACGGCGAGCTCCAGCGT 2271
Db 611 GAGCAGTGGGTCAAGAGTACTTGGACGTCTACTACTCTAACGACGGTGAGTCCAGCGT 670
QY 2272 GACGTGAGCTGCAGGCGTGGTGAAGGAGGTGCGT 2307
Db 671 GATGTGAGCTGCAGGCAATTGGTGAAGAGAGTGGT 706

RESULT 14
CA164910
LOCUS
DEFINITION
5', mRNA sequence. 674 bp mRNA linear EST 24-SEP-2003
SCSBRZ3124H05.g RZ3 Saccharum officinarum cDNA clone SCSBRZ3124H05

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
CA164910
CA164910.1 GI:35082793
EST.
Saccharum officinarum
Saccharum officinarum

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.
1 (bases 1 to 674)
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089

Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 124 row: H column: 05
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1..674
/organism="Saccharum officinarum"

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 23, 2004, 03:44:22 ; Search time 85 Seconds
(without alignments)
2948.466 Million cell updates/sec

Title: US-10-059-909-16
Perfect score: 4723
Sequence: 1 MFVHGVDRLTGKNKEAWSE.....VTGKAEGLTAMGIPNSISI 887

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4723	100.0	887	AAO27494	Corn (Zea
2	3478	73.6	837	ADA48504	Rice prot
3	2987.5	63.3	863	ADC53139	9'-specif
4	2936.5	62.2	862	AAU99691	Barley wi
5	2936.5	62.2	862	ABG30566	Wild type
6	2929.5	62.0	862	AAU99693	Barley wi
7	2929.5	62.0	862	AAU99692	Barley wi
8	2929.5	62.0	862	ABG30567	Mutant ty
9	2860	60.6	864	ABG30571	Barley lo
10	2829.5	59.9	865	AAR23797	Rice lipo
11	2829.5	59.9	865	AAR20670	Lipoxygen
12	2799.5	59.3	859	ABO19443	Wine grap
13	2777.5	58.8	862	ABO19442	Wine grap
14	2724.5	57.7	862	ABP70404	Amino aci
15	2630.5	55.7	857	AAB46803	Potato LO
16	2491.5	52.8	857	ABG30570	Glycine m
17	2486	52.6	865	ABG30569	Glycine m
18	2476	52.4	880	AAO27492	Balsam pe
19	2423.5	51.3	878	AAB11500	C. sativu
20	2423.5	51.3	878	AAB86036	Cucumber
21	2375	50.3	853	AAR50220	Soybean l
22	2369.5	50.2	864	AAR24042	Lipoxygen
23	2355.5	49.9	839	ABG30568	Glycine m
24	1760.5	37.3	491	AAE39891	Human lip
25	1634	34.6	924	AAE38266	Rice dise

26	1623	34.4	901	4	AAV97741	Aay97741 H. annus
27	1588.5	33.6	923	2	AAR61136	Aar61136 Plant bli
28	1478	31.3	922	5	AAU76150	Aau76150 Rice lipo
29	1459	30.9	445	6	AAO27493	Aao27493 Garden ba
30	805.5	17.1	301	3	AAG24811	Aag24811 Arabidops
31	771	16.3	464	6	AAO27495	Aao27495 Corn (Zea
32	736.5	15.6	312	3	AAG23228	Aag23228 Arabidops
33	681.5	14.4	222	4	AAG83338	Aag83338 P patens
34	681.5	14.4	222	4	AAG80888	Aag80888 Lipid deg
35	575	12.2	242	3	AAG23229	Aag23229 Arabidops
36	547	11.6	131	5	ABP04662	Abp04662 Human ORF
37	540.5	11.4	240	3	AAG23230	Aag23230 Arabidops
38	524.5	11.1	193	3	AAG24812	Aag24812 Arabidops
39	516	10.9	244	4	AAB86035	Aab86035 Cucumber
40	513.5	10.9	676	2	AAW93832	Aaw93832 Human 15S
41	513.5	10.9	676	4	AAE00935	Aae00935 Human 15S
42	513.5	10.9	676	5	ABG61866	Abg61866 Prostata
43	513.5	10.9	676	6	ABU89734	Abu89734 Protein d
44	513	10.9	556	3	AAB19381	Aab19381 Amino aci
45	513	10.9	711	3	AAI19379	Aai19379 Amino aci

ALIGNMENTS

RESULT 1
AAO27494
ID AAO27494 standard; protein; 887 AA.

XX AAO27494;
AC AAO27494;
XX 06-NOV-2003 (first entry)
DT 06-NOV-2003 (first entry)
XX Corn (Zea mays) lipoxygenase isozyme 4 amino acid sequence.
DE Lipoxigenase; hydroperoxidation; polyunsaturated fatty acid; plant;
KW fatty acid metabolite synthesis; signal molecule; growth regulation;
KW development regulation; plant development; wound response;
KW genetic mapping; hyperoxidation catalysis; Corn; enzyme.
XX Zea mays.
OS Zea mays.
XX US2003074693-A1.
PN 17-APR-2003.
PD 29-JAN-2002; 2002US-00059909.
XX 10-FEB-1999; 99US-0119597P.
PR 09-FEB-2000; 2000US-00501422.
XX (CAHO/) CAHOON E B.
PA (KINN/) KINNEY A J.
PA (KLEI/) KLEIN T M.
PA (LEEJ/) LEE J.
PA (PEAR/) PEARLSTEIN R W.
PA (RAFA/) RAFALSKI J A.
PA (SHEN/) SHEN J B.
PA (THOR/) THORPE C J.
PA (TING/) TINGEY S V.
PA (WENG/) WENG Z.
XX Cahoon EB, Kinney AJ, Klein TM, Lee J, Pearlstein RW;
PI Rafalski JA, Shen JB, Thorpe CJ, Tingey SV, Weng Z;
PI WPI; 2003-567325/53.
DR N-PSDB; AAL57714.
XX New isolated polynucleotides encoding plant lipoxygenases, useful in
PT genetic mapping, particularly in catalyzing hyperoxidation of
PT polyunsaturated fatty acids.
XX Claim 19; Page 29-31; 36pp; English.

XX This invention relates to novel nucleotide sequences which encode
CC proteins which have lipoxigenase activity. Lipoxigenases are membrane
CC bound ubiquitous enzymes which catalyse the hydroperoxidation of
CC polyunsaturated fatty acids in the first step of fatty acid metabolite
CC synthesis. Products of this pathway are found as signal molecules
CC involved in growth and development regulation. A knowledge of the amino
CC acid sequence of lipoxigenases may allow the understanding of plant
CC development and wound response. The polynucleotides, polypeptides and
CC lipoxigenases of the invention may therefore be useful in genetic mapping
CC and particularly for catalysing hydroperoxidation of polyunsaturated
CC fatty acids. The present sequence is the amino acid sequence of the Corn
CC (Zea mays) lipoxigenase protein 4 of the invention
XX
SQ Sequence 887 AA;

Query Match 100.0%; Score 4723; DB 6; Length 887;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 887; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFHWGVADRLTGKKEAWSEGKIRGTGTVRLVKKEVLVDGDFNASLLDGVHRLGWDDGVAF 60
Db |||||
QY 61 QLVSAATAADPSNGGRGKVGKAAHLEAAVSLKSTADGETVYRVSEFWEDESQIPGAVLVR 120
Db |||||
QY 121 NLQHAFFFLKTLTLEGVPGKGTGVVAVNSWVYPHKLYSQERIFFFANDTYLPSKMPAALVP 180
Db |||||
QY 181 YRQDELKILRGDDNPGPYQEHDRVYRYDYNDLGDPPDKGEEHARPILGSGQEHYPYRRCR 240
Db |||||
QY 241 TGRHPTKDPNSESRLFLNLNIYVPRDERFGHLKMSDFLGYSLKTIIEAVLPTLGTTFVD 300
Db |||||
QY 301 DTPKEFDSFEDILGLYELGPEAPNPLIAEIRKKIPEFLRSILPNNGSHDPLKMPLPNV 360
Db |||||
QY 361 IKSDVLKKAPEKFGWRTDEEFARETLAGVNPVVIKRLTEPPAKSTLDPROYGDHTSKIT 420
Db |||||
QY 421 EAHIRHNGGLSVQNALRNKRLFLDHDHFMPLYDEINELEGNFIYASRTLLFLKDDGT 480
Db |||||
QY 481 LKPLAIELSLPHDPGQQRGAQVSKVYTPAHTGVEGHVQALAKAYACVNDSAWHQLISHWLN 540
Db |||||
QY 541 THAVTEPFVIATNRQLSVVHPVKLLSPHYRDTLINALARQTLINAGGVFERTVFPKY 600
Db |||||
QY 601 ALGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPYAVDGLVIWVAIE 660
Db |||||
QY 661 RWVKEYLDIYYPNDGELQRDVELQAWKEVREEAHGDLKDRDWPRMDTVQOLARACTTI 720
Db |||||
QY 721 IWVASALHAAVNFGQYPYAGYLPNRPTASRRPMPEPGSHDYKKGAGQKEADVMVFIRIT 780
Db |||||
QY 781 SQFTILGISLIEILSKHSSDEVYLGQRDEPDRWTSDAKALDAFKRFGSLVQIENRIKT 840

Db 781 SQFTILGISLIEILSKHSSDEVYLGQRDEPDRWTSDAKALDAFKRFGSLVQIENRIKT 840
QY 841 MNDSPLKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887
Db 841 MNDSPLKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887
RESULT 2
ADA48504
ID ADA48504 standard; protein; 837 AA.
XX ADA48504;
XX 20-NOV-2003 (first entry)
XX Rice protein conferring disease resistance in plants.
DE disease resistance; pathogen tolerance; plant pathogen; rice.
KW Oryza sativa.
OS WO2003000906-A2.
XX 03-JAN-2003.
XX 21-JUN-2002; 2002WO-IB002453.
XX 22-JUN-2001; 2001US-0300112P.
XX 26-SEP-2001; 2001US-0352277P.
XX 22-MAR-2002; 2002US-0366535P.
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
PA Glazebrook J, Briggs S, Cooper B, Goff SA, Moughamer T;
PI Katagiri F, Krepis J, Provart N, Ricke D, Zhu T;
DR WPI; 2003-184052/18.
DR N-PSDB; ADA48503.
XX New polynucleotide comprising a plant nucleotide sequence having an open
PT reading frame that encodes a polypeptide associated with disease
PT resistance, useful for conferring resistance or tolerance to a plant
PT pathogen.
XX Claim 10; SEQ ID NO 574; 299pp; English.
XX The invention relates to a novel isolated polynucleotide comprising a
CC plant nucleotide sequence having an open reading frame that encodes a
CC polypeptide associated with disease resistance or its fragment having
CC substantially the same activity as the full-length polypeptide. The
CC polynucleotide of the invention is useful for conferring resistance or
CC tolerance to a plant pathogen. The present sequence represents a protein
CC conferring disease resistance used in the invention.
XX Sequence 837 AA;
SQ

Query Match 73.6%; Score 3478; DB 6; Length 837;
Best Local Similarity 75.3%; Pred. No. 2.3e-314;
Matches 666; Conservative 68; Mismatches 98; Indels 52; Gaps 8;

QY 5 GVADRLTGKKEAWSEGKIRGTGTVRLVKKEVLVDGDFNASLLDGVHRLGWDDGVAFQLVS 64
Db |||||
QY 65 ATAADPSNGGRGKVGKAAHLEAAVSLKSTADGETVYRVSEFWEDESQIPGAVLVRNLQH 124
Db |||||
QY 125 ABEFLKTLTLEGVPGKGTGVVAVNSWVYPHKLYSQERIFFFANDTYLPSKMPAALVPYRQD 184
Db |||||
QY 103 SEFFLKTLLTDGVPKGTGVVAVNSWIYPADNYQYERVFAND--LPSKMPAPLIPYRQE 160

QY 185 ELKILRGDDNPGPYQEHDRVYRYDYNDLGDGPDKEEHARPILGSGQEHYPYPRRCRTGRH 244
Db 161 ELNILRGDGKIGPYKEHDRIYRYDYNDLQDPDKGSKLVRPVLGSGQELPYPRRGRTGRA 220
QY 245 PTK-KDPNSESRLFILNLNIYVPRDERFEGHLMKSDFLGYSLKTIIEAVLPTLGTFFVDDTP 303
Db 221 PTKTSDPNTESRLPLDLNIYVPRDERFEGHLMKSDFLGYSLKAIVEGVLPIRTYVDTTP 280
QY 304 KEFDSFEDILGLYELGPEAPNNPLIAEIRKKIPSEFLRSILPNGSHDHPKMPPLPNVIKS 363
Db 281 KEFDSFQDIMELEYEGGLKVANASALAEIKRVPPELIKSLLPVAG-DQVLKPLPHVIKE 339
QY 364 DVLKKAPEKFGWRTDEEFARETLAGVNPVVIKRLTEFFPAKSTLDPKQYGDHTSKITEAH 423
Db 340 -----KFAWRTDEEFAREMLAGVNPVMIKRLT-----STLDPNVTYGDHTSKITEAH 385
QY 424 IRHNMGGLSVQNALRNKRLFILDDHDFMPYLDINELEGNFIYASRTLLFLKDDGTLKP 483
Db 386 IKHNMGLTVQNALKGNRLFILDDHDFMPFLDKINKLDGNFIYASRTLLFLKDDGTLKP 445
QY 484 LAIELSLPHPDGQQRGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSAWHQLISHWLNTHA 543
Db 446 LAIELSLPHPDGQQRGAVSKVYTPANTGVESQIWQLAKAYASVNDSAWHQLISHWLNTHA 505
QY 544 VIEPFIATNRQLSVVHPVHKLLSPHYRDTLNINALARQTLINAGGVFERTVFPKAYALG 603
Db 506 VIEPFIATNRQLSVVHPVHKLLSPHYRDTLNINALARQTLINADGIFEKTVPFGKYLE 565
QY 604 MSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKOYPYAVDGLVIWAIERWV 663
Db 566 MSSVYKWKWTFEQALPVDLVKRGVAVPDPTSPYNVRLLIKOYPYAVDGLVIWAIERWV 625
QY 664 KEYLDIYPNDGELQRDVELQAWKKEVREEAHGDLKDRDWPRMDTVQQLARACTTIWV 723
Db 626 GEYLAIYPNDGVLGDEELQAWKKEVREVGHGDLKDQDWPKMDTVQELTRACTTIWV 685
QY 724 ASALHAAVNFQGYPYAGYLPNRPTASRRPMPPEGSHDYKLGAGQKEADMVFIRTITSQF 783
Db 686 ASALHAAVNFQGYPYAGYLPNRPTVSRRPMPPEGTEEYAKLERGGDEADLVFIHTITSQF 745
QY 784 QTILGISLIEILSKHSSDEVYLGQRDEPDRTWTSDAKALDAFKRFGSLVQIENRIKTMND 843
Db 746 QTILGISLIEILSKHSSDEVYLGQRDTPE-WTSDAKALDAFKRFGSLVQIENRIKOMNG 804
QY 844 SPDLKNRKGVPVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
Db 805 NSALKNRNGPVKMPYMLLYP-----GLTAMGIPNSISI 837
RESULT 3
ID ADC53139 standard; protein; 863 AA.
XX
AC ADC53139;
XX
DT 18-DEC-2003 (first entry)
XX
DE 9'-specific lipoxxygenase gene derived protein.
XX
KW 9-specific lipoxxygenase; 9'-specific lipoxxygenase activity; microbe;
XX animal; plant.
OS Unidentified.
XX
PN JP2002325577-A.
XX
PD 12-NOV-2002.
XX
PF 27-APR-2001; 2001JP-00133611.
XX
PR 27-APR-2001; 2001JP-00133611.
XX
PA (SHIS) SHISEIDO CO LTD.

XX WPI; 2003-460714/44.
DR N-PSDB; ADC53127.
XX
PT A new rice-derived 9-specific lipoxxygenase gene useful for production of
PT 9-specific lipoxxygenase.
XX
PS Disclosure; Page 7-10; 17pp; Japanese.
XX
CC The invention relates to a novel 9-specific lipoxxygenase comprising a
CC fully defined sequence of 863 amino acid residues, as given in the
CC specification and a derivative having 9'-specific lipoxxygenase activity.
CC The 9-specific lipoxxygenase gene is useful for production of the 9-
CC specific lipoxxygenase in microbes, animal or plant cells. This sequence
CC represents the protein from the 9'-specific lipoxxygenase gene of the
CC invention.
XX
SQ Sequence 863 AA;
Query Match 63.3%; Score 2987.5; DB 7; Length 863;
Best Local Similarity 64.4%; Pred. No. 1.3e-268;
Matches 569; Conservative 111; Mismatches 179; Indels 25; Gaps 10;
QY 5 GVADRLTGKKEAWSEKIRGTVRLVKKEVLVDGDFNASLLDGVHRLGWDGVAFLVLS 64
Db 4 GLKDKLTGKN-----GNKIKGLAVLMSRKLLDPRDFTASLLDNVHEVFG--NSITCQLVS 56
QY 65 ATAADPSNGGRGKVGKAAHLEAVVSLKSTADGETVYRVVSFEWD-ESQIGPGAVLVRNLQ 123
Db 57 ATVADQNNNEGRGIVGSEANLEOGLTDLPSVSGESKLTVRFNWEMDKHGVPGAIKKNHH 116
QY 124 HAEFFLKTLLTLEGVPGKGTVVVANSWVYVPHKLYSQERIFFFANDTYLPSKMPAALVPYRQ 183
Db 117 STKFFLKTITLHDVPGCDTIVFVANSWIYVPGKYHYNRIFFANISYPPSQMPEALRPYRE 176
QY 184 DELKILRGDDNPGPYQEHDRVYRYDYNDLGDGPDKEEHARPILGSGQEHYPYPRRCRTGR 243
Db 177 DELRYLRGEDRQGPYQEHDRYRYDYNDLGEFDR--DNPRPVLGSGQKHPYPRRGRTGR 234
QY 244 HPTKDPNSESRLFILNLNIYVPRDERFEGHLMKSDFLGYSLKTIIEAVLPTLGTFFVDDTP 303
Db 235 IPTKDPNSESRLSLE-QIYVPSDERFAHLMKSDFAGYSIKAIVQGLPAIRTYVDLTP 293
QY 304 KEFDSFEDILGLYELGPEAPNNPLIAEIRKKIPSEFLRSILPNGSHDHPKMPPLPNVIKS 363
Db 294 GEFDSFEDILKLYRGGLKPLSIPALEELRKSFPVQLIKDLLPVGG-SYLLKFFKPDIIK- 351
QY 364 DVLKKAPEKFGWRTDEEFARETLAGVNPVVIKRLTEFFPAKSTLDPKQYGDHTSKITEAH 423
Db 352 -----ENEVAWRTDEEFAREILAGLNPVIRRLTEFFPKSTLDPKQYGDQSTITPAH 404
QY 424 IRHNMGGLSVQNALRNKRLFILDDHDFMPYLDINELEGNFIYASRTLLFLKDDGTLKP 483
Db 405 IEKNLEGLSVQQLDSNRLYILDHHDHFMPELIDINSLDGIFTYATRTLFLRDDDTLKP 464
QY 484 LAIELSLPHPDGQQRGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSAWHQLISHWLNTHA 543
Db 465 LAIELSLPHIEGNLTSAKSKVHTPASSGIESWWQWQLAKAYAVAVNDSGWRQLISHWLNTHA 524
QY 544 VIEPFIATNRQLSVVHPVHKLLSPHYRDTLNINALARQTLINAGGVFERTVFPKAYALG 603
Db 525 VMKPFVIATNRQLSVTHPVYKLLQPHYRDTMTINALARQTLINAGGVFERTVFPKAYALG 584
QY 604 MSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKOYPYAVDGLVIWAIERWV 663
Db 585 MSSAVYKWNWFAEQGLPDDDLIKRGIAIKDPSSPSKVLLIKDYPYATDGLAIWQAIQWV 644
QY 664 KEYLDIYPNDGELQRDVELQAWKKEVREEAHGDLKDRDWPRMDTVQQLARACTTIWV 723
Db 645 TEYCAIYYPNDGVLQDVALQAWKKEVREVGHGDLKDADWPKMQSLPBLTACTTIWI 704
QY 724 ASALHAAVNFQGYPYAGYLPNRPTASRRPMPPEGSHDYKLGAGQKEADMVFIRTITSQF 783

Db 705 ASALHAAVNFQYPYAGYLPNRPPTISRRPMPPEPGSKEYTEL---DENPEKFFIRITTSQF 761
QY 784 QTILGISLIEILSKHSSDEVILQORDEPDRTWSDAKALDAPKRFSGRLVQIENRIKTMND 843
Db 762 QTILGVSLEILSKHSADEIVLQORDTPE-WTSDPKALEAFKRFSQLVEIESKVLNMNK 820
QY 844 SPDLKVRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887
Db 821 DPLKVRVGPANFPYTLMPNTSDNKG-AAEGITARGIPNSISI 863

RESULT 4

AAU99691
ID AAU99691 standard; protein; 862 AA.
AC AAU99691;
XX
DT 07-OCT-2002 (first entry)
DE Barley wild-type lipoxigenase 1, LOX-1.
XX
KW Barley; plant; enzyme; lipoxigenase-1; LOX-1; transgenic; beer; beverage;
KW malt; organoleptic property; brewing; trans-2-nonenal; T2N;
KW elevated storage temperature; flavour stability; shelf-life.
XX
OS Hordeum vulgare.
XX WO200253720-A1.
PN
XX
PD 11-JUL-2002.
XX
PF 29-DEC-2000; 2000WO-IB002045.
XX
PR 29-DEC-2000; 2000WO-IB002045.
XX
PA (CARL-) CARLSBERG RES LAB.
PA (HETB) HEINEKEN TECH SERVICES BV.
PA (BRAS-) BRASSERIES KRONENBOURG SA.

PI Douma AC, Doderer A, Cameron-Mills V, Skadhauge B, Bech LM;
PI Schmitt N, Heistek JC, Van Mechelen JR;
XX WPI; 2002-557741/59.
DR N-PSDB; ABK88441.
XX
PT Novel barley cultivar having reduced lipoxigenase 1 activity and which
PT expresses mutant lipoxigenase protein, useful in brewing processes to
PT reduce formation of off-flavors in brewed products e.g. beer during
PT storage.
XX
PS Example 3; Page 86-89; 112pp; English.
XX

CC The invention relates to a barley plant or portion comprising a mutant
CC lipoxigenase-1 (LOX-1) protein, characterised by a reduction or absence
CC of LOX activity as compared to a non-mutated control, or comprising a
CC heterologous nucleic acid sequence expressing an antisense sequence to a
CC portion of a transcribed region of barley lox-1 gene, operably linked to
CC a promoter and a transcription terminator sequence. Also included are
CC grain or plant progeny produced from the barley plant or its portion, a
CC plant product produced from the barely plant or its portion or progeny,
CC and a beverage e.g. beer, manufactured using the plant product, plant or
CC its portion or progeny. The mutated barley plant, portions, progeny and
CC products are useful in the manufacture of a beverage, preferably malt or
CC beer, for stabilising organoleptic properties of a brewed product over a
CC measured period of time for the manufacture of a brewed product having
CC reduced levels of free trans-2-nonenal (T2N) over a measured period of
CC time or under conditions of elevated storage temperature and for the
CC preparation of beverage presenting organoleptic qualities that remain
CC stable over a measured period of time or at elevated storage
CC temperatures. Beer with significantly enhanced flavour stability, both
CC during storage and on exposure to elevated storage temperatures is
CC obtained. These properties enhance the quality of beer and are useful to
CC extend its shelf-life and reduce the need to cool beer during transport

CC and storage. The present sequence is the wild-type LOX-1 protein
XX
SQ Sequence 862 AA;
Query Match 62.2%; Score 2936.5; DB 5; Length 862;
Best Local Similarity 63.1%; Pred. No. 7.6e-264;
Matches 562; Conservative 110; Mismatches 187; Indels 31; Gaps 12;
QY 1 MFHWGVADRLTGKKEAWSEGKIRGTVRLVKKEVLVDGDFNASLLDGVHRLGWDGVAF 60
Db 1 MLLGLIDTLTGANKSA-----RLKGTVLMRKVNLDLNDFGATIIDGIGEFLLG--KGVTC 54
QY 61 QLVSATAADPSNGGRGKVKAAHLEAAVSVLSKSTADGETTVYRVVSFEWD-ESQGIPGAVLV 119
Db 55 QLISSTAVDQDNGGRGKVGAEAELEQWVTSLSPLTGTGESKFGLTFTDWEVEKLGVPGAIVV 114
QY 120 RNLQHAEPFLKTLTLEGVPGK-GTVVFVANSWVPHKLYSQERIFFFANDTVLPSPKMPAAL 178
Db 115 NNYHSSEFLKTTITLHDVPGRSNLTFFVANSWIYPAANYRYSRVFFANDTVLPSPQMPAAL 174
QY 179 VPYRQDELKILRGDDNPGPYQEHDRVYRYDYNLDGDDPKGEEHARPILGSGQEHYPYPRR 238
Db 175 KPYRDELRLNRGDDQGGPYQEHDRYRYDVYNDLGE-----GRPILGNSDHPYPRR 227
QY 239 CRTGRHPTKKDPNSESRLFLNLNLIYVPRDERFGLKMSDFLGYSLKTIIEAVLPTLGTG 298
Db 228 GRTERKPNASDPSLESRLSLE-QIYVPRDERFGLKTSDFLGYSIKAITQCILPAVRTY 286
QY 299 VDDTPKEFDSFEDILGLYELGPEAPNPNLIAETRKIPSEFLRSILPNGSHDHPKMLPLP 358
Db 287 VDTTPGEFDSFQDIINLYEGGIKLPKVAALDELRKQFFLQLIKOLLPPVG-DSLLKLPVP 345
QY 359 NVIKSDVLKKAPEFKFGWRTDEEFARETLAGVNPVVIKRLTEFFPAKSTLDPRQYGDHTSK 418
Db 346 HIHQ-----ENKQAWRTDEEFAREVLAGVNPVMITRLTEFFPKSSLDPSKFGDHTST 397
QY 419 ITEAHIRHNMGGLSVQNALRNKRLFLDHHDFMPYLDINELEGNFIYASRTLLFLKDD 478
Db 398 ITAEHIEKNLEGLTVQALLESNRLYILDHDFMPFLIDVNNLPGNFYATRTLFFLRGD 457
QY 479 GTLKPLAIELSLPHPDGQORGAVSKVYTPAHTG-VEGVWQLAKAYACVNDSAWHQLISH 537
Db 458 GRLTPLAIELSEPIQGGLTTAKSKVYTPVPSGVEGVWELAKAYAVNDSGWHQLVSH 517
QY 538 WLNTHAVIEPFVIATNRQLSVVHPVHKLLSPHYRDTLNINALARQTLINAGGVFERTVFP 597
Db 518 WLNTHAVMEPFVISTNRHLSVTHPVHKLLSPHYRDTMTINALARQTLINAGGIFEMTVFP 577
QY 598 AKVALGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPPYAVDGLVIWW 657
Db 578 GKFALGMSAVVYKDWKFTQGLPDDLIKRGMAVEDPSSPYKVRLLVSDYPYAADGLAIWH 637
QY 658 AIERWVKEYLDIYYPNDGELQRDVELQAMWKEVREEAHGDLKDRDWPRMDTVQQLARAC 717
Db 638 AIEQYVSEYLAIVYPNDGVLGQDTEVQAMWKETREVGHGDLKDAWPWKQSVPELAKAC 697
QY 718 TTIWVASALHAAVNFQYPYAGYLPNRPPTASRRRPMPEPGSHDYKKGAGQKEADMVFIR 777
Db 698 TTIWIGSALHAAVNFQYPYAGYLPNRPPTVSRRRMPEPGTEEYAEI---ERDPERAFIH 754
QY 778 TITSQFOTILGISLIEILSKHSSDEVILQORDEPDRTWSDAKALDAFKRFGSRLVQIENR 837
Db 755 TITSQIQTIIIGVSLLEVLKSHSSDELYLGQDTPPE-WTSDPKALEVFKRFSDRLVEIESK 813
QY 838 IKTMNDSPLKVRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887
Db 814 VVGMNHDPELKNRNGPAKFPYMLLYPNTSDHKG-AAAGLTAKGIPNSISI 862

RESULT 5
ABG30566
ID ABG30566 standard; protein; 862 AA.
XX

FT /note= "Wild-type Gly substituted by Asp"

XX WO200253720-A1.

FN 11-JUL-2002.

XX 29-DEC-2000; 2000WO-IB002045.

PF 29-DEC-2000; 2000WO-IB002045.

XX (CARL-) CARLSBERG RES LAB.

PA (HETB) HEINEXEN TECH SERVICES BV.

PA (BRAS-) BRASSERIES KRONENBOURG SA.

XX Douma AC, Doderer A, Cameron-Mills V, Skadhauge B, Bech LM,

PI Schmitt N, Heistek JC, Van Mechelen JR;

XX WPI; 2002-557741/59.

DR Novel barley cultivar having reduced lipoxigenase 1 activity and which

XX expresses mutant lipoxigenase protein, useful in brewing processes to

PT reduce formation of off-flavors in brewed products e.g. beer during

PT storage.

XX Claim 10; Page; 112pp; English.

XX The invention relates to a barley plant or portion comprising a mutant

CC lipoxigenase-1 (LOX-1) protein, characterised by a reduction or absence

CC of LOX activity as compared to a non-mutated control, or comprising a

CC heterologous nucleic acid sequence expressing an antisense sequence to a

CC portion of a transcribed region of barley lox-1 gene, operably linked to

CC a promoter and a transcription terminator sequence. Also included are

CC grain or plant progeny produced from the barley plant or its portion, a

CC plant product produced from the barley plant or its portion or progeny,

CC and a beverage e.g. beer, manufactured using the plant product, plant or

CC its portion or progeny. The mutated barley plant, portions, progeny and

CC products are useful in the manufacture of a beverage, preferably malt or

CC beer, for stabilising organoleptic properties of a brewed product over a

CC measured period of time for the manufacture of a brewed product having

CC reduced levels of free trans-2-nonenal (T2N) over a measured period of

CC time or under conditions of elevated storage temperature and for the

CC preparation of beverage presenting organoleptic qualities that remain

CC stable over a measured period of time or at elevated storage

CC temperatures. Beer with significantly enhanced flavour stability, both

CC during storage and on exposure to elevated storage temperatures is

CC obtained. These properties enhance the quality of beer and are useful to

CC extend its shelf-life and reduce the need to cool beer during transport

CC and storage. The present sequence represents a mutant of the LOX-1

CC protein. Note: The present sequence is not shown in the specification but

CC was created by the indexer using the wild-type LOX-1 protein and the

CC information in Claim 10

XX

SQ Sequence 862 AA;

Query Match 62.0%; Score 2929.5; DB 5; Length 862;

Best Local Similarity 63.0%; Pred. No. 3.4e-263;

Matches 561; Conservative 110; Mismatches 188; Indels 31; Gaps 12;

Qy 1 MFVHGVADRLTGKNEAWSEKIRGTVRLVKKEVLVDGDFNALSLLDGVHRLGWDDGVAF 60

Db 1 MLLGGLIDTLTGANKSA---RLKGTVVLMRKNVLDLNDGFIIDGIGEFGLG--KGVTC 54

Qy 61 QLVSAATAADPSNGGRKVGKAAHLEAAVSLKSTADGETVYRVSEWD-ESQGIPIGAVLV 119

Db 55 QLISSTAVDQDNGGRKVGABAELEQWVTSLSLTGSEKFGLTFTDWEVEKLGVPGAIVV 114

Qy 120 RNLOHAEFFLTKLTLEGVPGK-GTVVVFVANSWVYPHKLKYSQERIFFANDTYLPSKMPAAL 178

Db 115 NNYHSSEFLKTTITLHDVPGSGNLTFTVANSWIYPAANYRYSRVFFANDTYLPSQMPAAL 174

Qy 179 VPYRQDELKILRGDDNPGPYQEHDRVYRYDYNDLGDGPDKGEHARPILGSGQEHYPYRR 238

Db 175 KPYRDELRNLRGDDQGPYQEHDRYRYDYNDLGE-----GRPILGNSDHPYPRR 227

QY 239 CRTGRHPTKCDPNSESRFLNLNLIYVPRDERFGHLKMSDFLGYSLKTIIEAVLPTLGT 298

Db 228 GRTERKPNASDPSELSLSLE-QIYVPRDEKFGHLKTSDFLGYSIKAITQGLPAVRTY 286

QY 299 VDDTPKEFDSFEDILGLYELGPEAPNNPLIAEIRKIKPSEFLRSILPNGSHDHLKMLPL 358

Db 287 VDTTPEGFDSFQDIINLYEGIKLPKVALEELRKQPLQIKDLLPVG-DSLLKLPVP 345

QY 359 NVIKSDVLKKAPEFKGWRTEDEFARETLAGVNPVVIKRLTEFFPAKSTLDPQYGDHTSK 418

Db 346 HIIQ-----ENKQAWRTDEEFAREVLADVNPVMIITRLTEFFPKSSLDPSKFGDHTST 397

QY 419 ITEAHIRHNMGGLSVQNALRNKRLFILDDHHDHFMPLDINELEGNFIYASRTLLFLKDD 478

Db 398 ITAEHIEKNLEGLTVQQALESNRLYILDHHDHFMPLDINNLPGNFIYATRTLEFLRGD 457

QY 479 GTLKLPLAIELSLPHPDGQQRGAISKVYTPAHTG-VEGHVWQLAKAYACVNDNSAWHQLISH 537

Db 458 GRLTPLAIELSEPIIOGGLTTAKSKVYTPVPSGSGVEGWVWELAKAYAVVNDNSGWHQLVSH 517

QY 538 WLNTHAVIEPPFIATNRQLSVVHPVKLLSPHYRDTLNINALARQTLINAGGVFERTVFP 597

Db 518 WLNTHAVMEPPFVISTNRHLSVTHPVHKLSPHYRDTLNINALARQTLINAGGVFERTVFP 577

QY 598 AKYALGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKOYPYAVDGLVIWM 657

Db 578 GKFAIGMSAVVYKDWKFTQGLDDDLIKRGMAVEDPSSPYKVRLLVSDYPYAADGLAIWH 637

QY 658 AIERWVKEYLDIYPNDGELQRDVELQAWKKEVREAHGDLKDRDWPRMDTVQQLARAC 717

Db 638 AIEQVSEYLAIIYPNDGVLQGDTEVQAWKETREYVGHGDLKADAPWPKMQSVPELAKAC 697

QY 718 TTIWVASALHAAVNFQYVYAGYLPNRPTASRRRNPPEPGSHDYKKLGAQKEADVMVFI 777

Db 698 TTIWIGSALHAAVNFQYVYAGYLPNRPTVSRRRNPPEPGTEEYAEEL---ERDPERAFIH 754

QY 778 TITSQFTILGISLIEILSKHSSDEVYLGQRDEPDRTWTSADAKALDAFKRFGSRLVQIENR 837

Db 755 TITSQITIGVSLLEVLKSSSDELYLGQRDTPE-WTSDPKALEVFKRFSRDLVEIESK 813

QY 838 IKTMNDSPDLKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887

Db 814 VVGMNHDPELKNRNGPAKFPYMLLYPNTSDHKG-AAAGLTAKGIPNSISI 862

RESULT 7

ID AAU99692 standard; protein; 862 AA.

AC AAU99692;

DT 07-OCT-2002 (first entry)

DE Barley wild-type lipoxigenase 1, LOX-1, mutant #1.

KW Barley; plant; enzyme; lipoxigenase-1; LOX-1; transgenic; beer; beverage;

KW malt; organoleptic property; brewing; trans-2-nonenal; T2N;

KW elevated storage temperature; flavour stability; shelf-life; mutant;

muten.

OS Hordeum vulgare.

OS Synthetic.

FX Key Location/Qualifiers

FT Misc-difference 368

FT /label= OTHER

FT /note= "Wild-type Gly substituted by an acidic, basic or

FT polar amino acid, especially Glu or Asp, encoded by NNN"

XX WO200253720-A1.

XX 11-JUL-2002.

PI Douma AC, Doderer A, Cameron-Mills V, Skadhauge B, Bech LM;
PI Schmitt N, Heistek JC, Van Mechelen JR;
XX WPI; 2002-557742/59.
DR N-PSDB; ABK88516.
XX Novel barley plants having low lipoxygenase activity useful in the
PT production of plant products such as malt or brewed beverages,
PT particularly beer having increased stability and flavor.
XX
PS Claim 8; Page 94-96; 112pp; English.
XX
CC The invention describes a barley plant (I) having a mutant lipoxygenase-1
CC (LOX-1) protein, the plant or plant portion characterised by a reduction
CC or absence of LOX activity as compared to a non-mutated control, or
CC comprising a heterologous nucleic acid sequence expressing an antisense
CC sequence to a transcribed region of barley lox-1 gene, operably linked to
CC a promoter and a transcription terminator sequence. (I), a plant (II)
CC produced using (I) or a plant product (III) is useful in the manufacture
CC of a beverage, preferably malt or beer, for stabilising organoleptic
CC properties of a brewed product over a measured period of time as compared
CC to a control brewed product produced using a non-mutated barley plant or
CC its portion, grain or plant progeny, or plant product, and for the
CC manufacture of a brewed product having reduced levels of free trans-2-
CC nonenal over a measured period of time or under conditions of elevated
CC storage temperature, as compared to a control brewed product produced
CC using a non-mutated barley plant or its portion, grain or plant product.
CC Beer with significantly enhanced flavour stability, both during storage
CC and on exposure to elevated storage temperatures is obtained. These
CC properties enhance the quality of beer and are useful to extend its shelf
CC -life and reduce the need to cool beer during transport and storage. This
CC is the amino acid sequence of a mutant barley low-lipoxygenase 1 (lox-1)
CC protein
XX
SQ Sequence 862 AA;
Query Match 62.0%; Score 2929.5; DB 5; Length 862;
Best Local Similarity 63.0%; Pred. No. 3.4e-263;
Matches 561; Conservative 110; Mismatches 188; Indels 31; Gaps 12;
QY 1 MFHWGVADRLTGKKEAWSEGKIRGTURLVKKEVLVCGDFNASLLDGVHRLGWDGVA 60
Db 1 MLLGLIDTLTGANKSA----RLKGTWLMRKVNLDLDFGATIIDGIGEFLLG-KGVT 54
QY 61 QLVSAATAADPSNGGRGKVGKAAHLEAVVSLKSTADGETVYRVSEWD-ESQIGPGLV 119
Db 55 QLISSTAVDQDNGGRGKVGABAELEQWVTSLSLTGSGKFLTFDWEVEKLGVP 114
QY 120 RNLQHAFFELKTLTLEGVPGK-GTVVFFVANSWVYPKLYSQERIFFANDTYLPSKMPA 178
Db 115 NVHSSEFLKTLTLDVPGSGNLTFFVANSWIYPAANYRSRVFFANDTYLPSQMPA 174
QY 179 VPYRQDELKILRGDNDPGPYQEHDRVYRYDYNDLGDGPKGEEHARPILGSGQEHYP 238
Db 175 KPYRDELRLNRGDQDQGPYQEHDRYRYDYNDLGE-----GRPILGSGSDHPY 227
QY 239 CRTGRHPTKDPNSESRLFLNLNIYVPRDERFGLHKLMSDFLGYSKLKTIIEAVLPTL 298
Db 228 GRTERKENASDPSLESRLSLE-QIYVPRDEKFGHLKTSDFLGYSIKAITQGILPA 286
QY 299 VDDTPKEFDSFEDILGLYELGPEAPNNPLIAEIRKIPSEFLRSILPNSGSHDPLK 358
Db 287 VDTTFGEFDSFQDIINLYEGGKLPKVALEELRKQFFLQIKDLPVGG-DSLLKLP 345
QY 359 NVTKSDVLKKAPEFKFGWRTDEEFARETLAGVNPVIKRLTEFFPAKSTLDPRQYGD 418
Db 346 HIQ-----ENKQAWRTDEEFAREVLAXVNPVITRLTEFFPKSSLDPSKFGDHT 397
QY 419 ITEAHIRNMGGLSVQNALRNKRLFLDHDHFMFYLDEINELEGNFIYASRTLLFLK 478
Db 398 ITAEHIEKNLEGLTVQQALESNRLYILDHHDHFMFYLDEINELEGNFIYATRTL 457
QY 479 GTLKLPLAIELSLPHDPDGGQQRGAWSKVYTPAHTG-VEGHVWQLAKAYACVND 537

Db 458 GRLTPLAIELSEPIIOGGLTTAKSKVYTPVSGSGVEGWVWELAKAYAVAVNDSGHQLVSH 517
QY 538 WLNTHAVIEPPFVIATNRQLSVVHPVHKLLSPHYRDTLNLNALARQTLINAGGVFERTV 597
Db 518 WLNTHAVMEPPFVISTNRHLSVTHPVHKLLSPHYRDTLNLNALARQTLINAGGIFEM 577
QY 598 AKYALGMSADVYKSWNFENEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIAVDGLV 657
Db 578 GKFAIGMSAVVYKDWKFTQGLPDDDLIKRGMAVEDPSSPYKVRLLVSDYPYAADGL 637
QY 658 AIERWVKEYLDIYYPNDGELQBDVLOAWWKEVREEAHGDLDKDRDWPRMDTVQQLAR 717
Db 638 AIEQYVSEYLAIIYYPNDGVLQDTEVQAWWKETREVGCHGDLKDAPWPKMQSVPELA 697
QY 718 TTIWVASALHAAVNFQYVAGYLPNRPPTASRRPMPPEGSHDYKLGAGQKEADMV 777
Db 698 TTIWIGSALHAAVNFQYVAGYLPNRPPTVSRRRMPPEGTEEYAEEL---ERDPERAF 754
QY 778 TITSQFTILGISLIEILSKHSSDEVYLGQDEPDRTSDAKALDAFKRFGSRLVQIENR 837
Db 755 TITSQITIIIGVLSLLEVLKSSDELYLGQDTPETWSDPKALEVFKRFSRDLVEIESK 813
QY 838 IKTMNDSPDLKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887
Db 814 VVGWVNDPELKNRNGPAKFPYMLLYPNTSDHKG-AAAGLTAKGIPNSISI 862
RESULT 9
ABG30571
ID ABG30571 standard; protein; 864 AA.
XX
AC ABG30571;
XX
DT 07-OCT-2002 (first entry)
XX
DE Barley low-lipoxygenase 2 (LOX-2).
XX
KW Lipoxygenase-2; LOX-2; beverage; malt; beer; organoleptic property;
KW brewing; trans-2-nonenal; flavour stability; storage; shelf-life;
KW low-lipoxygenase 1; barley.
OS Hordeum vulgare.
XX
PN WO200253721-A1.
XX
PD 11-JUL-2002.
XX
PF 22-JAN-2001; 2001WO-IB000207.
XX
PR 29-DEC-2000; 2000US-00751587.
PR 29-DEC-2000; 2000WO-IB002045.
XX
PA (CARL-) CARLSBERG RES LAB.
PA (HETB) HEINEKEN TECH SERVICES BV.
PA (BRAS-) BRASSERIES KRONENBOURG SA.
XX
PI Douma AC, Doderer A, Cameron-Mills V, Skadhauge B, Bech LM;
PI Schmitt N, Heistek JC, Van Mechelen JR;
XX
DR WPI; 2002-557742/59.
XX
PT Novel barley plants having low lipoxygenase activity useful in the
PT production of plant products such as malt or brewed beverages,
PT particularly beer having increased stability and flavor.
XX
PS Disclosure; Fig 22A-B; 112pp; English.
XX
CC The invention describes a barley plant (I) having a mutant lipoxygenase-1
CC (LOX-1) protein, the plant or plant portion characterised by a reduction
CC or absence of LOX activity as compared to a non-mutated control, or
CC comprising a heterologous nucleic acid sequence expressing an antisense
CC sequence to a transcribed region of barley lox-1 gene, operably linked to
CC a promoter and a transcription terminator sequence. (I), a plant (II)
CC produced using (I) or a plant product (III) is useful in the manufacture
CC of a beverage, preferably malt or beer, for stabilising organoleptic
CC properties of a brewed product over a measured period of time as compared
CC to a control brewed product produced using a non-mutated barley plant or
CC its portion, grain or plant progeny, or plant product, and for the
CC manufacture of a brewed product having reduced levels of free trans-2-
CC nonenal over a measured period of time or under conditions of elevated
CC storage temperature, as compared to a control brewed product produced
CC using a non-mutated barley plant or its portion, grain or plant product.
CC Beer with significantly enhanced flavour stability, both during storage
CC and on exposure to elevated storage temperatures is obtained. These
CC properties enhance the quality of beer and are useful to extend its shelf
CC -life and reduce the need to cool beer during transport and storage. This
CC is the amino acid sequence of a mutant barley low-lipoxygenase 1 (lox-1)
CC protein

Db 117 AAEFFLKTITLDNVPGHGAVVFWANSWIYPASKYRYNRVFFSNDTSLPSKMAAALKPYRD 176
QY 184 DELKILRGDDNPGPYQEHDRVYDYNDLGDGKEEHARPILGSGEHPYPRRCRTGR 243
Db 177 DELRNLRGDDQCGPYQEHDRVYDYNDLGEPSG--NPRPVLGSPDRPYPRRGRTGR 234
QY 244 HPTKDPNSESRLFLNLNIYVPRDERFGLKMSDFLGYSKLTIIIEAVLPTLGTFFVDDTP 303
Db 235 KPTKTDPTAESRLSLE-NIYVPRDERFGLKMAADFLGYSIKALVDGIVPAIRTYVDLTP 293
QY 304 KEFDSFEDIILGLYELGPEAPNPLIAEIRKKTIPSEFLRSILPNGSHDHPKMPPLPNVKS 363
Db 294 GEFDSFKDILKLYEGGLKPLPSIPALEELRKRFPLQVKDLIPGG--DYLKLPMPHVIRE 351
QY 364 DVLKKAPEFKFGRWTDDEFARETLAGVNPVIKRLTEFFPAKSTLDPROYGDHTSKITEAH 423
Db 352 D--KKA-----WMTDDEFAREILAGVNPWVIARLTFEPPE-PLDPAHYGDTSTITAHA 402
QY 424 IRHNMGGLSVQNALRNKRLFILDHHDHFMPIYLDINELEGNFYASRTLLFLKDDGTLKP 483
Db 403 VERGLEGLTVQQAIDGNLLYVVDHHDHFMPIYLDINSDDNFYATRTLLFLRGDGTLL-A 461
QY 484 LAIELSLPH-PDGOQRGAVSKVYTPAHT-----GVEGHVWOLAKAYACVNDSAWHQLISH 537
Db 462 LAIELSLPHLQDDGLITARSTVYTPAAAAAPALEWVWVWOLAKAYVNVNDYCWHLISH 521
QY 538 WLNTHAVIEPFVIATNRQLSVVHPVHKLLSPHYRDTLNINALARQTLINAGGVFERTVFP 597
Db 522 WLNTHAVMEPFVIATNRQLSVVHPVHKLLSPHYRDTMTINGLARQTLINGGIFEMTVFP 581
QY 598 AKYALGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVIW 657
Db 582 RNDALAMSSAFYKDWSPADQALPDDLKVRGVRT-DPASPYKVRLLIEDPYANDGLAVCT 640
QY 658 AIERWVKEYLDIYENDGELORDVELQAWKVEVREZAHGDLKDRDWPRMDTVQQLARAC 717
Db 641 PIEQWATEYLAIYENDGVLGDAELQAWKVEVREVGHDIKDATWPEMKTADVVKAC 700
QY 718 TTIWVASALHAAVNFQGYPYAGYLPNRPPTASRRPMPEPGSHDYKKGAGQKEADMVFR 777
Db 701 ATIIWIGSALHAAVNFQGYPYAGYLPNRPSPSRAMPEPGTKEYDELA--RDPEKVFVR 757
QY 778 TITSQFQITLIGISLIEILSKHSSDEVYLGQRDEPDRWTSDAKALDAFKRFGSRLVQIENR 837
Db 758 TITKQMAIVIGISLLEILSKHSSDEVYLGQRDTPE-WTSDAKALEAFKRFGARLTEIESR 816
QY 838 IKTMNDSPDLKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887
Db 817 VVAMNKDPRHKNRVGPTNFPYTLTYPNTSCLKGD-AAGLSARGIPNSISI 865

RESULT 11

AAR20670

ID AAR20670 standard; protein; 865 AA.

XX AAR20670;

DT 24-OCT-2003 (revised)

DT 04-NOV-1992 (first entry)

XX Lipoxigenase.

XX Temperature; denaturation; rice; pRLC11; enzyme.

XX Oryza sativa; (Nihonbare).

XX JP04094681-A.

XX 26-MAR-1992.

XX 13-AUG-1990; 90JP-00211470.

XX

PR 13-AUG-1990; 90JP-00211470.
XX (MITS-) MITSUI GYOSAI SHOKU.
PA WPI; 1992-156052/19.
DR N-PSDB; AAQ24234.
XX Prodn. of protein in E.coli without denaturation - by culturing transformed E.coli at low temp.
PT Disclosure; Fig 1 (1-4); 5pp; Japanese.
XX mRNA was extracted from a rice plant and used to prepare a cDNA library. A clone contg. cDNA encoding the full length lipoxigenase gene was isolated (pRLC11) and used to transform E.coli. The transformant was deposited as FERM P-11635. pRLC11 was then ligated with an expression vector to obtain clone ET3a/RL0X2, which was used to transform E.coli BL21(DE3). The obtained clone was deposited as FERM P-11636. This clone was inoculated to ampicillin contg. LB medium, and cultured at 37 degrees C overnight. IPTG was then added, and the mixt. cultured below 20 degrees C, e.g. 18 or 15 degrees C for 16 hrs. Cells were collected and disrupted by ultrasonification to recover the enzyme solution. (Updated on 24-OCT-2003 to standardise OS field)

XX SQ Sequence 865 AA;

Query Match 59.9%; Score 2829.5; DB 2; Length 865;

Best Local Similarity 62.1%; Pred. No. 7.2e-254;

Matches 553; Conservative 113; Mismatches 189; Indels 35; Gaps 17;

QY 5 GVADRLTGKNEAWSEGKIRGTVRLVKKEVLDVGDVFNASLLDGVHRIIGWDDGVAFQLVS 64
Db 4 GIIGGLTG-NKNA-----RLKGLVLMRKNALDINDFGATVIERISEFLG--RGVTCQLVS 56
QY 65 ATAADPSNGGRKVGKAAHLEAAVSLKSTADGETVYRVSEFWD-ESQGIPGAVLVRNLQ 123
Db 57 SSLVDPNNGNRGRVGTSEASLEQWLTSLPSLTGTGESKFGVTFEWEVEKMGIPGAIIVKNH 116
QY 124 HAEFFLKTITLDNVPGHGAVVFWANSWIYPASKYRYNRVFFSNDTSLPSKMAAALKPYRD 176
Db 117 AAEFFLKTITLDNVPGHGAVVFWANSWIYPASKYRYNRVFFSNDTSLPSKMAAALKPYRD 176
QY 184 DELKILRGDDNPGPYQEHDRVYDYNDLGDGKEEHARPILGSGEHPYPRRCRTGR 243
Db 177 DELRNLRGDDQCGPYQEHDRVYDYNDLGEPSG--NPRPVLGSPDRPYPRRGRTGR 234
QY 244 HPTKDPNSESRLFLNLNIYVPRDERFGLKMSDFLGYSKLTIIIEAVLPTLGTFFVDDTP 303
Db 235 KPTKTDPTAESRLSLE-NIYVPRDERFGLKMAADFLGYSIKALVDGIVPAIRTYVDLTP 293
QY 304 KEFDSFEDIILGLYELGPEAPNPLIAEIRKKTIPSEFLRSILPNGSHDHPKMPPLPNVKS 363
Db 294 GEFDSFKDILKLYEGGLKPLPSIPALEELRKRFPLQVKDLIPGG--DYLKLPMPHVIRE 351
QY 364 DVLKKAPEFKFGRWTDDEFARETLAGVNPVIKRLTEFFPAKSTLDPROYGDHTSKITEAH 423
Db 352 D--KKA-----WMTDDEFAREILAGVNPWVIARLTFEPPE-PLDPAHYGDTSTITAHA 402
QY 424 IRHNMGGLSVQNALRNKRLFILDHHDHFMPIYLDINELEGNFYASRTLLFLKDDGTLKP 483
Db 403 VERGLEGLTVQQAIDGNLLYVVDHHDHFMPIYLDINSDDNFYATRTLLFLRGDGTLL-A 461
QY 484 LAIELSLPH-PDGOQRGAVSKVYTPAHT-----GVEGHVWOLAKAYACVNDSAWHQLISH 537
Db 462 LAIELSLPHLQDDGLITARSTVYTPAAAAAPALEWVWVWOLAKAYVNVNDYCWHLISH 521
QY 538 WLNTHAVIEPFVIATNRQLSVVHPVHKLLSPHYRDTLNINALARQTLINAGGVFERTVFP 597
Db 522 WLNTHAVMEPFVIATNRQLSVVHPVHKLLSPHYRDTMTINGLARQTLINGGIFEMTVFP 581
QY 598 AKYALGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVIW 657
Db 582 RNDALAMSSAFYKDWSPADQALPDDLKVRGVRT-DPASPYKVRLLIEDPYANDGLAVCT 640

OS Nicotiana tabacum.
XX WO200299112-A2.
FN 12-DEC-2002.
XX
PF 06-JUN-2002; 2002WO-FR001943.
XX
XX 07-JUN-2001; 2001FR-00007470.
PR 07-NOV-2001; 2001FR-00014358.
XX
XX (RHOB-) RHOBIO.
XX
PI Mene-Saffrane L, Esquerre-Tugaye M, Fournier J, Beffa R;
PI Grosjean-Cournoyer M;
XX
XX WPI; 2003-156858/15.
DR N-PSDB; ABZ68210.
XX
XX Reducing sensitivity of plants to diseases and pathogens, by
PT overexpressing a lipoxygenase, also vectors and cassettes for the process
PT and transformed plants.
XX
XX Claim 7; Page 39-41; 47pp; French.
XX
XX The present sequence represents a lipoxygenase-1 (LOX-1) gene. LOX-1 is
CC an enzyme that catalyses the dioxygenation of polyunsaturated fatty acids
CC having a pentadiene system. Overexpression of LOX-1 can be used to reduce
CC the sensitivity of plants to diseases and attack by pathogens.
CC Overexpression of LOX-1 improves resistance to viruses, bacteria, fungi
CC and insects, in a wide range of crops, particularly the Solanaceae, e.g.
CC tobacco, tomato, potato and pepper
XX
XX Sequence 862 AA;
XX
Query Match 57.7%; Score 2724.5; DB 6; Length 862;
Best Local Similarity 59.9%; Pred. No. 4.4e-244;
Matches 533; Conservative 111; Mismatches 215; Indels 31; Gaps 11;
QY 1 MFHWGVADRLTGKKEAWSEG-KIRGTVRLVKKEVLVDGDFNASLLDGVHRIILGWDDGVA 59
Db 1 MFLEKIVDAITGD-----DGKKVKGTVLMKKNVLDFTDINASVLDGVLEFLG--RRVS 53
QY 60 FQLVSATAADPSNGGRGKVGKAAHLEAAVSVLSKSTADGETVYRVSEFWEDESQ-GIPGAVL 118
Db 54 LELISSVNADPANGLOKRSKAAYLENLWLTNSTPIAAGESAFRTVDWDDDEFGVPGAFI 113
QY 119 VRNLQHAEEFFLKTLTLEGVPGKGTVVVANSWVYVPHKLYSQERIFFANDTILPCKMPAAL 178
Db 114 IKNLHSEFFLKSLTLEDVNHGKHVFCVNSWVYVANKYKSDRIFFANQAYLPSETPTDL 173
QY 179 VPRQDELKILRGDDNPGYQEHDRVYDYNDLGDPPDKGEEHARPILGSGSEHPYPRR 238
Db 174 RKYRENELVTLRG-DGTGKLEEWDRVYDYAYNDLGDPPDKGQDLSPVLCGSSEYPPRR 232
QY 239 CRIGRHPTKDPNSESRL-FLNLNIYVPRDERFGLKMSDFLGYSLSKTIIEAVLPTLGT 297
Db 233 GRIGRKPTKTDPNSESRIPLMSLDIYVPRDERFGLKMSDFLTFALKSTIVQLLLPEFKA 292
QY 298 FVDDTPKEFDSFEDILGLYELGPEAPNPLIAEIRKKIPSEFLRSILPNSGSHDHLKMP 357
Db 293 LFDSTHNEFDSFEDVLKLYEGGIKLPQGILLKATDTSIPLEILKELL-RSDGEGLFKYPT 351
QY 358 PNVKSDVLKKAPEKFGWRTDEEFARETLAGVNPVILKRLTEFFPAKSTLDPRQYGDHTS 417
Db 352 PQVIQED-----XTAWRTDEEFGREMLAGVNPVILSRLOEFPKSKLDPKIYGNQNS 403
QY 418 KITEAHIRHNMGGLSVQNALRNKRLFILDHHDHFMFYLDEINELEGNFTYASRTLLFLKD 477
Db 404 TITREQIEDKLDGLTIDEAIKTNRLFILNHDILMPYLRRINTSTDTKTYASRTLLFLQD 463
QY 478 DGTCLKPLAIELSLPHPDGQORGAVSKVYTPAHTGVGHWQOLAKAYACVNDSSAWHQLISH 537

Db 464 NGTLKPSAIELSLPHPDGQDFGAVSKVYTPADQGVGSIWQLAKAYAAVNDSGVHQLISH 523
QY 538 WLNTHAVIEPEFVIATNRQLSVVHPVHKLSPHYRDTILNALARQTLINAGGVFERTVEP 597
Db 524 WLNTHAAIEPEFVIATNRQLSALHPIYKLLHPHFRFTWNLARQILINGGGLLELTVEP 583
QY 598 AKYALGMSADVYKSNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIAVDGLVIMW 657
Db 584 AKYSMEMSAVYKDWVFPPEQALPTDLIKRGVAVEDSSSPILGIRLLIQDYPYAVDGLKWS 643
QY 658 AIERWVKEYLDIYYPNDGELQDVELQAWKKEVREEAHGDLKDRDWPRMDTVQQLARAC 717
Db 644 AIKSWVTEYCNYYKSDDAVQKDTLOAWKELREEGHGDKDEPWWPKMQTVQELIDSC 703
QY 718 TTIIWVASALHAAVNFQGYPIAGYLPNRPTASRRPMPEPESHDKKLKAGQKEADMVFI 777
Db 704 TITTIWASALHAAVNFQGYPIAGYLPNRPTLSRNFMPPEGSPEYEEL---KTNPKVFLX 760
QY 778 TITTSQFQTLIGISLIEILSKHSSDEVYLGQDEPDRWTSDAKALDAFKRFGSRLVQIENR 837
Db 761 TITPQLQTLIGISLIEILSRHSSDTLYLGQRESPE-WTKDQEPPLSAFARFGKLSLIEDQ 819
QY 838 IKTMNDSPDLKNRKGPVEMPMYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
Db 820 IMQNVNDEKWNRSRGPVKVPTLLPPTSEG-----GLTGKGIPIPSVSI 862
RESULT 15
AAB46803
ID AAB46803 standard; protein; 857 AA.
XX
AC AAB46803;
XX
DT 23-APR-2001 (first entry)
XX
DE Potato LOX protein.
XX
KW Potato; LOX protein; lipoxygenase; arachidonic acid; mutant; plant;
KW 11-arachidonate-lipoxygenase; 11-hydroperoxy-arachidonic acid.
XX
OS Solanum tuberosum.
XX
PN WO200104323-A2.
XX
PD 18-JAN-2001.
XX
PF 10-JUL-2000; 2000WO-EP006539.
XX
PR 08-JUL-1999; 99DE-01031819.
XX
PA (IPBP-) IPB INST PFLANZENBIOCHEMIE.
XX
PI Feussner I, Hornung E, Rosahl S;
XX
DR WPI; 2001-081054/09.
XX
XX New nucleic acid encoding lipoxygenase useful for producing 11-
PT hydroperoxy- or hydroxy-arachidonic acid.
XX
PS Disclosure; Fig 3; 18pp; German.
XX
CC This invention describes a novel nucleic acid (I) encoding a potato
CC lipoxygenase protein, LOX, (II) is new. The invention also describes (1)
CC (II), a sequence of 857 amino acids (aa), given in the specification; (2)
CC a vector (III) comprising (I); (3) a host cell (IV) comprising (I) or
CC (III); (4) a plant or part of a plant comprising (IV); (5) enhancing the
CC specificity of a plant lipoxygenase for position 11 of arachidonic acid
CC comprises mutating at least one amino acid of the wild type lipoxygenase;
CC (6) producing 11-hydroperoxy-arachidonic acid or the reduced 11-hydroxy-
CC derivative comprises treating arachidonic acid with (II) and further
CC reducing the obtained hydroperoxy form to the hydroxy form; (7) the
CC arachidonic acid derivative, comprising a hydroperoxy group or a hydroxy
CC group at position 11. (II) is useful for producing 11- hydroperoxy-

CC	and/or 11-hydroxy-arachidonic acid. The lipoxxygenase is specific for																																																									
CC	position 11 of arachidonic acid																																																									
XX																																																										
SQ	Sequence 857 AA;																																																									
	Query Match	55.7%;	Score	2630.5;	DB	4;	Length	857;																																																		
	Best Local Similarity	58.9%;	Pred.	No. 2.6e-235;																																																						
	Matches	511;	Conservative	113;	Mismatches	218;	Indels	25;	Gaps	9;																																																
QY	22	KIRGTVRLVKKEVL	DVGDFNASLLDGV	HRILGWDDGVA	FQLVSATAA	DP	SGRGKVGKA	81																																																		
Db	15	KVKGTVMMKQNAL	DFDLAGSLTDK	IFEALG--QKVS	FQLISSVQSD	PANGLQGGH	SNP	72																																																		
QY	82	AHLEEAUVSLKSTAD	GETVYRVSF	FEWDESQGI	PGAVLVRNLQ	HA	EFFLKTLTLEGV	PGKG	141																																																	
Db	73	AYLENFLTTLPLA	AGETA	FGVTFD	WNEEFGVPG	FAFIK	NTHINEFFLKS	LTLEDV	PNHG	132																																																
QY	142	TVVTVANSWVYP	PHKLYS	QERIF	PANDTYLPS	KMPAALV	PYRQDELKIL	RGGDND	PNP	QYEH	201																																															
Db	133	KVHFVCNSWVYP	SFRYKSDRI	FFANQ	PYP	LPSE	TELLRKYRENE	LLTLRG-D	GTG	KREAW	191																																															
QY	202	DRVRYDYNDL	GDPPDKG	EEHAR	PILGGS	QEH	PPR	CR	TGRH	PTKDPN	SESRL-FLN	260																																														
Db	192	DRIYDYDVNDL	GNPDQGE	QNVRTL	GG	SADY	PYP	PR	GR	TGR	PT	RTDPKSESRI	PLLS	251																																												
QY	261	LNIVPRDER	FHGLKMSD	FLGYS	LKTIIEA	V	PLT	GTFV	DD	TPKE	FS	FEDILGL	YELGP	320																																												
Db	252	LDIYVPRDER	FHGLKMSD	FLTYALKS	IVQ	FIL	PEL	HAL	F	DG	T	PN	EF	DSFEDVLRL	YEGGI	311																																										
QY	321	EAPNPLIAE	IRKKIPSE	FLRSIL	PNGSHD	HLK	MPL	PN	VIKSD	VLKKA	PE	FK	FGW	RTDE	380																																											
Db	312	KLPQGPLFKAL	TAAIPLEM	KELLRTD	G-EGIL	R	P	T	PLVIK-----	DSK	T	A	W	RTDE	362																																											
QY	381	EFARETLAGVNP	VIIKRLTE	FP	AKS	TLD	PR	Q	Y	GH	TS	KITEA	HIRH	NMG	GLSV	QNALRNK	440																																									
Db	363	EFAREMLAGVNP	IIISRLQ	EP	PKS	KLD	PE	A	Y	G	N	S	TITAE	HIED	KLDGLT	VDEAMNN	422																																									
QY	441	RLFILDHDFMP	YLDEINE	LEGNFI	YASRTL	FL	KD	DG	T	L	KPLA	I	E	L	SIL	PH	PDG	Q	Q	RGA	500																																					
Db	423	KLFILNHH	DV	LIP	YLR	R	INT	TTTK-TY	ASRTL	FL	QD	NS	L	KPLA	I	E	L	SIL	PH	PDG	Q	Q	FGV	481																																		
QY	501	VSKVYTPAHT	GV	EH	VW	Q	LAKAYAC	VN	D	S	A	W	H	Q	L	I	S	H	W	L	N	T	H	AV	I	E	P	F	V	I	A	T	N	R	Q	L	S	V	VH	560																		
Db	482	ISKVYTPSDQ	GV	ESSI	W	Q	LAKAYAV	N	D	S	G	V	H	Q	L	I	S	H	W	L	N	T	H	AV	I	E	P	F	V	I	A	T	N	R	Q	L	S	V	LH	541																		
QY	561	PVHKLLSPHYR	D	T	L	N	I	N	A	L	A	R	Q	T	L	I	N	A	G	V	F	E	R	T	V	P	P	A	K	A	L	G	M	S	A	D	V	Y	K	S	W	N	E	Q	A	L	P	620										
Db	542	PIHKLLYPH	FRD	T	M	N	I	N	A	M	A	R	Q	I	L	I	N	A	G	V	L	E	S	T	V	P	P	S	K	F	A	M	E	M	S	A	V	Y	K	D	W	V	F	P	D	Q	A	L	P	601								
QY	621	ADLVKRGVAV	P	DQ	SS	P	Y	G	V	R	L	L	I	K	D	P	Y	A	V	D	G	L	V	I	W	A	E	R	W	V	K	E	Y	L	D	I	Y	P	N	D	G	E	L	Q	R	D	680											
Db	602	ADLVKRGVAV	E	D	S	S	P	H	G	V	R	L	L	I	E	D	P	Y	A	V	D	G	L	E	I	W	S	A	I	K	S	W	V	T	D	C	S	F	Y	G	S	D	E	E	I	L	K	D	661									
QY	681	VELQAWK	VE	RE	A	H	G	D	L	K	D	R	D	W	P	R	M	D	T	V	Q	L	A	R	A	C	T	T	I	I	W	V	A	S	A	L	H	A	A	V	N	F	G	O	Y	P	Y	A	G	740								
Db	662	NELQAWK	EL	REV	H	G	D	K	K	N	E	P	W	P	E	M	E	T	P	Q	E	L	I	D	S	C	T	T	I	I	W	A	S	A	L	H	A	A	V	N	F	G	O	Y	P	Y	A	G	721									
QY	741	YLPNR	P	T	A	S	R	R	P	M	P	E	P	G	S	H	D	Y	K	L	G	A	G	Q	K	E	A	D	M	V	F	I	R	T	I	T	S	Q	F	O	T	I	L	G	I	S	L	I	E	I	L	S	K	H	S	800		
Db	722	YLPNR	P	T	V	S	R	R	F	M	P	E	P	G	T	P	E	Y	E	E	L	--K	K	N	P	D	K	A	F	L	K	T	I	T	A	Q	L	O	T	L	L	G	V	S	L	I	E	I	L	S	R	H	T	778				
QY	801	DEVY	L	G	O	R	D	E	P	D	R	W	T	S	A	K	A	L	D	A	F	K	R	F	G	S	R	L	V	Q	I	E	N	R	I	K	T	M	N	D	S	P	D	L	K	N	R	K	G	P	V	E	M	P	Y	M	L	860
Db	779	DEIY	L	G	O	R	E	S	P	E	-W	T	K	D	E	F	L	A	F	D	K	F	G	K	L	T	D	I	E	K	Q	I	I	O	R	N	G	D	N	I	L	T	N	R	S	G	P	V	N	A	P	Y	T	L	837			
QY	861	LYPNT	S	D	V	T	G	E	K	A	E	G	L	T	A	M	G	I	P	N	S	I	S	I	887																																	
Db	838	LFT	S	E	G	-----G	L	T	K	G	I	P	N	S	V	S	I	857																																								

Search completed: March 23, 2004, 06:59:05
Job time : 92 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 06:57:53 ; Search time 26 Seconds
(without alignments)
1761.240 Million cell updates/sec

Title: US-10-059-909-16

Perfect score: 4723

Sequence: 1 MFVHGVDRLTGKNKEAWSE.....VTGKAEGLTAMGIPNSISI 887

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3049	64.6	864	4	US-09-810-268-3
2	2936.5	62.2	862	4	US-09-751-687-9
3	2929.5	62.0	862	4	US-09-751-687-12
4	2860	60.6	864	4	US-09-751-687-18
5	2491.5	52.8	857	4	US-09-751-687-17
6	2486	52.6	865	4	US-09-751-687-16
7	2355.5	49.9	839	4	US-09-751-687-15
8	513.5	10.9	676	3	US-09-061-768A-2
9	513.5	10.9	676	4	US-09-764-246-2
10	513	10.9	556	4	US-09-547-435-6
11	513	10.9	711	4	US-09-547-435-2
12	513	10.9	867	4	US-09-547-435-24
13	507	10.7	677	3	US-09-061-768A-4
14	507	10.7	677	4	US-09-764-246-4
15	503.5	10.7	701	3	US-09-087-727-2
16	503.5	10.7	701	4	US-09-853-053-2
17	485.5	10.3	692	4	US-09-252-991A-19668
18	475	10.1	582	3	US-09-413-814-83
19	430	9.1	663	4	US-09-641-638-653
20	427	9.0	460	4	US-09-547-435-12
21	427	9.0	615	4	US-09-547-435-10
22	427	9.0	662	3	US-09-061-768A-25
23	427	9.0	662	4	US-09-764-246-25
24	427	9.0	771	4	US-09-547-435-28
25	380.5	8.1	291	4	US-09-547-435-14
26	294.5	6.2	195	4	US-09-547-435-20
27	253.5	5.4	334	4	US-09-547-435-8

28	253.5	5.4	489	4	US-09-547-435-4	Sequence 4, Appli
29	253.5	5.4	645	4	US-09-547-435-26	Sequence 26, Appl
30	139	2.9	139	4	US-09-547-435-18	Sequence 18, Appl
31	121	2.6	69	4	US-09-547-435-16	Sequence 16, Appl
32	118	2.5	560	4	US-09-252-991A-22343	Sequence 22343, A
33	111.5	2.4	1675	4	US-09-540-236-1994	Sequence 1994, Ap
34	111	2.4	943	4	US-09-540-236-3458	Sequence 3458, Ap
35	111	2.4	982	4	US-09-623-326-12	Sequence 12, Appl
36	111	2.4	1231	4	US-09-107-532A-5150	Sequence 5150, Ap
37	109.5	2.3	883	2	US-08-953-492-2	Sequence 2, Appli
38	108.5	2.3	640	4	US-09-687-538B-2	Sequence 2320, Ap
39	108.5	2.3	751	4	US-09-540-236-2320	Sequence 5, Appli
40	108.5	2.3	986	4	US-09-403-618A-5	Sequence 11, Appl
41	107.5	2.3	949	4	US-09-623-326-11	Sequence 7, Appli
42	106.5	2.3	423	1	US-08-844-064-7	Sequence 7, Appli
43	106.5	2.3	423	3	US-09-009-433-7	Sequence 28773, A
44	106.5	2.3	1007	4	US-09-252-991A-28773	Sequence 9, Appli
45	106.5	2.3	2311	4	US-08-934-386-9	

ALIGNMENTS

RESULT 1
US-09-810-268-3
; Sequence 3, Application US/09810268
; Patent No. 6627797
; GENERAL INFORMATION:
; APPLICANT: Duvick, Jon
; APPLICANT: Maddox, Joyce R.
; APPLICANT: Keller, Nancy P.
; TITLE OF INVENTION: Maize Lipoxxygenase Polynucleotide and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 1269
; CURRENT APPLICATION NUMBER: US/09/810,268
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/190,950
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 864
; TYPE: PRT
; ORGANISM: Zea mays
US-09-810-268-3

Query Match	64.6%	Score	3049;	DB	4;	Length	864;
Best Local Similarity	66.2%	Pred. No.	4.8e-285;				
Matches	585;	Conservative	100;	Mismatches	175;	Indels	24;
Gaps	10;						
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QY	65	ATAADPSNGGRGKVGKAAHLEAAVWSLKSTADGETVYRVSVFWD-ESQIGPQAVLVRLNQ	123				
Db	58	STLVLDANNGNRGRVGAENLEQWLTSLPSLTGSKFGVTDFWEVEKLGVPQAVVVKNNH	117				
QY	124	HAFFFLKTLTLEGVPGKGTVFVANSWVYPHKLYSQERIFFANDTYLPSKMPAALVPYRQ	183				
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Db	178	DELNLRGDDQGGPYQEHDRVYRYDYNDLGEPPDG--NPRPILGGSADHPYRRCRTGR	235				
QY	244	HPTKDPNSESRLFLNLNLYVPRDERFGLKMSDFLGYSLKTIIEAVLPTLGTFFVDDTP	303				
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QY	304	KEFDSFEDILGLYELGPEAPNPNLIAEIRKKIPSEFLRSILPNGSHDHPKMLPNVIXS	363				
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Db 354 D-----KNAWRTDEEFAREVLAGVNPVITRLTEFFPKSTLDPKSYGDHTSITTAEH 405
QY 424 IRHNMGLSVQNALRNKRLFILDHHDHFMFYLDEINELEGNEFIYASRTLLFLKDDGTLPK 483
Db 406 IEKNLEGLTVQOALDGNRLYILDHHDHFMFPLIDVNNLEGNFIYATRTLFFLRGDLAP 465
QY 484 LAIELSLPHDPGQQRGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSSAWHQLISHWLNTA 543
Db 466 LAIELSEPIDGDLTVAKSKVYTPASSGVEAWVWQLAKAYAVAVNDSSGHWQLVSHWLNTA 525
QY 544 VIEPFVIATNRQLSVVHPVHKLLSPHYRDTLNALARQTLINAGGVFERTVFPKVALG 603
Db 526 VMEPFVIATNRQLSVTHPVHKLLSSHFRDTMTINALARQTLINGGGIFEMTVFPGKVALG 585
QY 604 MSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPPYAVDGLVINWAIERWV 663
Db 586 MSSVVYKSWNFTEQGLPADLVKRGVAVADPSSPYKVRLLIEDYPPYASDGLAIWHAIEQWV 645
QY 664 KEYLDIYPNDGELQRDVELQAWWKEVREEAHGDLKDRDWPRMDTVQQLARACTTIWV 723
Db 646 GEYLAIYPPDDGALRGDEELQAWWKEVREVGHDHDKDAPWPKMQAVSELASACTTIWI 705
QY 724 ASALHAAVNFQYQPYAGYLPNRPTASRRMPPEPGSHDYKLGAGQKEADVMVFTITSQF 783
Db 706 ASALHAAVNFQYQPYAGYLPNRPTVSRRRMPPEPGSKEYEEL--ERDPERGFHTITSQI 762
QY 784 QTILGISLIEILSKHSSDEVILGQDEPDRTWTSDAKALDAFKRFGSRLVQIENRIKTMND 843
Db 763 QTIIGISLIEILSKHSSDEVILGQDTPPE-WTSDARALAAFKRFSDALVKIEGVVGENR 821
QY 844 SPDLKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887
Db 822 DPQLNRNGPAEFYMLLYPNTSDHSG-AAAGLTAKGIPNSISI 864

RESULT 2

US-09-751-687-9
; Sequence 9, Application US/09751687
; Patent No. 6660915

GENERAL INFORMATION:

; APPLICANT: Douma, Anneke
; APPLICANT: Doderer, Albert
; APPLICANT: Cameron-Mills, Verena
; APPLICANT: Skadhauge, Birgitte
; APPLICANT: Bech, Lene
; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY
; FILE REFERENCE: 11225.11US01
; CURRENT APPLICATION NUMBER: US/09/751,687
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 9

; LENGTH: 862

; TYPE: PRT

; ORGANISM: Hordeum vulgare

US-09-751-687-9

Query Match 62.2%; Score 2936.5; DB 4; Length 862;
Best Local Similarity 63.1%; Pred. No. 3.5e-274;
Matches 562; Conservative 110; Mismatches 187; Indels 31; Gaps 12;

QY 1 MFHWGADRLTGKKEAWSEKIRGTVRLVKKEVLVDVGFNLSLLDGVHRLGWDGVA 60
Db 1 MLLGGLIDTLTGANKSA----RLKGTVMRKNVLDLNDFGATIIDGIGEFGLG--KGVTC 54
QY 61 QLVSATAADPSNGGRGKVGKAAHLEAAVSLKSTADGETVYRVVSFEWD-ESQIPGAVLV 119
Db 55 QLISSTAVDQDNGGRGKVGAAEAEQWVTSPLSTGTGESKFGLTFTDWEVEKLGVPGAIVV 114
QY 120 RNLQHAEEFFLKTLTLEGVPCK-GTVVFNANSWVYPHKLYSQERIFFFANDTYLPKMPAAL 178

Db 115 NNYHSSEFLTKTITLHDVPGRSGNLTFFVANSWIYPAANYRSRVFFANDTYLPKMPAAL 174
QY 179 VPYRQDELKILRGDDNPGPYQEHDRVYRYDYNDLGDPPDKGEEHARPILGSGQEHYPYPR 238
Db 175 KPYRDELRNLRGDDQGGPYQEHDRYRYDYNDLGE-----GRPILGNSDHPYPR 227
QY 239 CRTGRHPTKDPNSESRLFLMLNLNIVVPRDERFGHLKMSDFLGYSLKTIIEAVLPTLGT 298
Db 228 GRTERKPNASDPSLESRLSLE-QIYVPRDEKFGHLKTSDFLGYSIKAITQGIPLAVRTY 286
QY 299 VDDTPKEFDSFEDIILGYELGPEAPNPNPLIAEIRKIPSEFLRSILPNSHCHPLKMLP 358
Db 287 VDTTPGEFDSFQDIINLYEGGIKLPKVALEELRKQFPLQIKDLLPVGG-DLLKLPVP 345
QY 359 NVIKSDVLKKAPEKFGWRTDEEFARETLAGVNPVVIKRLTEFFPAKSTLDPQYGDHTSK 418
Db 346 HIIQ-----ENKQAWRTDEEFAREVLAGVNPVITRLTEFFPKSSLDPSKFGDHTST 397
QY 419 ITEAHIRHNMGGLSVQNALRNKRLFILDHHDHFMFYLDEINELEGNEFIYASRTLLFLKDD 478
Db 398 ITAEHIEKNLEGLTVQOALESNRLYILDHHDHFMFPLIDVNNLEGNFIYATRTLFFLRGD 457
QY 479 GTLKLPLAIELSLPHDPGQQRGAVSKVYTPAHTG-VEGHVWQLAKAYACVNDSSAWHQLISH 537
Db 458 GRLTPLAIELSEPIIQGGLTAKSKVYTPVPSGSGVEGWVWELAKAYAVAVNDSSGHWQLVSH 517
QY 538 WLNTHAVIEPFVIATNRQLSVVHPVHKLLSPHYRDTLNALARQTLINAGGVFERTVFP 597
Db 518 WLNTHAVMEPFVISTNRHLSVTHPVHKLLSPHYRDTMTINALARQTLINAGGIFEMTVFP 577
QY 598 AKYALGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPPYAVDGLVWV 657
Db 578 GKFAIGMSAVVYKDWKFTQGLPDDLIKRGMAVEDPSSPYKVRLLVSDYPPYADGLAIWH 637
QY 658 AIERWVKEYLDIYYPNDGELQRDVELQAWWKEVREEAHGDLKDRDWPRMDTVQQLARAC 717
Db 638 AIEQYVSEYLAIIYYPNDGVLCQDTEVQAWWKETREVGHDGLKADPWPMPQSVPELAKAC 697
QY 718 TTIIVWASALHAAVNFQYQPYAGYLPNRPTASRRMPPEPGSHDYKLGAGQKEADVMVFI 777
Db 698 TTIIWGSALHAAVNFQYQPYAGYLPNRPTVSRRRMPPEGTEEYAEEL---ERDPERAFIH 754
QY 778 TITSQFQTLIGISLIEILSKHSSDEVILGQDEPDRTWTSDAKALDAFKRFGSRLVQIENR 837
Db 755 TITSQIQTIIIGVSLLEVLKSHSSDELYLGQDTPPE-WTSDPKALEVFKRFRSRLVVEIESK 813
QY 838 IKTMDSPDLKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887
Db 814 VVGMNHDPELKNRNGPAKFPYMLLYPNTSDHKG-AAAGLTAKGIPNSISI 862

RESULT 3

US-09-751-687-12
; Sequence 12, Application US/09751687
; Patent No. 6660915

GENERAL INFORMATION:

; APPLICANT: Douma, Anneke
; APPLICANT: Doderer, Albert
; APPLICANT: Cameron-Mills, Verena
; APPLICANT: Skadhauge, Birgitte
; APPLICANT: Bech, Lene
; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY
; FILE REFERENCE: 11225.11US01
; CURRENT APPLICATION NUMBER: US/09/751,687
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 12

; LENGTH: 862

; TYPE: PRT

; ORGANISM: Hordeum vulgare

; FEATURE:

Db 704 WTGSALHAAVNFQYPYSGYHPNKPASRRPMPVQSGSEYAEI---ERDPEKAFIRITTS 760
Qy 782 QFQTILGISLIEILSKHSSDEVYLGQRDEPDRWTSDAKALDAFKRFGSRLVQIENRIKTM 841
Db 761 QFHALVGISLMEILSKHSSDEVYLGQHDTF-AWTSDAKALEAFKRFQAKLEGIEKQVAM 819
Qy 842 NSDPDLKNRKGPVEMPYMLYPNTSDVTGEKAEGLTAMGIPNSISI 887
Db 820 NSDPQLKNRTPAKFPYMLYPNTSDHTGQ-AEGLTARGIPNSISI 864
RESULT 5
US-09-751-687-17
; Sequence 17, Application US/09751687
; Patent No. 6660915
; GENERAL INFORMATION:
; APPLICANT: Douma, Anneke
; APPLICANT: Doderer, Albert
; APPLICANT: Cameron-Mills, Verena
; APPLICANT: Skadhauge, Birgitte
; APPLICANT: Bech, Lene
; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY
; FILE REFERENCE: 11225.11US01
; CURRENT APPLICATION NUMBER: US/09/751,687
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 17
; LENGTH: 857
; TYPE: PRT
; ORGANISM: Glycine max
US-09-751-687-17

Query Match 52.8%; Score 2491.5; DB 4; Length 857;
Best Local Similarity 55.3%; Pred. No. 3.4e-231;
Matches 487; Conservative 135; Mismatches 210; Indels 49; Gaps 14;

Qy 22 KIRGTVRLVKKVLDVG-----DFNASLLDGVHRILGWDDGVAFLVSATAA 68
Db 11 KIKGTVLMRKNVLDVNSVTSVGGIIGQGLDLVGSTLDTLTAFGL--RSVSLQLISATKA 68
Qy 69 DPSNGGRGKVGKAAHLEAVVSLKSTADGETVYRVSEFWEDESQGIPIGAVLVRNLQHAEFF 128
Db 69 DAN--GKGKLGKATFLEGIITSLPTLGAGQSAFINFEWDDGSGIPGAFYIKNFMQTEFF 126
Qy 129 LKTLTLEGVPGKGTVVVANSWVYPHKLVSQRIFFANDTYLPSKMPAALVPYRQDELKI 188
Db 127 LVSLTLEDIPNHGSIHFVCSWIIYNAKLFKSDRIFFANQTYLPSETPAPLVKYREEELHN 186
Qy 189 LRGGDNPQYQEHDRVYDYNDLGDPPDKGEEHARPILGSGQEHYPYRRCRTGRHPTKK 248
Db 187 LRQ-DGTGERKEWERIYDYNDLGDPPDKGENEARPVLGGNDTFYPYRGRGTGRKPTRK 245
Qy 249 DPNSERLFLNLNIYVPRDERFGLKMSDFLGYSLKTIIEAVLPTLGTFFVD--DTPKEF 306
Db 246 DPNSER---SNDVYLPDRDEAFGLKSSDFLTGLKSVSQNVLPQLQSAFDLNFPTREF 301
Qy 307 DSPEDILGLYELGPEAPNPLIAEIRKXIPSEFLRSILPNGSHDHPKMLPNVIKSDVL 366
Db 302 DSPFVHGLYSGGIKLPD-IISKIS--PLPVLKEIFRTDG-EQALKFPPPKVIQVS-- 354
Qy 367 KKAPEFKFGWRTDEEPARETLAGVNPVIIKRLTPEPAKSTLDPROYGDHTSKITEAHIRH 426
Db 355 -----KSAWMTDEEPAREMLAGVNPNIIRCLDPPRSLKDSQVYGDHTSQITKEHLEP 408
Qy 427 NMGGLSVQNALNRKLFILDDHDFMPYLDEINELEGNFIYASRTLLFLKDDGTLKPLAI 486
Db 409 NLEGLTVDEAIQNKRLFLDDHDPIMPYLRINATSTK-AYATRTILFKNDGTLRPLAI 467
Qy 487 ELSLPHPDGQORGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSAHWQLISHWLNTHAVIE 546
Db 468 ELSLPHPDGQSGAFSQVFLPADEGVESSIWLAKAYVVVNDSCYHQLVSHWLNTHAVVE 527

Qy 547 PFVIATNRQLSVVHPVHKLSPHYRDTLNLINALARQTLINAGGVFERTVFPKAYALGMSA 606
Db 528 PFIIATNRHLSVVHPIYKLLPHPHYRDTMNINGLARLSLVNDGGVIEQTFWLGYSVEMSA 587
Qy 607 DVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVYRLLIKDYPYAVDGLVWIAERWVKEY 666
Db 588 VVYKDWVFTDQALPADLTKRGMALIEDPSCPHGIRLVIEDYPTVTDGLEIWDIAKTWVHEY 647
Qy 667 LDIIYPNDGELQRDVLOAWKKEVREEAHGDLKDRDWPRMDTVQQLARACTTIIWVASA 726
Db 648 VFYYKSDDTLREDPELQACWELVEVGHGDKKNEPWPWPKMQTREELVEACAIITWASA 707
Qy 727 LHAAVNFGQYPYAGYLPNRPASRRPMPPEGSHDYKKLGAGQKEADWMVFIITTSQFQTI 786
Db 708 LHAAVNFGQYPYGGILNRPRTLRRFEMPEKGSAYEEL---RKNPQKAYLKTITPKFQTL 764
Qy 787 LGISLIEILSKHSSDEVYLGQRDEPDRWTSDAKALDAFKRFGSRLVQIENRIKTMNDSPD 846
Db 765 IDLSVIEILSRHASDEVYLGGERDNPW-WTSDTRALEAFKRFGNKLAQIENKLSERNNDK 823
Qy 847 LKNRKGPVEMPYMLYPNTSDVTGEKAEGLTAMGIPNSISI 887
Db 824 LRNRGVPQMPYTLTLLPSSK-----EGLTFRGIPNSISI 857

RESULT 6

US-09-751-687-16
; Sequence 16, Application US/09751687
; Patent No. 6660915
; GENERAL INFORMATION:
; APPLICANT: Douma, Anneke
; APPLICANT: Doderer, Albert
; APPLICANT: Cameron-Mills, Verena
; APPLICANT: Skadhauge, Birgitte
; APPLICANT: Bech, Lene
; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY
; FILE REFERENCE: 11225.11US01
; CURRENT APPLICATION NUMBER: US/09/751,687
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 16
; LENGTH: 865
; TYPE: PRT
; ORGANISM: Glycine max
US-09-751-687-16

Query Match 52.6%; Score 2486; DB 4; Length 865;
Best Local Similarity 54.5%; Pred. No. 1.2e-230;
Matches 487; Conservative 137; Mismatches 196; Indels 74; Gaps 15;

Qy 22 KIRGTVRLVKKVLD---VGDFN-----ASLLDGVHRILGWDDGVAFLV 63
Db 18 KIKGTVLMRKNVLDVNSVADLTGKNGVGLTGLNVVGSTLDNLTAFLG--RSVALQLI 75
Qy 64 SATAADPSNGGRGKVGKAAHLEAVVSLKSTADGETVYRVSEFWEDESQGIPIGAVLVRNLQ 123
Db 76 SAT--KPLANGKVGKDTFLEGIIVSLPTLGAGESAFNIQFEWDESMGIPGAFYIKNYM 133
Qy 124 HAEFFLKTTLLEGVPGKGTVVVANSWVYPHKLVSQRIFFANDTYLPSKMPAALVPYRQ 183
Db 134 QVEFYKSLTLEDVNPQGTIRFCNSWVYNTKLYSVRIFFANHTYVPSETPAALVGYRE 193
Qy 184 DELKILRGDDNPGYQEHDRVYDYNDLGDPPDKGEEHARPILGSGQEHYPYRRCRTGR 243
Db 194 EELKNLRG-DGKERKEHDRIYDYDVYNDLGNPDHGENFARPIGSGSSTHYPRGRTRGR 252
Qy 244 HPTKDPNSESRLFLNLNIYVPRDERFGLKMSDFLGYSLKTIIEAVLPTLGTFFVD--D 301
Db 253 YPTRKQDNSEK-----PGEVYVPRDENFGLKSSDFLAYGIKLSQYVLPAFESVFDLNF 307
Qy 302 TPKEFDSFEDILGLYELGPEAPNPLIAEIRKXIPSEFLRSILP-----NGSHDHPL 353

Db 308 TPNEPDSFQDVRDLHEGG-----IKLPTEVISTIMPLPVVKELFRDTGEQVL 354.
QY 354 KMPLFNVIKSDVLKKAPEKFGWRTDEFARETLAGVNPVVKRLTEFFPAKSTLDPQY 413
Db 355 KFPPEHVIQVS-----KSAWMTDEEFAREMVAGVNPVIRGLQEFPPKSNLDPTIYG 406
QY 414 DHTSKITEAHIRHNMGGSLSVONALRNKRLFILDHHDHMPYLDINELEGNFYASRTLL 473
Db 407 EQTSKITADAL--DLDDGYTVDEALASRRFLMDYHDVEMPYIRRIQNTYAK-AYATRTIL 463
QY 474 FLKDDGTLKPLAIELSLPHDPGQORGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSSAWHQ 533
Db 464 FLRENGTLKPVAIELSLPHDPAGDLGAVSQVILPAKEGVESTIWLAKAYVVVNDSCYHQ 523
QY 534 LISHWLNTHAVIEPFVIAIATNRQSLVWHPVVKLLSPHYRDTLNINALARQTLINAGGVFER 593
Db 524 LMSHLNTHAVIEPFIIATNRHLSALHPYIKLLTPHYRDTMNINALARQSLINADGIEK 583
QY 594 TVFPAKVALGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPYAVDGL 653
Db 584 SELPSKHSVEMSSAVYKNWVFTDQALPADLVKRGVAVPDQSSPYGVRLLIKDYPYAVDGL 643
QY 654 VINWAIERWVKEYLDIYYPNDELQORDVELQAWWKEVEEAHGDLDKRDWPRMDTVQOL 713
Db 644 EIWAALKTWVQYVSLYARDVDPKSELQWQWKEAVEKGHGDLDKDPWPKLQTIIEEL 703
QY 714 ARACTIITWVASALHAAVNFQYQYPYAGYLPNRPTASRRPMPPEPGSHDYKKLGAGQKEADM 773
Db 704 VEICTIITWASALHAAVNFQYQYPYGGFILNRPTSSRRLLPEKGTPEYEEMVKSQKA-- 761
QY 774 VIRTITSQFOTILGISLIEILSKHSSDEVYLGQDEPDRWTSADAKALDAFKRFGSRLVQ 833
Db 762 -YLRITTSKFOTLVDLSVIEILSRHASDEVYLGQDNP-HWTSDSKALQAFQKFGNKLKE 819
QY 834 IENRIKTMNDSPDLKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887
Db 820 IEEKLARKNDQSLSNRLGPVQLPYTLLHPN-----SEGLTCRGIPNSISI 865

RESULT 7

US-09-751-687-15
; Sequence 15, Application US/09751687
; Patent No. 6660915
; GENERAL INFORMATION:
; APPLICANT: Douma, Anneke
; APPLICANT: Doderer, Albert
; APPLICANT: Cameron-Mills, Verena
; APPLICANT: Skadhauge, Birgitte
; APPLICANT: Bech, Lene
; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY
; FILE REFERENCE: 11225.11US01
; CURRENT APPLICATION NUMBER: US/09/751,687
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Glycine max
US-09-751-687-15

Query Match 49.9%; Score 2355.5; DB 4; Length 839;
Best Local Similarity 53.4%; Pred. No. 4.5e-218;
Matches 465; Conservative 140; Mismatches 223; Indels 43; Gaps 14;

QY 22 KIRGTVRLVKKEVLVDGDFENASLLDGVHRILGWDDGVAFLVSAATAADPSNGGRGKVGKA 81
Db 7 KIKGTVVLMPKNELEVNP-DGSAVDNLNAFLG--RSVSLQLISATKADAH--GKGKVGKD 61
QY 82 AHLEEAUVSLKSTADGETVYRVSFWEDESQIGPQAVLVRNLQHAEPFLKTLTLEGVPGKG 141
Db 62 TFLEGINTSLPTLGAGESAFNIHFEWDGSMGIPGAFYIKNYMQVEFLKSLTLEAISNOG 121

QY 142 TVVFVANSWVYPHKLYSQERIFFANDTYLPSKMPAALVPYRQDELKILRGDDNPGPYQEH 201
Db 122 TIRFVCNCSWVYNTKLYKSVIRIFANHTYVPSETPAPLVSYREELKSLRG-NGTGERKEY 180
QY 202 DRVYRYDYNLDGDPDKGEEHARPILGSGQEHYPYRRCRTGRHPTKKDPNSESER--LFL 259
Db 181 DRIYDYDYNLDGNPDKSEKLAPPVLGSGSTFFYPYRRCRTGRGPTVTDPTNTEKQGEVF-- 238
QY 260 NLNIYVPRDERFGLKMSDFLGYSLKTIIEAVLPTLGTFFVD--DTPKEFDSFEDILGLYE 317
Db 239 ----YVPRDENLGHLSKSDALEIGTKSLSQIVQPAFESAFDLKSTPIEFHSFQDVHDLYE 294
QY 318 LGPEAPNPNLIAEIRKKIPSEFLRSILPNGSHDHPKXPLPNVIXSDVLKKAPEKFGWR 377
Db 295 GGIKLPDVIISTIIPLPVIKELYRT-----DGHILKEFPQPHVQVS-----QSAWM 341
QY 378 TDEEFARETLAGVNPVVKRLTEFFPAKSTLDPQYGDHSTKITEAHIRHNMGGSLVQNAL 437
Db 342 TDEEFAREMIAGVNPVIRGLEEFFPKSNLDPAIYGDOSSKITADSL--DLDDGYTMDAL 399
QY 438 RNKELFILDHDFMPYLDINELEGNFYIASRTILLEKDDGTLKPLAIELSLPHDPGQQ 497
Db 400 GSRRLFMDYHDFIMPYVTRQINQNSAKTYATRTILFLREDGTLKPVAIELSLSHSAGDL 459
QY 498 RGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSSAWHQLISHWLNTHAVIEPFVIAIATNRQLS 557
Db 460 SAAVSQVVLPAKEGVESTIWLAKAYVIVNDSCYHQLMSHLNTHAAMEPFVIAIATNRHLS 519
QY 558 VVHPVHKLLSPHYRDTLNINALARQTLINAGGVFERTVFPKAYALGMSADVYKSWNFNEQ 617
Db 520 VLHFIYKLLTPHYRNNMNINALARQSLINANGIIETTFPLPSKYSVEMSSAVYKNWVFTDQ 579
QY 618 ALPADLVKRGVAVPDQSSPYGVRLLIKDYPYAVDGLVIWAIERWVKEYLDIYVNDGEL 677
Db 580 ALPADLIKRGVAIKDPPSTPHGVRLIIEYDYPYAADGLEIWAIAKTWVQYVPLYARDDDV 639
QY 678 QRDVELQAWWKEVREEAHGDLDKRDWPRMDTVQOLARACTTIIWVASALHAAVNFQY 737
Db 640 KNDSELQHWKAEAVEKGHGDLDKDPWPKLQTLLEDLVEVCLIIIIWIASALHAAVNFQY 699
QY 738 YAGYLPNRPTASRRPMPPEGSHDYKKLGAGQKEADMVFIRITTSQFOTILGISLIEILSK 797
Db 700 YGGLIMNRPTASRRLLPEKGTPEYEEMINNEKA---YLRITTSKLTLSLSVIEILST 756
QY 798 HSSDEVYLGQDEPDRWTSADAKALDAFKRFGSRLVQIENRIKTMNDSPDLK-NRKGPVEM 856
Db 757 HASDEVYLGQDNP-HWTSDSKALQAFQKFGNKLKEIEEKLVRNNDPSLQGNRLGPVQL 815
QY 857 PYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887
Db 816 PYTLLYPSE-----EGLTFRGIPNSISI 839

RESULT 8

US-09-061-768A-2
; Sequence 2, Application US/09061768A
; Patent No. 6204037
; GENERAL INFORMATION:
; APPLICANT: BRASH, ALAN R.
; APPLICANT: BOEGLIN, WILLIAM E.
; APPLICANT: JISAKA, MITSUO
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARLES A. TAYLOR, JR.
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
; COMPUTER: IBM PC/XT/AT compatible

OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/061,768A
FILING DATE: APRIL 16, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA: NONE
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 676 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-09-061-768A-2

Query Match 10.9%; Score 513.5; DB 3; Length 676;
Best Local Similarity 31.2%; Pred. No. 2.7e-40;
Matches 164; Conservative 74; Mismatches 193; Indels 95; Gaps 17;

QY 376 WRTDEEFARETLAGVNPVVIKRLTEFFPAKSTLDPQYGDHSTKITEAHIRHNMG-GLSVQ 434
Db 232 WQEDAFFASQFLNGLNPVLIIRCHYLP-----KNFPVTDAMVASLLGPGTSLQ 279
QY 435 NALRNKRLFIIDHDFMPYLDEI--NELEG--NFIYASRTLLFLKDD-GTLKPLAIELS 489
Db 280 AELEKGSFLVDH----GILSGIQTNVINGKPKQFSAAPMTLLYQSPGCGPLPLAQLS 334
QY 490 LPHPDGQORGAVSKVYTPAHTGVEGHVWQAKAYACVNDSAWHQLISHWLNTHAVIEPFV 549
Db 335 -----QTPGNSPIFLPTDDKWD---WLLAKTWVRNABFSFHEALTHLLSHLLPEVFT 385
QY 550 IATNRQLSVVHPVKLLSPHYRDTLNINALARQTLNAGGVFERTVFPKAYALGMSADVY 609
Db 386 LATLRQLPHCHPLFKLLIPHTRYTLHINTLARELLIVPGQVDRST-----GIGIEGF 438
QY 610 -----KSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIAVDGLVIWAIER 661
Db 439 SELIQRMKQLNYSLCLPDIRTRGVED-----IPGYYYRDDGMQINGAVER 486
QY 662 WKKEYLDIYPNDGELQRDVELQAWKEVREEAHGDLKDRDWPRMDTVQQLARACTIIT 721
Db 487 FVSEIIGIYPSDESVDQDRELQAWVREIFSKGFLNQESSGIPSSLETREALVQYVTMVI 546
QY 722 WVASALHAAVNFQGYPYAGYLPNRPPTASRRPMPPEPGSHDYKKLGAGQKEADMVFIRTITS 781
Db 547 FTCSAKHAAVSAGQFSDCAWPNLPPSMQLPPP-----TSKGLATCEG----FIATLPP 596
QY 782 QFQTILGISLIEILSKHSSDEVYLGQRDEPDRWTSDAKALDAFKRFGSRLVQIENRIKTM 841
Db 597 VNATCDVILALWLLSKEPGDQRLPG--TYPDEHFTTEAPRRSIATFQSRLLAQISRGIOER 654
QY 842 NDSPLDKNRKGPVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
Db 655 N-----RGLV-LPYTYLDPPL-----IENSVSI 676

RESULT 9

US-09-764-246-2
Sequence 2, Application US/09764246
Patent No. 6649355
GENERAL INFORMATION:
APPLICANT: BRASH, ALAN R.
BOEGLIN, WILLIAM B.

JISAKA, MITSUO
TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARLES A. TAYLOR, JR.
STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
CITY: DURHAM
STATE: NORTH CAROLINA
COUNTRY: USA
ZIP: 27707
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/764,246
FILING DATE: 17-Jan-2001
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 676 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-764-246-2

Query Match 10.9%; Score 513.5; DB 4; Length 676;
Best Local Similarity 31.2%; Pred. No. 2.7e-40;
Matches 164; Conservative 74; Mismatches 193; Indels 95; Gaps 17;

QY 376 WRTDEEFARETLAGVNPVVIKRLTEFFPAKSTLDPQYGDHSTKITEAHIRHNMG-GLSVQ 434
Db 232 WQEDAFFASQFLNGLNPVLIIRCHYLP-----KNFPVTDAMVASLLGPGTSLQ 279
QY 435 NALRNKRLFIIDHDFMPYLDEI--NELEG--NFIYASRTLLFLKDD-GTLKPLAIELS 489
Db 280 AELEKGSFLVDH----GILSGIQTNVINGKPKQFSAAPMTLLYQSPGCGPLPLAQLS 334
QY 490 LPHPDGQORGAVSKVYTPAHTGVEGHVWQAKAYACVNDSAWHQLISHWLNTHAVIEPFV 549
Db 335 -----QTPGNSPIFLPTDDKWD---WLLAKTWVRNABFSFHEALTHLLSHLLPEVFT 385
QY 550 IATNRQLSVVHPVKLLSPHYRDTLNINALARQTLNAGGVFERTVFPKAYALGMSADVY 609
Db 386 LATLRQLPHCHPLFKLLIPHTRYTLHINTLARELLIVPGQVDRST-----GIGIEGF 438
QY 610 -----KSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIAVDGLVIWAIER 661
Db 439 SELIQRMKQLNYSLCLPDIRTRGVED-----IPGYYYRDDGMQINGAVER 486
QY 662 WKKEYLDIYPNDGELQRDVELQAWKEVREEAHGDLKDRDWPRMDTVQQLARACTIIT 721
Db 487 FVSEIIGIYPSDESVDQDRELQAWVREIFSKGFLNQESSGIPSSLETREALVQYVTMVI 546
QY 722 WVASALHAAVNFQGYPYAGYLPNRPPTASRRPMPPEPGSHDYKKLGAGQKEADMVFIRTITS 781
Db 547 FTCSAKHAAVSAGQFSDCAWPNLPPSMQLPPP-----TSKGLATCEG----FIATLPP 596
QY 782 QFQTILGISLIEILSKHSSDEVYLGQRDEPDRWTSDAKALDAFKRFGSRLVQIENRIKTM 841

Db 597 VNATCDVILALWLLSKEPGDQRLG--TYPDEHFTTEAPRRSIATFQSLAQISRGIQER 654
QY 842 NDSPDLKXKRGKGVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
Db 655 N-----RGLV-LPTYLDPL-----IENSVSI 676

RESULT 10

US-09-547-435-6
; Sequence 6, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-547-435-6

Query Match 10.9%; Score 513; DB 4; Length 556;
Best Local Similarity 29.3%; Pred. No. 2.1e-40;
Matches 154; Conservative 85; Mismatches 192; Indels 94; Gaps 16;

QY 376 WRTDEEFARETLAGNVPVIIKRLTEFPAPKSTLDPROYGHTSKITEAHIRHNMG-GLSVQ 434
Db 113 WCEDHFFGYQYLVGNVPMVLMHCISLPSK-----LPVTNDMVAPLLGQDTCLO 160
QY 435 NALNRKRLFILDDHDFMPYLDE--INELEG--NFIYASRTLLFLKDDGTLKPLAIELS- 489
Db 161 TELERGNIFLADYW-----ILAEAPTHCLNGRQYVAAPCLLWLSPOGALVPLAIQLSQ 215
QY 490 LPHPDGQORGAVSKVYTPAHTGVEGHVWQAKAYACVNDSAWHQLISHWLNTHAVIEPFV 549
Db 216 TPGPD-----SPIFLPTDSEWD---WLLAKTWVRNSEFLVHENTHFLCTHLLCEAFA 265
QY 550 IATNRQLSVVHPVHKLLSPHYRDTLINALARQTLINAGGVFERTVFPKAYALGMSADV 609
Db 266 MATLRQLPLCHPIYKLLPHTRYTLQVNTIARATLLNPEGLVDQVT-----SIGRQGLIY 320
QY 610 -----KSNWFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVIWAIERWV 663
Db 321 LMSTGLAHFTYTNFCLPDSLARGV-----LAIPNYHYRDDGLKIWAIESFV 368
QY 664 KEYLDIYPNDGELQRDVELQAWKKEVREEAHGDLKDRDWPRMDTVQQLARACTTIWV 723
Db 369 SEIVGYYPDSASVQDSELOQWTEIIFAQAFLGRESSGFPSSRLCTPGEMVKFLTAIFN 428
QY 724 ASALHAAVNFQGYPYAGYLPNRPRTASRRPMPE-PGSHDYKKGAGQKEADMFVIRTITSQ 782
Db 429 CSAQHAAVNSGQHDGFWAMPNAPSSMRQPPPTKGTTLK-----TYLDTLPEV 477
QY 783 FQTLIGISLIEILSKHSSDEVVLGQDEPDRTWTSDAKALDAFKRFGSLRVQIENIKTMN 842
Db 478 NISCNLLLFVLVSQEPKQDRPLG--TYPDEHFTTEAPRRSIAAFQSLRAQI----- 527
QY 843 DSPDLKXKRGKGVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
Db 528 -SRDIQERNQGLALPYTYLDPPL-----IENSVSI 556

RESULT 11

US-09-547-435-2

; Sequence 2, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-547-435-2

Query Match 10.9%; Score 513; DB 4; Length 711;
Best Local Similarity 29.3%; Pred. No. 3.3e-40;
Matches 154; Conservative 85; Mismatches 192; Indels 94; Gaps 16;

QY 376 WRTDEEFARETLAGNVPVIIKRLTEFPAPKSTLDPROYGHTSKITEAHIRHNMG-GLSVQ 434
Db 268 WCEDHFFGYQYLVGNVPMVLMHCISLPSK-----LPVTNDMVAPLLGQDTCLO 315
QY 435 NALNRKRLFILDDHDFMPYLDE--INELEG--NFIYASRTLLFLKDDGTLKPLAIELS- 489
Db 316 TELERGNIFLADYW-----ILAEAPTHCLNGRQYVAAPCLLWLSPOGALVPLAIQLSQ 370
QY 490 LPHPDGQORGAVSKVYTPAHTGVEGHVWQAKAYACVNDSAWHQLISHWLNTHAVIEPFV 549
Db 371 TPGPD-----SPIFLPTDSEWD---WLLAKTWVRNSEFLVHENTHFLCTHLLCEAFA 420
QY 550 IATNRQLSVVHPVHKLLSPHYRDTLINALARQTLINAGGVFERTVFPKAYALGMSADV 609
Db 421 MATLRQLPLCHPIYKLLPHTRYTLQVNTIARATLLNPEGLVDQVT-----SIGRQGLIY 475
QY 610 -----KSNWFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVIWAIERWV 663
Db 476 LMSTGLAHFTYTNFCLPDSLARGV-----LAIPNYHYRDDGLKIWAIESFV 523
QY 664 KEYLDIYPNDGELQRDVELQAWKKEVREEAHGDLKDRDWPRMDTVQQLARACTTIWV 723
Db 524 SEIVGYYPDSASVQDSELOQWTEIIFAQAFLGRESSGFPSSRLCTPGEMVKFLTAIFN 583
QY 724 ASALHAAVNFQGYPYAGYLPNRPRTASRRPMPE-PGSHDYKKGAGQKEADMFVIRTITSQ 782
Db 584 CSAQHAAVNSGQHDGFWAMPNAPSSMRQPPPTKGTTLK-----TYLDTLPEV 632
QY 783 FQTLIGISLIEILSKHSSDEVVLGQDEPDRTWTSDAKALDAFKRFGSLRVQIENIKTMN 842
Db 633 NISCNLLLFVLVSQEPKQDRPLG--TYPDEHFTTEAPRRSIAAFQSLRAQI----- 682
QY 843 DSPDLKXKRGKGVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
Db 683 -SRDIQERNQGLALPYTYLDPPL-----IENSVSI 711

RESULT 12

US-09-547-435-24
; Sequence 24, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides

; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 867
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-547-435-24

Query Match 10.9%; Score 513; DB 4; Length 867;
Best Local Similarity 29.3%; Pred. No. 4.6e-40;
Matches 154; Conservative 85; Mismatches 192; Indels 94; Gaps 16;
QY 376 WRTDEEFARETLAGVNPVILKLTFFPAKSTLDPQYGDHTSKITEAHIRHNMG-GLSVQ 434
Db 424 WCEDHFGYQYLVGNVPMVLMHCISLPSK-----LPVNDMVAPLLGQDTCLQ 471
QY 435 NALRNKRLFLDHHDFMPYLDE--INELEG--NFIYASRTLLFLKDDGTLKPLAIELS- 489
Db 472 TELERGNIFLADYW-----ILAEAPTHCLNGRQYVAAPLCLLWLSPOGALVPLAIQLSQ 526
QY 490 LPHPDGQORGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSAWHQLISHWLNTHAVIEPFV 549
Db 527 TPGPD-----SPIFLPTDSEWD---WLLAKTWVRNSEFLVHENNTHFLCTHLLCEAFA 576
QY 550 IATNRQLSVVHPVHKLSPHYRDTLNINALAROTLINAGGVFERTVFPKAYALGMSADVY 609
Db 577 MATLRQLPLCHPIYKLLPLPHTRYTLQVNTIARATLLNPEGLVDQVT-----SIGRQGLIY 631
QY 610 -----KSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPPYAVDGLVIWVAIERWV 663
Db 632 LMSTGLAFTYTNFCLPDSLARGV-----LAIPNYHYRDDGGLKIWAIESFV 679
QY 664 KEYLDIYPNDGELQRDVELQAWKVEVREEAHGDLKDRDWMPRMDTVQQLARACTTIIWV 723
Db 680 SEIVGYYPDSASVQDSELOAWTGEIFAQAFGLGESSGPPSRLCTPGEMVKFLTAIEN 739
QY 724 ASALHAAVNFGQYPYAGYLPNRPFTASRRPMPE-PGSHDYKKLKAGQKEADMVFIRITISQ 782
Db 740 CSAQHAAVNSGQHDGFGAWMPNAPSSMRQPPQTKGTTLK-----TYLDTLPEV 788
QY 783 FQTLIGLSLIEILSKHSSDEVILQORDEPRDRTSDAKALDAFKRFGSLVQIENRIKTMN 842
Db 789 NISCNLLFLWLSQEPKQDRPLG--TYPDEHFTTEAPRRSIAAFQSRLAQI----- 838
QY 843 DSPDLKNRKGPVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
Db 839 -SRDIQERNQGLALPYTYLDPPL-----IENSVSI 867

RESULT 13
US-09-061-768A-4
; Sequence 4, Application US/09061768A
; Patent No. 6204037
; GENERAL INFORMATION:
; APPLICANT: BRASH, ALAN R.
; APPLICANT: BOEGLIN, WILLIAM E.
; APPLICANT: JISAKA, MITSUO
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARLES A. TAYLOR, JR.
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
; COMPUTER: IBM PC/XT/AT compatible

; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORD PERFECT 6.1 and ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/061,768A
; FILING DATE: APRIL 16, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: NONE
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: ARLES A. TAYLOR, JR.
; REGISTRATION NUMBER: 39,395
; REFERENCE/DOCKET NUMBER: 1242/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 493-8000
; TELEFAX: (919) 419-0383
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 677 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
US-09-061-768A-4

Query Match 10.7%; Score 507; DB 3; Length 677;
Best Local Similarity 29.8%; Pred. No. 1.1e-39;
Matches 160; Conservative 83; Mismatches 192; Indels 102; Gaps 20;
QY 369 APEFKFG-WRTDEEFARETLAGVNPVILKLTFFPAKSTLDPQYGDHTSKITEAHIRHN 427
Db 225 AAEEYFAHWQEDAFFASQFLNGINPVLIRRHCHSLP-----NNFPVTDEMVAAPV 272
QY 428 MG-GLSVQNALRNKRLFLDHHDFMPYLDEINELEG--NFIYASRTLLFLKDD- 477
Db 273 LGPGTSLQAELEKSGSLFLVDHGLSGVH-----TNILNGKPFQFSAAPMTLLHQSSG 323
QY 478 DGTLLKPLAIEL-SLPHPDGQORGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSAWHQLIS 536
Db 324 SGPLLPALQKOTPGPD-----NPIFLPSDDTDW---WLLAKTWVRNSEFYIHEAVT 373
QY 537 HWLNTHAVIEPFVFIATNRQLSVVHPVHKLSPHYRDTLNINALAROTLINAGGVFERTV 596
Db 374 HLLHAHLIPEVFALATLRQLPRCHPLFKLLIPHIRYTHINTLARELLVAPGKLIDKS-- 431
QY 597 PAKYALGMSADVYK---SWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDG 652
Db 432 -TGLGTGFGSDLIKRNMEQLNYSVLCLPEDIRARGVED-----IPGYIYRDDG 478
QY 653 LVIWVAIERWVKEYLDIYPNDGELQRDVELQAWKVEVREEAHGDLKDRDWMPRMDTVQ 712
Db 479 MQIWAIAKSFVSEIVSIYYPSTSVQDDQELQAWVREIFSEGLGESSGMPSLDRTREA 538
QY 713 LARACTTIIWVASALHAAVNFGQYPYAGYLPNRPFTASRRPMPEPGSHDYKKLKAGQKEAD 772
Db 539 LVQYITMVIPTCSAKHAAVSSGQFDSVWMPNLPPTMQLPPP-----TSKQARPE 589
QY 773 MVFIRITISQFQTLIGLSLIEILSKHSSDEVILQORDEPRDRTSDA--KALDAFKRFGSR 830
Db 590 S-FIATLPVAVNSSYHIIALWLLSAEPGDQRPGLGHYPD-EHFTEDAPRRSVAAPQR---K 644
QY 831 LVQIENRIKTMNDSPDLKNRKGPVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
Db 645 LIQI-----SKGIRERNRGLALPYTYLDPPL-----IENSVSI 677

RESULT 14
US-09-764-246-4
; Sequence 4, Application US/09764246
; Patent No. 6649355
; GENERAL INFORMATION:
; APPLICANT: BRASH, ALAN R.
; APPLICANT: BOEGLIN, WILLIAM E.

JISAKA, MITSUO
TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARLES A. TAYLOR, JR.
STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
CITY: DURHAM
STATE: NORTH CAROLINA
COUNTRY: USA
ZIP: 27707
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/764,246
FILING DATE: 17-Jan-2001
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 677 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-764-246-4

Query Match 10.7%; Score 507; DB 4; Length 677;
Best Local Similarity 29.8%; Pred. No. 1.1e-39;
Matches 160; Conservative 83; Mismatches 192; Indels 102; Gaps 20;
QY 369 APEFKFG-WRTDEEFARETLAGVNPVVKRLTEFPKSTLDPKQYGDHTEAHIRHN 427
Db 225 AAEYVFAHQWQEDAFFASQFLNGINPVLIRCHSLP-----NNPVTDEMVA 272
QY 428 MG-GLSVQNALRNKRLFLDH-----HDHFMPLYLDEINELEG--NFIYASRTLLFLKD- 477
Db 273 LGPQTSLOAELEKGLFLVDHGILSGVH-----TNILNGKQFSAAPMTLLHQSSG 323
QY 478 DGTILKPLAIEL-SLPHPDGQORGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSAWHQLIS 536
Db 324 SGPLLPALQKQTPGPD-----NPIFLPSDDTDW---WLLAKTWVRNSEFYIHEAVT 373
QY 537 HMLNTHAVIEPFIATNRQLSVVHPVHKLLSPHYRDTLNINALARQTLINAGGVFERTVF 596
Db 374 HLLHAHLIPEVFALATLRQLPRCHPLFKLLIPHIRYTLHINTLARELLVAPGKLIDKS-- 431
QY 597 PAKYALGMSADVYK---SWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDG 652
Db 432 -TGLTGGFSDLIKRNMEQLNYSVLCLPEDIRARGVED-----IPGYIYRDDG 478
QY 653 LVINWAIERWVKEYLDIYYPNDGELQDVELQAWKEVREEAHGDLKDRDWMFRMDTVQQ 712
Db 479 MQIWAIGKSFVSEIVSIYIPSDTSVQDDQELQAWREIFSEGFLGRESSGMPSLDRTREA 538
QY 713 LARACTIIVWASALHAAVNFQYPIYAGYLPNRPASRRPMPPEPGSHDYKYLKAGQKEAD 772
Db 539 LVQYITWVIFTCSAKHAAVSSGQFSDSCVWMPNLPPTMQLPFP-----TSKGQARPE 589
QY 773 MVFIRITTSQFQITLIGISLILSKHSSDEVYLGQDEPDRWTSDA--KALDAFKRFGSR 830

Db 590 S-FIATLPAVNSSSYHIIALWLLSAEPGDQRPGLCHYPD-EHFTEDAPRRSVAAAFQ---K 644
QY 831 LVQIENRIKTMNDSPDLKRNKGPVEMPYMLLYENTSDVTGKAEGLTAMGINSISI 887
Db 645 LIQI-----SKGIRERNRGLALPYTYLDPPL-----IENSVSI 677
RESULT 15
US-09-087-727-2
; Sequence 2, Application US/09087727A
; Patent No. 6103496
; GENERAL INFORMATION:
; APPLICANT: Brash, Alan R
; APPLICANT: Boeglin, William E
; APPLICANT: Kim, Richard B
; TITLE OF INVENTION: Isolated and Purified 12R-lipoxygenase Protein and
; TITLE OF INVENTION: Nucleic Acids
; FILE REFERENCE: Attorney Docket No. 6103496 1242-7
; CURRENT APPLICATION NUMBER: US/09/087,727A
; CURRENT FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 701
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-087-727-2

Query Match 10.7%; Score 503.5; DB 3; Length 701;
Best Local Similarity 26.0%; Pred. No. 2.6e-39;
Matches 205; Conservative 108; Mismatches 249; Indels 227; Gaps 36;
QY 130 KTLIEGVPGKGTTFVANSWVYPKLYSQERIFFANDTYLPSKMPAALVPRQDELKIL 189
Db 109 ETLALREATGKTTA-----DDSLP-----VLEHRKBEIRA- 139
QY 190 RGDNPQPYQEHDRVRYDYNDLGDGDPKGEHARPIILG--SQEH--PYPRCRTRGRHP 245
Db 140 -----KQDFY-----HWRVPLPGLPSYVHIPSPYRPPVRRHRNP 172
QY 246 TKXDPNSESRLFLNLNIYVPRDERFGLKMSDFGLYSKLTIEAVLPTLGTGFYDDTPKE 305
Db 173 NRPEWNG-----YIPGFPILINFKATKFLNLNR--YSFLKTASFFV----- 212
QY 306 FDSFEDILGLYELGPEAPNPLIAEIRKKIPSEF-----LRSILPNGSHDPLKMPLP 358
Db 213 -----RLGPMA-----LAFKVRGLLDCSHWKRLKDIRKIFPGK----- 246
QY 359 NVIKSDVLKKAPEFKFGWETDEEFARETLAGVNPVVKRLTEFPKSTLDPKQYGDHTEAH 418
Db 247 ---KSVVSEYVAEH---WAEDTFGYQYLVNPNGLIRRCTRIPDK-----FP 288
QY 419 ITEAHIRNMG-GLSVQNALRNKRLFLDHHDHFMPLYLDEINELEGNFY--ASRTLLFL 475
Db 289 VTDDMVAPFLGEGTCLQAELEKGNIIYLDY--RMEGIPTV-ELSGRKQHHCAPLCLLHF 345
QY 476 KDDGTLKPLAIELS-LPHPDGQORGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSAWHQL 534
Db 346 GPEGKMPPIAIQLSQTPGPD-----CPIFLPSSEWD---WLLAKTWVRYAEFFYSHEA 395
QY 535 ISHMLNTHAVIEPFIATNRQLSVVHPVHKLLSPHYRDTLNINALARQTLINAGGVFERT 594
Db 396 IAHLETHLIAEAFCLALLRNLPMPCHPLYKLLIPHRYTVQINSIGRAVLNNEGSL---- 451
QY 595 VFPKALGMSADV-----YKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIK 644
Db 452 -----SAKGMSLGVEGFAGVMVRALSELTYSLYLNDPVERGV-----QDLP----- 494
QY 645 DYPYAVDGLVIWAIERWVKEYLDIYYPNDGELQDVELQAWKEVREEAHGDLKDRD-- 702
Db 495 GYTYRDDDSLAVWNVALEKYVTEIITYYPSDAAVEGDELOQSWVQEIFKEC-----LLGRESS 551
QY 703 WWPR-MDTVQQLARACTTIIVWASALHAAVNFQYPIYAGYLPNRPASRRPMPPEPGSHDY 761

Db	552	GFPRCLRTVPELIRYVTIVITCSAKHAAVNTGMEFTAWMPNFPASMRNP-----PI	604
Qy	762	KKLGAGQKEADMVVFIRITTSQFQTLIGISLIEILSKHSSDEVYLGQRDEPD-RWTSDA--	818
Db	605	QTKGLTLE---TFMDTLPDVKTTCITLLVLTLSREPDRRPLGH--FPDIHFVEEAPR	659
Qy	819	KALDAFKRFGSRLVQIENRIKTWNDSPLKNRKGVPVEMPYMLLYPNTSDVTGEKABGLTA	878
Db	660	RSIEAFRQ---RLNQI-----SHDIRQNRKCLPIPYVYLDP-----	692
Qy	879	MGIPNSISI	887
Db	693	VLIENSISI	701

Search completed: March 23, 2004, 07:02:07
Job time : 30 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 07:01:04 ; Search time 333 Seconds
(without alignments)
689.770 Million cell updates/sec

Title: US-10-059-909-16
Perfect score: 4723
Sequence: 1 MFHWGVADRLTGKKNKEAWSE.....VTGEKAEGLTAMGIPNSISI 887

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 1049977

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	4723	100.0	887	14	US-10-059-909-16
2	4723	100.0	887	14	US-10-132-350-22
3	4723	100.0	887	14	US-10-132-350-24
4	4575	96.9	897	12	US-10-425-114-39463
5	4498	95.2	926	12	US-10-425-114-69756
6	4487	95.0	887	14	US-10-132-350-18
7	4487	95.0	887	14	US-10-132-350-20
8	3039	64.3	864	14	US-10-132-350-10
9	3039	64.3	864	14	US-10-132-350-12
10	2958	62.6	873	14	US-10-132-350-2
11	2958	62.6	873	14	US-10-132-350-4
12	2958	62.6	891	12	US-10-425-114-62915
13	2936.5	62.2	862	10	US-09-751-687-9
14	2929.5	62.0	862	10	US-09-751-687-12
15	2860	60.6	864	10	US-09-751-687-18
					Sequence 16, Appl
					Sequence 22, Appl
					Sequence 24, Appl
					Sequence 39463, A
					Sequence 69756, A
					Sequence 18, Appl
					Sequence 20, Appl
					Sequence 10, Appl
					Sequence 12, Appl
					Sequence 2, Appli
					Sequence 4, Appli
					Sequence 62915, A
					Sequence 9, Appli
					Sequence 12, Appl
					Sequence 18, Appl

16	2833	60.0	871	14	US-10-132-350-14	Sequence 14, Appl
17	2833	60.0	871	14	US-10-132-350-16	Sequence 16, Appl
18	2799.5	59.3	859	10	US-09-978-522-3	Sequence 3, Appli
19	2777.5	58.8	862	10	US-09-978-522-1	Sequence 1, Appli
20	2663.5	56.4	859	12	US-10-424-599-213159	Sequence 213159, A
21	2661	56.3	864	12	US-10-425-114-46828	Sequence 46828, A
22	2633	55.7	887	12	US-10-425-114-54449	Sequence 54449, A
23	2495.5	52.8	857	12	US-10-424-599-215976	Sequence 215976, A
24	2495.5	52.8	860	12	US-10-425-114-45769	Sequence 45769, A
25	2495.5	52.8	863	12	US-10-425-114-54429	Sequence 54429, A
26	2495.5	52.8	863	12	US-10-425-114-55253	Sequence 55253, A
27	2491.5	52.8	857	10	US-09-751-687-17	Sequence 17, Appl
28	2486.5	52.6	866	12	US-10-424-599-239573	Sequence 239573, A
29	2486	52.6	865	10	US-09-751-687-16	Sequence 16, Appl
30	2476	52.4	880	14	US-10-059-909-12	Sequence 12, Appl
31	2457.5	52.0	860	12	US-10-424-599-220216	Sequence 220216, A
32	2457	52.0	826	12	US-10-424-599-215973	Sequence 215973, A
33	2457	52.0	832	12	US-10-425-114-45631	Sequence 45631, A
34	2430	51.5	871	12	US-10-425-114-62385	Sequence 62385, A
35	2422	51.3	865	12	US-10-424-599-258944	Sequence 258944, A
36	2419.5	51.2	868	12	US-10-424-599-242598	Sequence 242598, A
37	2414.5	51.1	881	12	US-10-425-114-57754	Sequence 57754, A
38	2414.5	51.1	882	12	US-10-425-114-54555	Sequence 54555, A
39	2398.5	50.8	856	12	US-10-424-599-151512	Sequence 151512, A
40	2396	50.7	857	12	US-10-425-114-57794	Sequence 57794, A
41	2395	50.7	859	12	US-10-424-599-161981	Sequence 161981, A
42	2395	50.7	860	12	US-10-425-114-57755	Sequence 57755, A
43	2395	50.7	861	12	US-10-425-114-45728	Sequence 45728, A
44	2395	50.7	863	12	US-10-425-114-62362	Sequence 62362, A
45	2389.5	50.6	856	12	US-10-424-599-151513	Sequence 151513, A

ALIGNMENTS

RESULT 1
US-10-059-909-16
; Sequence 16, Application US/10059909
; Publication No. US20030074693A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Edgar B.
; APPLICANT: Kinney, Anthony
; APPLICANT: Klein, Theodore
; APPLICANT: Lee, Jian Ming
; APPLICANT: Pearlstein, Richard
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Shen, Jennie
; APPLICANT: Thorpe, Cathy
; APPLICANT: Tingey, Scott
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Lipoxigenases
; FILE REFERENCE: BB1333 US CIP
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: US/10/059,909
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: 60/119,597
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 16
; LENGTH: 887
; TYPE: PRT
; ORGANISM: Zea mays
US-10-059-909-16

Query Match 100.0%; Score 4723; DB 14; Length 887;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 887; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFHWGVADRLTGKKNKEAWSEKIRGTVRLVKKEVLVGVDFNASLLDGVHRLGWDGVAF 60
DB 1 MFHWGVADRLTGKKNKEAWSEKIRGTVRLVKKEVLVGVDFNASLLDGVHRLGWDGVAF 60

QY 61 QLVATAADPSNGGRGKVGKAAHLEAAVSLKSTADGETVYRVSEFWEDESQIGPGLVLR 120
Db 61 QLVATAADPSNGGRGKVGKAAHLEAAVSLKSTADGETVYRVSEFWEDESQIGPGLVLR 120
QY 121 NLQHAEEFLKTLTLEGVPGKGTGVFVANSWVYPHKLYSQERIFFANDTYLPSKMPAALVP 180
Db 121 NLQHAEEFLKTLTLEGVPGKGTGVFVANSWVYPHKLYSQERIFFANDTYLPSKMPAALVP 180
QY 181 YRQDELKILRGDDNPGPYQEHDRVYDYNDLGDPPDKGEEHARPILGSGQEHYPYRRCR 240
Db 181 YRQDELKILRGDDNPGPYQEHDRVYDYNDLGDPPDKGEEHARPILGSGQEHYPYRRCR 240
QY 241 TGRHPTKDPNSESRLFLNLNIYVPRDERFGLKMSDFLGYSLKTIIEAVLPTLGTFTVD 300
Db 241 TGRHPTKDPNSESRLFLNLNIYVPRDERFGLKMSDFLGYSLKTIIEAVLPTLGTFTVD 300
QY 301 DTPKEFDSFEDILGLYELGPEAPNPLIAEIRKKIPSEFLRSILPNGSHDHLKMPPLNV 360
Db 301 DTPKEFDSFEDILGLYELGPEAPNPLIAEIRKKIPSEFLRSILPNGSHDHLKMPPLNV 360
QY 361 IKSDVLKKAPEFKFGWRTDEEFARETLAGVNPVIIKRLTEFFPAKSTLDPQYGDHTSKIT 420
Db 361 IKSDVLKKAPEFKFGWRTDEEFARETLAGVNPVIIKRLTEFFPAKSTLDPQYGDHTSKIT 420
QY 421 EAHIRHNMGGLSVQNALRNKRLFLDHHDFMPYLDDEINELEGNFIYASRTLLFLKDDGT 480
Db 421 EAHIRHNMGGLSVQNALRNKRLFLDHHDFMPYLDDEINELEGNFIYASRTLLFLKDDGT 480
QY 481 LKPLAIELSLPHPDGQORGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSAWHQLISHWLN 540
Db 481 LKPLAIELSLPHPDGQORGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSAWHQLISHWLN 540
QY 541 THAVIEPFVIATNRQLSVVHPVHKLLSPHYRDTLNINALARQTLINAGGVFERTVFPKY 600
Db 541 THAVIEPFVIATNRQLSVVHPVHKLLSPHYRDTLNINALARQTLINAGGVFERTVFPKY 600
QY 601 ALGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPYAVDGLVIWVAIE 660
Db 601 ALGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPYAVDGLVIWVAIE 660
QY 661 RWVKEYLDIYYPNDGELQORDVELQAWKEVREEAHGDLKORDWWPRMDTVQQLARACTTI 720
Db 661 RWVKEYLDIYYPNDGELQORDVELQAWKEVREEAHGDLKORDWWPRMDTVQQLARACTTI 720
QY 721 IWVASALHAAVNFQYYPAGYLPNRPTASRRRPMPEPGSHDYKKGAGQKEADMVFIRITIT 780
Db 721 IWVASALHAAVNFQYYPAGYLPNRPTASRRRPMPEPGSHDYKKGAGQKEADMVFIRITIT 780
QY 781 SQFTILGISLIEILSKHSSDEVYLGQRDEPDRWTSDAKALDAFKRFGSRLVQIENRIKT 840
Db 781 SQFTILGISLIEILSKHSSDEVYLGQRDEPDRWTSDAKALDAFKRFGSRLVQIENRIKT 840
QY 841 MNDSPDLKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887
Db 841 MNDSPDLKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887

RESULT 2

US-10-132-350-22
; Sequence 22, Application US/10132350
; Publication No. US20030166855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Kolomiets, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxigenase Polynucleotides and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286,889

; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 887
; TYPE: PRT
; ORGANISM: Zea mays
US-10-132-350-22

Query Match 100.0%; Score 4723; DB 14; Length 887;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 887; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFWHGVADRLTGKNKEAMSEKIRGTVRLVKKVEVLVDGDFNASLLDGVHRILGWDDGVAF 60
Db 1 MFWHGVADRLTGKNKEAMSEKIRGTVRLVKKVEVLVDGDFNASLLDGVHRILGWDDGVAF 60
QY 61 QLVATAADPSNGGRGKVGKAAHLEAAVSLKSTADGETVYRVSEFWEDESQIGPGLVLR 120
Db 61 QLVATAADPSNGGRGKVGKAAHLEAAVSLKSTADGETVYRVSEFWEDESQIGPGLVLR 120
QY 121 NLQHAEEFLKTLTLEGVPGKGTGVFVANSWVYPHKLYSQERIFFANDTYLPSKMPAALVP 180
Db 121 NLQHAEEFLKTLTLEGVPGKGTGVFVANSWVYPHKLYSQERIFFANDTYLPSKMPAALVP 180
QY 181 YRQDELKILRGDDNPGPYQEHDRVYDYNDLGDPPDKGEEHARPILGSGQEHYPYRRCR 240
Db 181 YRQDELKILRGDDNPGPYQEHDRVYDYNDLGDPPDKGEEHARPILGSGQEHYPYRRCR 240
QY 241 TGRHPTKDPNSESRLFLNLNIYVPRDERFGLKMSDFLGYSLKTIIEAVLPTLGTFTVD 300
Db 241 TGRHPTKDPNSESRLFLNLNIYVPRDERFGLKMSDFLGYSLKTIIEAVLPTLGTFTVD 300
QY 301 DTPKEFDSFEDILGLYELGPEAPNPLIAEIRKKIPSEFLRSILPNGSHDHLKMPPLNV 360
Db 301 DTPKEFDSFEDILGLYELGPEAPNPLIAEIRKKIPSEFLRSILPNGSHDHLKMPPLNV 360
QY 361 IKSDVLKKAPEFKFGWRTDEEFARETLAGVNPVIIKRLTEFFPAKSTLDPQYGDHTSKIT 420
Db 361 IKSDVLKKAPEFKFGWRTDEEFARETLAGVNPVIIKRLTEFFPAKSTLDPQYGDHTSKIT 420
QY 421 EAHIRHNMGGLSVQNALRNKRLFLDHHDFMPYLDDEINELEGNFIYASRTLLFLKDDGT 480
Db 421 EAHIRHNMGGLSVQNALRNKRLFLDHHDFMPYLDDEINELEGNFIYASRTLLFLKDDGT 480
QY 481 LKPLAIELSLPHPDGQORGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSAWHQLISHWLN 540
Db 481 LKPLAIELSLPHPDGQORGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSAWHQLISHWLN 540
QY 541 THAVIEPFVIATNRQLSVVHPVHKLLSPHYRDTLNINALARQTLINAGGVFERTVFPKY 600
Db 541 THAVIEPFVIATNRQLSVVHPVHKLLSPHYRDTLNINALARQTLINAGGVFERTVFPKY 600
QY 601 ALGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPYAVDGLVIWVAIE 660
Db 601 ALGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPYAVDGLVIWVAIE 660
QY 661 RWVKEYLDIYYPNDGELQORDVELQAWKEVREEAHGDLKORDWWPRMDTVQQLARACTTI 720
Db 661 RWVKEYLDIYYPNDGELQORDVELQAWKEVREEAHGDLKORDWWPRMDTVQQLARACTTI 720
QY 721 IWVASALHAAVNFQYYPAGYLPNRPTASRRRPMPEPGSHDYKKGAGQKEADMVFIRITIT 780
Db 721 IWVASALHAAVNFQYYPAGYLPNRPTASRRRPMPEPGSHDYKKGAGQKEADMVFIRITIT 780
QY 781 SQFTILGISLIEILSKHSSDEVYLGQRDEPDRWTSDAKALDAFKRFGSRLVQIENRIKT 840
Db 781 SQFTILGISLIEILSKHSSDEVYLGQRDEPDRWTSDAKALDAFKRFGSRLVQIENRIKT 840
QY 841 MNDSPDLKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887
Db 841 MNDSPDLKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887

Db 841 MNDSPDLKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887

RESULT 3

US-10-132-350-24
; Sequence 24, Application US/10132350
; Publication No. US20030166855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Koloniets, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxigenase Polynucleotides and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286,889
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 887
; TYPE: PRT
; ORGANISM: Zea mays
US-10-132-350-24

Query Match 100.0%; Score 4723; DB 14; Length 887;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 887; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFVHGVADRLTGKKEAWSEGKIRGTVRLVKKEVLVDGDFNASLLDGVHRLGWDGVA 60
Db 1 MFVHGVADRLTGKKEAWSEGKIRGTVRLVKKEVLVDGDFNASLLDGVHRLGWDGVA 60

Qy 61 QLVSAATAADPSNGGRGKVGKAAHLEAAVSLKSTADGETVYRVSEFWEDESQIGIPGAVLVR 120
Db 61 QLVSAATAADPSNGGRGKVGKAAHLEAAVSLKSTADGETVYRVSEFWEDESQIGIPGAVLVR 120

Qy 121 NLQHAFFFLKTLTLEGVPGKGTGVFVANSWVYPHKLYSQERIFFANDTYLPSKMPAALVP 180
Db 121 NLQHAFFFLKTLTLEGVPGKGTGVFVANSWVYPHKLYSQERIFFANDTYLPSKMPAALVP 180

Qy 181 YRQDELKILRGDDNPGYPQEHDRVYRYDYNDLGDGPKGEEHARPILGSGQEHYPYRRCR 240
Db 181 YRQDELKILRGDDNPGYPQEHDRVYRYDYNDLGDGPKGEEHARPILGSGQEHYPYRRCR 240

Qy 241 TGRHPTKDPNSESRLFLNLNIYVPRDERFGLKMSDFLGYSLKTIIEAVLPTLTGTFVD 300
Db 241 TGRHPTKDPNSESRLFLNLNIYVPRDERFGLKMSDFLGYSLKTIIEAVLPTLTGTFVD 300

Qy 301 DTPKEFDSFEDILGLYELGPEAPNPLIAEIRKKIPSEFLRSILPNSGSHDHPKMPLPNV 360
Db 301 DTPKEFDSFEDILGLYELGPEAPNPLIAEIRKKIPSEFLRSILPNSGSHDHPKMPLPNV 360

Qy 361 IKSDVLKKAPEFKFGRTRDEEFARETLAGVNPVVIKRLTEFPAPKSTLDPROYGDHTSKIT 420
Db 361 IKSDVLKKAPEFKFGRTRDEEFARETLAGVNPVVIKRLTEFPAPKSTLDPROYGDHTSKIT 420

Qy 421 EAHIRHNMGGLSVQNALRNKRLFLDHDHDFMPYLDIENELEGNFYASRTLLFLKDDGT 480
Db 421 EAHIRHNMGGLSVQNALRNKRLFLDHDHDFMPYLDIENELEGNFYASRTLLFLKDDGT 480

Qy 481 LKPLAIELSLPHPDGQQRGAWSKVYTPAHTGVEGHVWQLAKAYACVNDSAWHQLISHWLN 540
Db 481 LKPLAIELSLPHPDGQQRGAWSKVYTPAHTGVEGHVWQLAKAYACVNDSAWHQLISHWLN 540

Qy 541 THAVIEPFVIATNRQLSVVHPVKLLSPHYRDTLNINALARQTLINAGGVFEERTVFPAPY 600
Db 541 THAVIEPFVIATNRQLSVVHPVKLLSPHYRDTLNINALARQTLINAGGVFEERTVFPAPY 600

Qy 601 ALGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIAVDGLVIWIAIE 660
Db 601 ALGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIAVDGLVIWIAIE 660

Qy 661 RWVKEYLDIYYPNDGELQRDVELQAWKKEVREEAHGDLKDRDWPRMDTVQOLARACTII 720
Db 661 RWVKEYLDIYYPNDGELQRDVELQAWKKEVREEAHGDLKDRDWPRMDTVQOLARACTII 720

Qy 721 IWVASALHAAVNFQOYPYAGYLPNRPTASRRPMPPEPGSHDYKKGAGQKEADMVFIRIT 780
Db 721 IWVASALHAAVNFQOYPYAGYLPNRPTASRRPMPPEPGSHDYKKGAGQKEADMVFIRIT 780

Qy 781 SQFOTILGISLIEILSKHSSDEVYLGQDEPDRTWTSDAKALDAFKRFGSRLVQIENRIKT 840
Db 781 SQFOTILGISLIEILSKHSSDEVYLGQDEPDRTWTSDAKALDAFKRFGSRLVQIENRIKT 840

Qy 841 MNDSPDLKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887
Db 841 MNDSPDLKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887

RESULT 4

US-10-425-114-39463
; Sequence 39463, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 39463
; LENGTH: 897
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700202892_FLI.pep
US-10-425-114-39463

Query Match 96.9%; Score 4575; DB 12; Length 897;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 861; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MFVHGVADRLTGKKEAWSEGKIRGTVRLVKKEVLVDGDFNASLLDGVHRLGWDGVA 60
Db 11 MDWGRTEQALTGKKEAWSEGKIRGTVRLVKKEVLVDGDFNASLLDGVHRLGWDGVA 70

Qy 61 QLVSAATAADPSNGGRGKVGKAAHLEAAVSLKSTADGETVYRVSEFWEDESQIGIPGAVLVR 120
Db 71 QLVSAATAADPSNGGRGKVGKAAHLEAAVSLKSTADGETVYRVSEFWEDESQIGIPGAVLVR 130

Qy 121 NLQHAFFFLKTLTLEGVPGKGTGVFVANSWVYPHKLYSQERIFFANDTYLPSKMPAALVP 180
Db 131 NLQHAFFFLKTLTLEGVPGKGTGVFVANSWVYPHKLYSQERIFFANDTYLPSKMPAALVP 190

Qy 181 YRQDELKILRGDDNPGYPQEHDRVYRYDYNDLGDGPKGEEHARPILGSGQEHYPYRRCR 240
Db 191 YRQDELKILRGDDNPGYPQEHDRVYRYDYNDLGDGPKGEEHARPILGSGQEHYPYRRCR 250

Qy 241 TGRHPTKDPNSESRLFLNLNIYVPRDERFGLKMSDFLGYSLKTIIEAVLPTLTGTFVD 300
Db 251 TGRHPTKDPNSESRLFLNLNIYVPRDERFGLKMSDFLGYSLKTIIEAVLPTLTGTFVD 310

Qy 301 DTPKEFDSFEDILGLYELGPEAPNPLIAEIRKKIPSEFLRSILPNSGSHDHPKMPLPNV 360
Db 311 DTPKEFDSFEDILGLYELGPEAPNPLIAEIRKKIPSEFLRSILPNSGSHDHPKMPLPNV 370

QY 361 IKSDVLKKAPEFKFGRWTDDEFARETLAGVNPVVIKRLTEFFPAKSTLDPROYGDHTSKIT 420
Db 371 IKSDVLKKAPEFKFGRWTDDEFARETLAGVNPVVIKRLTEFFPAKSTLDPROYGDHTSKIT 430
QY 421 EAHIRHNMGGLSVQNALRNKELFILDHHDHFMPIYDDEINELEGNFIYASRTLLFLKDDGT 480
Db 431 EAHIRHNMGGLSVQNALRNKELFILDHHDHFMPIYDDEINELEGNFIYASRTLLFLKDDGT 490
QY 481 LKPLAIELSLPHPDGQORGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSSAWHQLISHWLN 540
Db 491 LKPLAIELSLPHPDGQORGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSSAWHQLISHWLN 550
QY 541 THAVIEPFVIATNRQLSVVHPVHKLSPHYRDTILNINALARQTLINAGGVFERTVFPKY 600
Db 551 THAVIEPFVIATNRQLSVVHPVHKLSPHYRDTILNINALARQTLINAAASSAPCSLQKY 610
QY 601 ALGMSADVYKSWNFENEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVIWVAIE 660
Db 611 ALGMSADVYKSWNFENEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVIWVAIE 670
QY 661 RWKEYLDIYYPNDGELQRDVELQAWKVEVREAHGDLKORDWPMRMDTVQQLARACTTI 720
Db 671 RWKEYLDIYYPNDGELQRDVELQAWKVEVREAHGDLKORDWPMRMDTVQQLARACTTI 730
QY 721 IWVASALHAAVNFQGYPYAGYLPNRPTASRRPMPEPGSHDYKKGAGQKEADMVFIRTIIT 780
Db 731 IWVASALHAAVNFQGYPYAGYLPNRPTASRRPMPEPGSHDYKKGAGQKEADMVFIRTIIT 790
QY 781 SQFTILGISLIEILSKHSSDEVYLGQRDEPDRWTSDAKALDAFKRFGSRLVQIENRIKT 840
Db 791 SQFTILGISLIEILSKHSSDEVYLGQRDEPDRWTSDAKALDAFKRFGSRLVQIENRIKT 850
QY 841 MNDSPDLKNRKGPVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
Db 851 MNDSPDLKNRKGPVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 897

RESULT 5
US-10-425-114-69756
; Sequence 69756, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 69756
; LENGTH: 926
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17282G11_FLI.pep
US-10-425-114-69756

Query Match 95.2%; Score 4498; DB 12; Length 926;
Best Local Similarity 93.7%; Pred. No. 0;
Matches 831; Conservative 33; Mismatches 23; Indels 0; Gaps 0;
QY 1 MFHGVADRLTGKXKAWSEKIRGTVRLVKCEVLDVGDFENASLLDGVHRLGWDGVAIF 60
Db 40 MFHGVADRLTGKXKAWSEKIRGTVRLVKCEVLDVGDFENASLLDGVHRLGWDGVAIF 99
QY 61 QLVSATAADPSNGRGKVGKAAHLEAAVSLKSTADGETVYRVSVFEWDSQGPVAVLVR 120

Db 100 QLVSATAADPSNGRGKVGKAAHLEAAVSLKSTADGETVYRVSVFEWDSQGPVAVLVR 159
QY 121 NLQHAFFFLKTLTLEGVPGKGTWVFVANSWVYPHKLYSQERIFFANDTYLPSKMPAALVP 180
Db 160 NLQHAFFFLKSLTLEGVPGKGTWVFVANSWVYPHNLYSQERVFFANDTYLPSKMPAALVP 219
QY 181 YRQDELKILRGDDNPGPYQEHDRVYDYNDLGDGPDKGEHARPILGSGQEHYPYRRCR 240
Db 220 YRQDELKILRGDDNPGPYQEHDRVYDYNDLGDGPDKGEHARPILGSGQEHYPYRRCR 279
QY 241 TGRHPTTKDPNSESRLFLNLNIYVPRDERFGLHMSDFLGYSKLTIIIEAVLTLGTFTVD 300
Db 280 TGRHPTTKDPNSESRLFLNLNIYVPRDERFGLHMSDFLGYSKLTIIIEAVLTLGTFTVD 339
QY 301 DTPKEFDSFEDIILGYELGPEAPNPLIAEIRKIPSEFLRSILPNGSHDHLKMPPLPNV 360
Db 340 DTPKEFDSFEDIILGYELGPEAPNPLIAEIRKIPSEFLRSILPNGSHDHLKMPPLPNV 399
QY 361 IKSDVLKKAPEFKFGRWTDDEFARETLAGVNPVVIKRLTEFFPAKSTLDPROYGDHTSKIT 420
Db 400 IRSDVLKKAPEFKFGRWTDDEFARETLAGVNPVVIKRLTEFFPAKSTLDPROYGDHTSKIT 459
QY 421 EAHIRHNMGGLSVQNALRNKELFILDHHDHFMPIYDDEINELEGNFIYASRTLLFLKDDGT 480
Db 460 EAHIRHNMGGLSVQNALRNKELFILDHHDHFMPIYDDEINELEGNFIYASRTLLFLKDDGT 519
QY 481 LKPLAIELSLPHPDGQORGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSSAWHQLISHWLN 540
Db 520 LKPLAIELSLPHPDGQORGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSSAWHQLISHWLN 579
QY 541 THAVIEPFVIATNRQLSVVHPVHKLSPHYRDTILNINALARQTLINAGGVFERTVFPKY 600
Db 580 THAVIEPFVIATNRQLSVVHPVHKLSPHYRDTILNINALARQTLINAGGVFERTVFPKY 639
QY 601 ALGMSADVYKSWNFENEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVIWVAIE 660
Db 640 ALGMSADVYKSWNFENEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVIWVAIE 699
QY 661 RWKEYLDIYYPNDGELQRDVELQAWKVEVREAHGDLKORDWPMRMDTVQQLARACTTI 720
Db 700 RWKEYLDIYYPNDGELQRDVELQAWKVEVREAHGDLKORDWPMRMDTVQQLARACTTI 759
QY 721 IWVASALHAAVNFQGYPYAGYLPNRPTASRRPMPEPGSHDYKKGAGQKEADMVFIRTIIT 780
Db 760 IWVASALHAAVNFQGYPYAGYLPNRPTASRRPMPEPGSHDYKKGAGQKEADMVFIRTIIT 819
QY 781 SQFTILGISLIEILSKHSSDEVYLGQRDEPDRWTSDAKALDAFKRFGSRLVQIENRIKT 840
Db 820 SQFTILGISLIEILSKHSSDEVYLGQRDEPDRWTSDAKALDAFKRFGSRLVQIENRIKT 879
QY 841 MNDSPDLKNRKGPVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
Db 880 MNDSPDLKNRKGPVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 926

RESULT 6
US-10-132-350-18
; Sequence 18, Application US/10132350
; Publication No. US20030166855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Kolomiets, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxigenase Polynucleotides and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286,889
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; PRIOR FILING DATE: 2001-07-13


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; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 887
; TYPE: PRT
; ORGANISM: Zea mays
US-10-132-350-18

Query Match      95.0%; Score 4487; DB 14; Length 887;
Best Local Similarity 93.5%; Pred. No. 0;
Matches 829; Conservative 34; Mismatches 24; Indels 0; Gaps 0;

Qy      1 MFHGVADRLTGKKEAWSEKIRGTVRLVKKEVLVDGDFNASLLDGVHRLGWDGVA 60
Db      1 MFHGVADRLTGKKEAWNEKIRGTVRLVKKEVLVDGDFNASLLDGVHRLGWDGVA 60

Qy      61 QLVSAATAADPSNGRGKVGKAAHLEAAVSLKSTADGETVYRVSEFEWDSQGI 120
Db      61 QLVSAATAADPSNGRGKVGKAAHLEAAVSLKSTADGETVYRVSEFEWDSQGI 120

Qy      121 NLOHAEFFLKTLLTLEGVPGKGTVVVFVANSWVYPHKLYSQERIFFANDTYLPSK 180
Db      121 NLOHAEFFLKSLLTLEGVPGKGTVVVFVANSWVYPHNLYSQERVFFANDTYLPSK 180

Qy      181 YRQDELKILRGDDNPGPYQEHDRVYDYNDLGPDKGEEHARPILGSGQEHYP 240
Db      181 YRQDELKILRGDDNPGPYQEHDRVYDYNDLGPDKGEDHARPVLGSGQEHYP 240

Qy      241 TGRHPTKDPNSESRLFLNLNIYVPRDERFGLKMSDFLGYSLKTII EAVLPTLGT 300
Db      241 TGRPTETDPNSESRLFLNLNIYVPRDERFGLKMSDFLGYSLKTII EAVLPTLGR 300

Qy      301 DTPKEFDSFEDILGLYEPGPEAPNPLIAEIRKIPSEFLRSILPNGSHDHPK 360
Db      301 DTPKEFDSFEDILGLYEPGPEAPNPLVAEVRKIPSEFLRSILPDGSHDHPK 360

Qy      361 IKSDVLKKAPEFKFGRWTDDEEFARETLAGVNPVLIKRLTEFPKSTLDP 420
Db      361 IRSDVLKKAPEFKFGRWTDDEEFARETLAGVNPVLIKRLTEFPKSTLDP 420

Qy      421 EAHIRHNMGGLSVQNALRNKRLFILDHHDHFMPIYLNKINELEGNFIYAS 480
Db      421 EAHIQHMEGLSVQNALKNKRLFILDHHDHFMPIYLNKINELEGNFIYAS 480

Qy      481 LKPLAIELSLPHPDGQORGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSAW 540
Db      481 LKPLAVELSLPHPDGQOHGAVSKVYTPAHSAGAEHVWQLAKAYACVNDSAW 540

Qy      541 THAVIEPFVIATNRQLSVVHPVHKLSPHYRDTLNINALAROTLINAGGV 600
Db      541 THAVIEPFVIATNRQLSVVHPVHKLSPHYRDTLNINALAROTLINAGGV 600

Qy      601 ALGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPI 660
Db      601 ALGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPI 660

Qy      661 RWVKEYLDIYYPNDGELQDVELQAWWKEVREAHGDLKDRDWPRMDTV 720
Db      661 RWVKEYLDVYYPNDGELQDVELQAWWKEVREAHGDLKDRDWPRMDTV 720

Qy      721 IWVASALHAAVNFQYYPAGYLPNRPPTASRRRPMPEPGSHDYKKLGAG 780
Db      721 IWVASALHAAVNFQYYPAGYLPNRPPTVSRRRPMPEPGSDDYKKLEAG 780

Qy      781 SQQTILGISLIEILSKHSSDEVYLGQDEPDWTSDAKALDAFKRFGSRL 840
Db      781 SQQTILGISLIEILSKHSSDEVYLGQDEPDWTSDAKALDAFKRFGSRL 840

Qy      841 MNDSPDLXNRKGPVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
Db      841 MNDSPDLXNRKGPVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
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RESULT 7
US-10-132-350-20
; Sequence 20, Application US/10132350
; Publication No. US20030166855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Kolomiets, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxxygenase Polynucleotides and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286,889
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 887
; TYPE: PRT
; ORGANISM: Zea mays
US-10-132-350-20

Query Match      95.0%; Score 4487; DB 14; Length 887;
Best Local Similarity 93.5%; Pred. No. 0;
Matches 829; Conservative 34; Mismatches 24; Indels 0; Gaps 0;

Qy      1 MFHGVADRLTGKKEAWSEKIRGTVRLVKKEVLVDGDFNASLLDGVHRLGWDGVA 60
Db      1 MFHGVADRLTGKKEAWNEKIRGTVRLVKKEVLVDGDFNASLLDGVHRLGWDGVA 60

Qy      61 QLVSAATAADPSNGRGKVGKAAHLEAAVSLKSTADGETVYRVSEFEWDSQGI 120
Db      61 QLVSAATAADPSNGRGKVGKAAHLEAAVSLKSTADGETVYRVSEFEWDSQGI 120

Qy      121 NLOHAEFFLKTLLTLEGVPGKGTVVVFVANSWVYPHKLYSQERIFFANDTYLPSK 180
Db      121 NLOHAEFFLKSLLTLEGVPGKGTVVVFVANSWVYPHNLYSQERVFFANDTYLPSK 180

Qy      181 YRQDELKILRGDDNPGPYQEHDRVYDYNDLGPDKGEEHARPILGSGQEHYP 240
Db      181 YRQDELKILRGDDNPGPYQEHDRVYDYNDLGPDKGEDHARPVLGSGQEHYP 240

Qy      241 TGRHPTKDPNSESRLFLNLNIYVPRDERFGLKMSDFLGYSLKTII EAVLPTLGT 300
Db      241 TGRPTETDPNSESRLFLNLNIYVPRDERFGLKMSDFLGYSLKTII EAVLPTLGR 300

Qy      301 DTPKEFDSFEDILGLYELGPEAPNPLIAEIRKIPSEFLRSILPNGSHDHPK 360
Db      301 DTPKEFDSFEDILGLYEPGPEAPNPLVAEVRKIPSEFLRSILPDGSHDHPK 360

Qy      361 IKSDVLKKAPEFKFGRWTDDEEFARETLAGVNPVLIKRLTEFPKSTLDP 420
Db      361 IRSDVLKKAPEFKFGRWTDDEEFARETLAGVNPVLIKRLTEFPKSTLDP 420

Qy      421 EAHIRHNMGGLSVQNALRNKRLFILDHHDHFMPIYLNKINELEGNFIYAS 480
Db      421 EAHIQHMEGLSVQNALKNKRLFILDHHDHFMPIYLNKINELEGNFIYAS 480

Qy      481 LKPLAIELSLPHPDGQORGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSAW 540
Db      481 LKPLAVELSLPHPDGQOHGAVSKVYTPAHSAGAEHVWQLAKAYACVNDSAW 540

Qy      541 THAVIEPFVIATNRQLSVVHPVHKLSPHYRDTLNINALAROTLINAGGV 600
Db      541 THAVIEPFVIATNRQLSVVHPVHKLSPHYRDTLNINALAROTLINAGGV 600

Qy      601 ALGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPI 660
Db      601 ALGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPI 660
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QY 661 RWKVEYLDIYYPNDGELQRDVQLQAWKVEVEEAHGDLDKDRDWPRMDTVQQLARACTTI 720
Db 661 RWKVEYLDVYYPNDGELQRDVQLQAWKVEVEEAHGDLDKDRDWPRMDVAVQLARACTTV 720
QY 721 IWVASALHAANVFGQYPYAGYLEPNRPTASRRPMPEPGSHDYKKGAGQKEADMVFIIRIT 780
Db 721 IWVASALHAANVFGQYPYAGYLEPNRPTVSRPMPEPGSDDYKKLEAGQKEADAVFIIRIT 780
QY 781 SQFQTILGISLIEILSKHSSDEVYLGQRDEPRWTSADAKALDAFKRFGSRLVQIENRIKT 840
Db 781 SQFQTILGISLIEILSKHSSDEVYLGQRDEPRWTSADAKALDAFKRFGSRLVQIENRIKT 840
QY 841 MNDSPDLKNRKGPPVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
Db 841 MNDSPDLKNRKGPPVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887

RESULT 8

US-10-132-350-10
; Sequence 10, Application US/10132350
; Publication No. US20030166855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Kolomiets, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxigenase Polynucleotides and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286,889
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 864
; TYPE: PRT
; ORGANISM: Zea mays
US-10-132-350-10

Query Match 64.3%; Score 3039; DB 14; Length 864;
Best Local Similarity 66.1%; Pred. No. 4.8e-280;
Matches 584; Conservative 100; Mismatches 176; Indels 24; Gaps 10;

QY 5 GVADRLTGKKEAWSEGKIRGTVRLVKKEVLVDGDFNASLLDGVHRIWGDDGVAFQLVS 64
Db 4 GIIDGLTGANKHA----RLKGTVVLMRKNVLDLNDFGATVVDSEFLG--KGVTCQLIS 57
QY 65 ATAADPSNGGRGKVGKAAHLEAAVVSLSKSTADGETVYRVSFEDW-ESQGIPLGAVLVRNLQ 123
Db 58 STLVDANNNGRGRVGAEANLEQWLTSLPSTLTGSEKFGVTDFDWEVEKLGVPFVAVVKNH 117
QY 124 HAEFFLKTLTLEGVPGKGTVVVANSWVYPHKLYSQERIFFANDTYLPSKMPAALVPYRQ 193
Db 118 AAEFFLKTITLDDVPGRGAVTFVANSWVYPAGKYRKNRVFFSNDTYLPSQMPAALKPYRD 177
QY 184 DELKILRGDDNPGPYQEHDRVYRYDYNLDGDPDKGEEHARPILGGSQBHPYPRRCRTGR 243
Db 178 DELRLRGDDQQGPYQEHDRVYRYDVYNDLGEPPDG--NPRPILGGSADHPYPRRCRTGR 235
QY 244 HPTKDPNSESRLFLNLNIVPRDERFGLHKLMSDFGLYSKLTIIIEAVLPTLGTGFDVDDTP 303
Db 236 KPTKDPNDSRLSVE-QIYVPRDERFGLHKLMSDFGLYSIKAITQGIIPAVRTYVDVTTTP 294
QY 304 KEEDSFEDILGLYELGPEAPNPNPLIAEIRKIPSEFLRSILPNGSHDHLKMPLEPNVKS 363
Db 295 GEFDSPQDIINLYEGGIKLPKIQALEDMRKLFLQLVKDLLPAGG-DYLLKLPIPIQIIQE 353
QY 364 DVLKKAPEFKFGWRTDEBFARETLAGVNPVILKRLTEFFPAKSTLDPQYGDHTSKITEAH 423

Db 354 D-----KNAWRTDEEFAREVLAGVNPMTVITRLTEPFPKSTLDPSKYGDHTSTITAEH 405
QY 424 IRHNMGSLVQNALNRKRLFLDHDHDFMPYLDENIEEGNFIYASRTLLFLKDDGTLP 483
Db 406 IEXNLEGLTVQALDGNRLYILDHDFRMPFLIDVNNLEGNFIYATRTLFFLRGDRGLAP 465
QY 484 LAIELSLPHPDGQQRGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSAWHQLISHWLNTHA 543
Db 466 LAIELSEPIYIDGDLTVAKSKVYTPASSGVEAWVWQLAKAYAVAVNDSGWHQLVSHWLNTHA 525
QY 544 VIEPFIATNRQLSVVHPVHKLLSPHYRDTLNINALAQTLINAGGVFERTVFPKAYALG 603
Db 526 VMEPFIATNRQLSVTHPVHKLLSSHFRDVTMTINALAQTLINAGGVFERTVFPKAYALG 585
QY 604 MSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVIWAIERWV 663
Db 586 MSSVYKSWNFTEQGLPADLVKRGVAVADPSSLYKVRLLIEDYPIYASDGLAIWHAIEQWV 645
QY 664 KEYLDIYYPNDGELQRDVQLQAWKVEVEEAHGDLDKDRDWPRMDTVQQLARACTTIWV 723
Db 646 GEYLAIYYPDDGALRGDEELQAWKVEVEEGHGDHDKDAPWPKMQAVSELASACTTIWI 705
QY 724 ASALHAAVNFQYYPYAGYLEPNRPTASRRPMPEPGSHDYKKGAGQKEADMVFIIRITSQF 783
Db 706 ASALHAAVNFQYYPYAGYLEPNRPTVSRPMPEPGSKEYEEL---ERDPERGFIHTITSQI 762
QY 784 QTILGISLIEILSKHSSDEVYLGQRDEPRWTSADAKALDAFKRFGSRLVQIENRIKTMND 843
Db 763 QTILGISLIEILSKHSSDEVYLGQRDTPE-WTSADALAAAFKRFSDALVKIEGKVVGENR 821
QY 844 SPDLKNRKGPPVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
Db 822 DPQLNRNGPAEFFPYMLLYPNTSDHSG-AAAGLTAKGIPNSISI 864

RESULT 9

US-10-132-350-12
; Sequence 12, Application US/10132350
; Publication No. US20030166855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Kolomiets, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxigenase Polynucleotides and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286,889
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 864
; TYPE: PRT
; ORGANISM: Zea mays
US-10-132-350-12

Query Match 64.3%; Score 3039; DB 14; Length 864;
Best Local Similarity 66.1%; Pred. No. 4.8e-280;
Matches 584; Conservative 100; Mismatches 176; Indels 24; Gaps 10;

QY 5 GVADRLTGKKEAWSEGKIRGTVRLVKKEVLVDGDFNASLLDGVHRIWGDDGVAFQLVS 64
Db 4 GIIDGLTGANKHA----RLKGTVVLMRKNVLDLNDFGATVVDSEFLG--KGVTCQLIS 57
QY 65 ATAADPSNGGRGKVGKAAHLEAAVVSLSKSTADGETVYRVSFEDW-ESQGIPLGAVLVRNLQ 123
Db 58 STLVDANNNGRGRVGAEANLEQWLTSLPSTLTGSEKFGVTDFDWEVEKLGVPFVAVVKNH 117

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QY 124 HAEFFLKTILEGVPKGTGVFVANSWVYVPHKLYSQERIFPANDTYLPSKMPAALVPYRQ 183
Db 118 AAEFFLKTITLDDVPGRGAVTEFVANSWVYPAGKYRNYRNVFSDTYLPSQMPAALKPYRD 177
QY 184 DELKILRGDNDPGPYQEHDRVRYDYNDLGDGDPKGEHARPILGSGQEHYPYRRCTGR 243
Db 178 DELNLRGDDQQGPYQEHDRVRYDYNDLGEPDGG--NPRILGGSADHPYRRCTGR 235
QY 244 HPTKDPNSESRLFLNLNIYVPRDERFGLKMSDFLGYSLKTIIEAVLPTLGTFFVDDTP 303
Db 236 KPTKTDPSDSRLSLVE-QIYVPRDERFGLKMSDFLGYSKAITQGIIPAVRTYVDTTP 294
QY 304 KEFDSFEDILGLYELGPEAPNPLIABIRKPISEFLRSILPNSGSHDPLKMPLPNVIKS 363
Db 295 GEFDSFQDIINLYEGGKLPKIQALEDMRKLFPLQLVKDILLPAGG-DYLLKLPPIQLIQE 353
QY 364 DVLKKAPEFKFGWRTDEEFARETLAGVNPVLIKRLTEFPFAKSTLDPROQYGDHTSKITEAH 423
Db 354 D-----KNAWRTDEEFAREVLAGVNPVITRLTEFPFAKSTLDPSKYGDHTSITAETH 405
QY 424 IRHNMGLSVQNALRNKRLFILDDHDFMPYLDIENELEGNFIYASRTLLFLKDDGTLKP 483
Db 406 IEKNLEGLTVQALDGNRLYLIDHDFRMPFLIDVNNLEGNFIYATRLLFFLRGDRGLAP 465
QY 484 LAIELSLPHPDGQORGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSAWHQLISHWLNTHA 543
Db 466 LAIELSEPYIDGDLTVAKSKVYTPASSGVEAWVWQLAKAYAVANDSGWHQLVSHWLNTHA 525
QY 544 VIEPFVIATNRQLSVVHPVHKLLSPHYRDTLNINALAQTLINAGGVFERIVFPKAYALG 603
Db 526 VMEPFVIATNRQLSVTHPVHKLLSSHFRDNTINALAQTLINGGGIFEMTVFPKAYALG 585
QY 604 MSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVWIAERWV 663
Db 586 MSSVVYKSWNFTEQGLPADLVKRGVAVADPSSLYKVRLLIEDYPIYASDGLAIWHAIEQWV 645
QY 664 KEYLDIYPNDGELQRDVELQAWKKEVREBAHGDLDKDRDWPRMDTVQQLARACTTIWV 723
Db 646 GEYLAIYPDDGALRGDEELQAWKKEVREVGHGDKDAPWPKMQAVSELASACTTIWI 705
QY 724 ASALHAAVNFQGPYAGYLPNRPTASRRPMPEPGSHDYKKLGAGQKEADMVFIRITISQF 783
Db 706 ASALHAAVNFQGPYAGYLPNRPTVSRMRMPEPGSKYESEL---ERDPERGFIHTISQI 762
QY 784 QTILGISLIEILSKHSSDEVILGQRDEPDRWTSADKALDAFKRFGSRLVQIENRIKTMND 843
Db 763 QTILGISLIEILSKHSSDEVILGQRDTPE-WTSDARALAAAFKRFSDALVKIEGKVGENR 821
QY 844 SPDLKVRKGPVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
Db 822 DPQENRNGPAEFPYMLLYPNTSDHSG-AAAGLTAKGIPNSISI 864
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RESULT 10

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US-10-132-350-2
; Sequence 2, Application US/10132350
; Publication No. US20030166855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Kolomietz, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxigenase Polynucleotides and Methods
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286,889
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
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; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 2
; LENGTH: 873
; TYPE: PRT
; ORGANISM: Zea mays
; US-10-132-350-2

Query Match 62.6%; Score 2958; DB 14; Length 873;

Best local Similarity 63.6%; Pred. No. 2.6e-272;

Matches 561; Conservative 115; Mismatches 180; Indels 26; Gaps 11;

QY 10 LTGKNKEAWSEGKIRGTVRLVKVEV--LDVGDFNASLLDGVHRILGWDGVAQFQVLSATA 67

Db 14 LTGSNKNA-----HLKGNVVLVRKTVLGLDVTISIAGSLLDGIGCEFLG--RGVTCQLISSTV 67

QY 68 ADPSNGGRGKVGKAAHLEAAVVSLSKSTADGETVYRVVSFEWD-ESQIGPGLVLRNLQHA 126

Db 68 VDPNNGNRGKLGAEASLEQWLLNPPPLLSSENQFRVTDFWEVEKQGIPGAIIVKNNHASE 127

QY 127 FFLKTLILEGVPKGTGVFVANSWVYVPHKLYSQERIFPANDTYLPSKMPAALVPYRQDEL 186

Db 128 FFLKTLITLNDVPGHGTIVFVANSWVYVPHKLYSQERIFPANDTYLPSKMPAALVPYRQDEL 187

QY 187 KILRGDNDPGPYQEHDRVRYDYNDLGDGDPKGEHARPILGSGQEHYPYRRCTGRHPT 246

Db 188 RNLRGDNDPGPYQEHDRVRYDYNDLGLPDG--NPRPVLGCTKELPYRRCTGRKPT 245

QY 247 KKDPSSESRLFLNLNIYVPRDERFGLKMSDFLGYSLKTIIEAVLPTLGTFFVDDTPKEF 306

Db 246 KSDPSSESRLTLVDGVDVYVPRDERFGLKMSDFYGYAIKALVNAVIPAIRTYVDSLSPGEF 305

QY 307 DSFEDILGLYELGPEAPNPLIABIRKPISEFLRSILPNSGSHDPLKMPLPNVIKSDVL 366

Db 306 DSFKDINKLYEGGIQLPKIPALEDLRKQFPLELVKDVLPVGG-DYLLKLPMPQIIKED-- 362

QY 367 KKAPEFKFGWRTDEEFARETLAGVNPVLIKRLTEFPFAKSTLDPROQYGDHTSKITEAHIRH 426

Db 363 -----KTGWMTDEEFGREILAGVNPMLVKRLTEFPFRSSLDPSKYGDHTSTIREADLEN 416

QY 427 NMGLSVQNALRNKRLFILDDHDFMPYLDIENELEGNFIYASRTLLFLKDDGTLKPLAI 486

Db 417 KLEGLTVQALHGNRLYLIDHDFNEMPFVLRVNSLEGNFIYATRVLFLRGDGTLPVPAI 476

QY 487 ELSLPHPDGQORGAVSKVYTP-AHTGVEGHVWQLAKAYACVNDSAWHQLISHWLNTHAVI 545

Db 477 ELSLPELRDGLTTAKSTVTPKSTTGAEAWVWHLAKAYANVNDYCWHLISHWLNTHAVM 536

QY 546 EPFVIATNRQLSVVHPVHKLLSPHYRDTLNINALAQTLINAGGVFERIVFPKAYALGMS 605

Db 537 EPFVIATNRQLSVTHPVHKLLSPHYRDTMNINSNARQMLVNAVAGGIFETTVFPRQYAFEMS 596

QY 606 ADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVWIAERWVKE 665

Db 597 SVIYKDNWTFEQALPDDDLIKRGMAVADPSSPYKVRLLVEDYPIYASDGLAIWHAIEQWVTE 656

QY 666 YLDIYYPNDGELQRDVELQAWKKEVREBAHGDLDKDRDWPRMDTVQQLARACTTIWVAS 725

Db 657 YLAVYYPNDGVLRADVELQAWKKEAREVGHADLKDAPWPKMQTVAEVLKACTTIWIAS 716

QY 726 ALHAAVNFQGPYAGYLPNRPTASRRPMPEPGSHDYKKLGAGQKEADMVFIRITISQFQT 785

Db 717 ALHAAVNFQGPYAGYLPNRPSVSRKPMAPGSDGEYAEV---ERKPEKVFVTRITISQFQA 773

QY 786 ILGISLIEILSKHSSDEVILGQRDEPDRWTSADKALDAFKRFGSRLVQIENRIKTMNDSP 845

Db 774 LVGISLIEILSSHSSDEVILGQRDTKE-WTSDAKAQAEAFKRFGARLTIEIKRVVTMNDAP 832

QY 846 DLKVRKGPVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887

Db 833 RLKVRNGPAEFPYMLLYPNTSDTKGD-AAGITAKGIPNSISI 873

RESULT 11

Query Match	62.0%; Score 2929.5; DB 10; Length 862;
Best Local Similarity	63.0%; Pred. No. 1.3e-269;
Matches	561; Conservative 110; Mismatches 188; Indels 31; Gaps 12;
QY	1 MFWHGVADRLTGKKEAWSEKIRGTVRLVKKEVLVDGDFNASLLDGVHRILGWDDGVAF 60
Db	1 MLGLGLIDTLTGANKSA-----RLKGTVVLMRKKNVLDLNDFGATIIDGIGEFGL--KGVTC 54
QY	61 QLVSATAADPSNGGRGKVGKAAHLEAAVSLKSTADGETVYRVVSFEWD-ESQGIPGAVLV 119
Db	55 QLISSTAVDQDNGGRGKVGABAELEQWVTSPLSTTGESKFGLTFDWEVEKLGVPGAIVV 114
QY	120 RNLQHAFFLKTLLTEGVPGK-GTVVVFVANSWVYPHKLXSQERIFFANDTYLPSKMPAAL 178
Db	115 NNYHSSEFLKTIITLHDVPGRSNLTTFVANSWIIYPAANYRSRVFFANDTYLPSQMPAAL 174
QY	179 VPYRQDELKILRGDDNPGPYQEHDRVYRYDYNDLGDPKGEEHARPILGSGOEHPYPRR 238
Db	175 KPYRDELNLRGDDQCGPYQEHDRYRYDYNDLGE-----GRPILGNSDHPYPRR 227
QY	239 CRTGRHPTKKDPNSESRFLNLTNIYVPRDERFGLKMSDFLGYSLKXTIEAVLPTLGTF 298
Db	228 GRTERKPNASDPSLESRLSLE-QIYVPRDEKFGHLKTSDFLGYSIKAITQGILPAVRTY 286
QY	299 VDDTPKEFDSFEDILGLYELGPEAPNPLIAEIRKKIPSEFLRSILPENGSHDHPKMLPL 358
Db	287 VDTTPGEFDSFDIINLYEGGIKLPKVAALEELRKQFPLQLIKDLLPVGG-DSLLKLPVP 345
QY	359 NVIKSDVLKKAPEKFGKRTDEEFARETLAGVNPVITKRLTEFPKSTLDRQYGDHTSK 418
Db	346 HIIQ-----ENKQAWRTDEEFAREVLAXVNPVMITRLTEFPKSSLDPSKFGDHTST 397
QY	419 ITEAHRHNMGGLSVQNALRNKRLFILDHHDHFMPLYDINELEGNFYASRTLLFLKDD 478
Db	398 ITAEHIEKNLEGLTVQQALESRLYILDHHDHFMPLFDVNNLPGNFIYATRTLFLRGD 457
QY	479 GTLKLPLAIELSLPHPDGQORGAVSKVYTPAHTG-VEGHVWQLAKAYACVNDSAWHQLISH 537
Db	458 GRLTPLAIELSEPIIQGLTTAKSKVYTPVPSGVEGVWELAKAYAVANDSGWHQLVSH 517
QY	538 WLNTHAVIEPFIATNRQLSVVHPVHKLLSPHYRDTLININALARQTLINAGGVFEETVFP 597
Db	518 WLNTHAVMEPFIATNRHLSVTHPVHKLLSPHYRDTMTINALARQTLINAGGIFEMTVFP 577
QY	598 AKYALGMSADVYKSNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYVDGLVIWM 657
Db	578 GKFAIGMSAVVYKDKWKEFTEQGLPDDDLIKRGMAVEDPSSPYKVRLLVSDYPIYAADGLAIWH 637
QY	658 AIERWVKEYLDIYYPNDGELQRDVELQAWKVEVEEAHGDLDKRDWWPRMDTVQQLARAC 717
Db	638 AIEQYVSEYLAIYYPNDGVLGDTVEQAWKTEFEVGHGDLKDAPWWPKMQSPVELAKAC 697
QY	718 TTIIWVASALHAANFGQYPIAGYLPNRPTASRRPMPPEPGSHDYKKLGAGQKEADWVFIR 777
Db	698 TTIIWIGSALHAANFGQYPIAGFLPNRPTVSRMRPMPGTEEYAEI-----ERDPERAFIH 754
QY	778 TITSQFOTILGISLIEILSKHSSDEVYLGQRDEPRWTSDAKALDAFKRFGSRLVQIENR 837
Db	755 TITSQIQTIIIGVSLLEVLKSHSSDELYLGQRDTPE-WTSDPKALEVFVKRFSRDLVEIESK 813
QY	838 IKTMNDSDDLKNRKGVPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887
Db	814 VVGWNHDPELKNRNGPAKFPYMLLYPNTSDHKG-AAAGLTAKGIPNSISI 862

```

; APPLICANT: Cameron-Mills, Verena
; APPLICANT: Skadhauge, Birgitte
; APPLICANT: Bech, Lene
; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY
; FILE REFERENCE: 11225.11US01
; CURRENT APPLICATION NUMBER: US/09/751,687
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 864
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-09-751-687-18

Query Match      60.6%;   Score 2860;   DB 10;   Length 864;
Best Local Similarity 62.2%;   Pred. No. 5.7e-263;
Matches 551;   Conservative 117;   Mismatches 188;   Indels 30;   Gaps 11;

QY      5  GVADRLTGKKEAWSEGKIRGTVRLVKKEVLVDGDFNASLLDGVHRIILGWDDGVAFQLVVS 64
Db      6  GIVSDLTGGIRGA---HLKGSVLMRKNAALDFNDFGAHVMDGVTELLG--RGVTCQLIS 59

QY      65  ATAADPSNGGRGKVGKAAHLEAAVV--SLKSTADGETVYRVVSFEWD--ESQGIPGAVLVRN 121
Db      60  STNVDPHNGGRGKVGAAEANLEQWLLPTNLPHITGTGENKFAVTFDWSVDKLGVPGAIIKVN 119

QY      122  LQHAEFFLKTILEGVPKGKTVVFVANSWVYPHKLYSQERIFFANDTYLPSKMPAALVPY 181
Db      120  NHASEFFLKT-TLDNVPGRTIVFVANSWVYPQAKYRYNRVFFANDTYLPHQMPAALKPY 179

QY      182  RQDELKILRGDDNPGPYQEHDRVRYDYVNDLGDPPDKGEEHARPILGSGQEHYPYPRRCRT 241
Db      180  RDELRLNRGDDQGGPYLDHDRVRYDYVNDLGD-----SRDVLGGSKDLPYPRRCRT 232

QY      242  GRHPTKKDPNSESRLFLNLNIYVPRDERFGHLKMSDFGLYSLKTIIEAVLPTLGTTFVDD 301
Db      233  GRKPSDSKPDHESRLLLLVQNVYVLRDELFGHLKQSDLLGYTLKGWLDGILAIRTYVDL 292

QY      302  TPKEFDSFEDILGLYELGPEAPNNPLIAIRKKIPSEFLRSILPNSGSHDPLKMPLPNVI 361
Db      293  SPGEFDSFADILKLYEGGIKLPNIPALEEVKRFPLQLVKDLIPKGG-DFLKLPKPEII 351

QY      362  KSDVLKKAPBEKFGWRTDEEFARETLAGVNPVILKRLTEFFPAKSTLDPQYGDHTSKITE 421
Db      352  KVD--QKA-----WNTDEEFAREMLAGVNPMMIKRLTEFFPKSTLDPKYGDHTSTMTE 403

QY      422  AHIRHNMGSLVQNALRNKRLFLDHHDFMPYLDIENELEGNFIVASRTLLFLKDDGTL 481
Db      404  EHVAKSLEGLTVQALAGNRLIYVDQHDNLMPPFLIDINNLDASFVYATRTLLFLRGDGT 463

QY      482  KPLAIELSLPHDPDGGQORGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSAWHQLISHWLNT 541
Db      464  APVAIELSPLIQELTTAKSAVYTPQHAGVEGWIWQLAKAYASVNDYGMWHQLISHWLNT 523

QY      542  HAVIEPFVIATNRQLSVVHPVHKLLSPHYRDTLNINALARQTLINAGGVFERTVFPKAYA 601
Db      524  HAVMEPFVIATNRQLSVTHPVYKLLHPHYRDTMNINARAGLLINAGGVIENTVFPKHHA 583

QY      602  LGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPYAVDGLVIWMAIER 661
Db      584  MPMSSMVYKHWNFTEQALPADLIXRGMAVEDASSPHKVRLLIKDYPYATDGLAVWDAIEQ 643

QY      662  WVKEYLDIYYPNDGELQRDVELQAWWKEVREEAHGDLKORDWWPRMDTVQQLARACTTII 721
Db      644  WVSDYLTIIYYPNDGVLGQDVELQAWWKEVREVGHDLDKAAWPMKQIVAEELIKACATII 703

QY      722  WVASALHAAVNFGQYPYAGYLPNRPITASRRPMPPEGSHDYKKLGAQKEADWVFIRTITS 781
Db      704  WTGSALHAAVNFGQYPYSGYHPNKPASRRPMPVPQSGSEYAEI---ERDPEKAFIRTITS 760

QY      782  QFQTILGTSILEILSKHSSDEVILGQRPDRWTSDAKALDAFKRFGSRLVQIENRIKTM 841
Db      760  QFQTLGTSILEILSKHSSDEVILGQRPDRWTSDAKALDAFKRFGSRLVQIENRIKTM 841

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Db 761 QFHALVGISLMEILSKHSSDEVYLCQHDTTP-AWTSDAKALEAPKRFEGAKLEGIEKQVVAM 819

Qy 842 NDSPLKNRKGPVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887

Db 820 NSDPQLKNRTGTPAKFPYMLLYPNTSDHTGQ-AEGLTARGIPNSISI 864

Search completed: March 23, 2004, 07:11:45

Job time : 336 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 23, 2004, 06:36:23 ; Search time 30 Seconds
(without alignments)
2844.063 Million cell updates/sec

Title: US-10-059-909-16
Perfect score: 4723
Sequence: 1 MFHWGVADRLTGKNKEAWSE.....VTGEKAEGLTAMGIPNSISI 887

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:**
1: pir1:**
2: pir2:**
3: pir3:**
4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	3369.5	71.3	876	2 T05943	probable lipoxxygen
2	2936.5	62.2	862	2 T05941	lipoxxygenase (EC 1
3	2860	60.6	864	2 T05945	lipoxxygenase (EC 1
4	2829.5	59.9	865	1 S23454	lipoxxygenase (EC 1
5	2724.5	57.7	862	2 S57964	lipoxxygenase (EC 1
6	2695.5	57.1	862	2 T07775	lipoxxygenase (EC 1
7	2626.5	55.6	859	1 JQ2267	lipoxxygenase (EC 1
8	2597	55.0	861	2 S44940	lipoxxygenase (EC 1
9	2511	53.2	859	2 T06352	lipoxxygenase (EC 1
10	2510	53.1	859	2 T06339	lipoxxygenase (EC 1
11	2498.5	52.9	876	2 T07101	lipoxxygenase (EC 1
12	2486	52.6	865	1 DASYL1	lipoxxygenase (EC 1
13	2480.5	52.5	857	2 S01864	lipoxxygenase (EC 1
14	2458.5	52.1	864	1 S07075	lipoxxygenase (EC 1
15	2437	51.6	861	1 S01142	lipoxxygenase (EC 1
16	2433	51.5	877	2 T10085	lipoxxygenase (EC 1
17	2423.5	51.3	878	2 S74207	lipoxxygenase (EC 1
18	2420	51.2	865	2 T11852	lipoxxygenase (EC 1
19	2405.5	50.9	862	2 S22153	lipoxxygenase (EC 1
20	2394	50.7	853	2 T07036	lipoxxygenase (EC 1
21	2393.5	50.7	856	2 T06596	lipoxxygenase (EC 1
22	2393.5	50.7	868	2 T06827	lipoxxygenase (EC 1
23	2389	50.6	859	2 T06429	lipoxxygenase (EC 1
24	2385.5	50.5	858	2 T12142	lipoxxygenase (EC 1
25	2375	50.3	853	2 T07662	lipoxxygenase (EC 1
26	2370.5	50.2	864	2 S13381	lipoxxygenase (EC 1
27	2355.5	49.9	839	1 DASYL2	lipoxxygenase (EC 1
28	2353	49.8	839	2 T06354	lipoxxygenase (EC 1
29	2329.5	49.3	866	2 T06454	probable lipoxxygen

30	2295.5	48.6	868	2 S56655	lipoxxygenase (EC 1
31	2231	47.2	741	2 S18906	lipoxxygenase (EC 1
32	1827.5	38.7	517	2 T06274	probable lipoxxygen
33	1823	38.6	908	2 T07409	lipoxxygenase (EC 1
34	1823	38.6	914	2 T07065	probable lipoxxygen
35	1794.5	38.0	599	2 S18612	lipoxxygenase (EC 1
36	1721	36.4	926	2 E96749	probable lipoxxygen
37	1667.5	35.3	896	2 JQ2391	lipoxxygenase (EC 1
38	1648	34.9	899	2 T07062	probable lipoxxygen
39	1630	34.5	896	2 T07408	lipoxxygenase (EC 1
40	1606.5	34.0	899	2 T11578	probable lipoxxygen
41	1586.5	33.6	923	2 A53054	lipoxxygenase (EC 1
42	1569.5	33.2	917	2 B96699	probable lipoxxygen
43	1559	33.0	936	2 T06190	lipoxxygenase (EC 1
44	1552.5	32.9	870	2 T47454	lipoxxygenase AtLOX
45	1478	31.3	623	2 T07664	lipoxxygenase (EC 1

ALIGNMENTS

RESULT 1

T05943

Probable lipoxxygenase (EC 1.13.11.12) - barley

C:Species: Hordeum vulgare (barley)

C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-Jun-1999

C:Accession: T05943

R:van Mechelen, J.R.; Smits, M.; Graner, A.; Douma, A.C.; Schuurink, R.C.; Heidekamp, F.

Submitted to the EMBL Data Library, June 1997

A:Description: Barley grain lipoxxygenase isoenzymes: cDNA cloning, characterization and

A:Reference number: Z15464

A:Accession: T05943

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-876 <VAN>

A:Cross-references: EMBL:L37359; NID:g2182266; PIDN:AAB60715.1; PID:g2182267

A:Experimental source: cv. Triumph

C:Genetics:

A:Gene: LoxB

A:Map position: 4

C:Superfamily: lipoxxygenase

C:Keywords: oxidoreductase

Query Match		71.3%	Score 3369.5;	DB 2;	Length 876;
Best Local Similarity		72.5%	Pred. No. 7.5e-235;		
Matches		648;	Conservative	87;	Mismatches 134; Indels 25; Gaps 9;
Qy	1	MFHWGVADRLTGKNKEAWSEGKIRGTAVLVKKEVLDVGDVFNASLLDGVHRLGWDGVA	60		
Db	1	MLLHGLVDRLTGKNKEAWSEGKIRGTAVLVKSDVLDLGDHFASLLDGVHKLKDDGVSF	60		
Qy	61	QLVSATAADPSNGGRGKVGKAAHLEAVVSLKSTADGETVYRVSFENDESQIGPGLVR	120		
Db	61	RLVSATAPDPQNGSRGKVGKPAHLEEMVVTMKSTAAGESVFKVTFEWDSDSQVPGAVIVR	120		
Qy	121	NLQHAFFFLKTLTLEGVPGKGTVVVFVANSWVYPHKLVSQRIFFANDTYLPSKMPAALVP	180		
Db	121	NTYRSEYLLKTLTHGVPGKGTVVVFVANSWIYP-----NVDRLFFANDTYLPSKMPALLVQ	176		
Qy	181	YRQDELKILRGDDNPGPYQEHDRVYRYDYNDLGDGDPKGEHARPILGSGQEHYPRRCR	240		
Db	177	YRQDELNNLRGDDTTGEYKEADRVYRYDYNDLGEPD--NDNPRFVLGGTQELPYPRRCR	234		
Qy	241	TGRHPTKDPNSESRL-----FLLNLNIYPRDERFGLHKMSDFLGYSLKTIIEAVLPTLG	296		
Db	235	TGRPPTETDPRSESRIPKYIKIKEALNIYPRDERFGLHKLSDFLGYSLKAIKATEAILPITR	294		
Qy	297	TFVDDTPKEFDSFEDILGLYELGPEAPNNPLIAEIRKKIPSEFLRSILPNSGSHDPLKMP	356		
Db	295	TYVDSTPKFDSFQDIYNLYDGLLVKVPDNOHKLKLNK-SLQFIKSLAVAGDSDS--KLA	351		
Qy	357	LPNVIKSDVLKKAPEFKFGWRTDEEFARETLAGVNPVVIKRLTEFFAKSTLDPROYGDHT	416		

Db 352 LPHVIXSD-----QYAWRSDEEFAREMLAAVDPVCIRRLTKFPVKKYLDPSPVYGDQS 403

QY 417 SKITEAHIRHNM-GGLSVQNALRNKRLFLDHHDHMFYDEINELEGNFYASRTLLFL 475

Db 404 STIFEDQIQNLNEDGLTVRQMDKRLFLDHHDNFMPFLDRINKLEGNYIASRTLLFL 463

QY 476 KDDGTLKPLAIELSLPHPDGQORGAVSKVYTPA--HTGVEGHVWQLAKAYACVNDSAWHQ 533

Db 464 KADGTLKPLAIELSQPHPDGQORGAKSTVYLPADINSVGDQIWLAKAYASVDDSAWHQ 523

QY 534 LISHWLNTHAVIEPFVIATNRQLSVVHPVHKLLSPHYRDTLNINALARQTLINAGGVFER 593

Db 524 LISHWLNTHAVIEPFVIATNRQLSVVHPVHKLLSPHYRDTLNINALARQTLINAGGVFER 583

QY 594 TVFPAKYGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGL 653

Db 584 TVFPGYALEMSAVVYKSWNKLTEQGLPDDLKRGMAVVPDESSPYGIRLLIKDYPIYAVDGL 643

QY 654 VIWAIERWVKEYLDIYYPNDGELQRDVELQAWKVEVEEAHGDLDKORDWPRMDTVQOL 713

Db 644 VIWAIERWVNEYLAIYYPNDGVLRADKELEEWKVEVEVGHGDLKDADWPKWTVQEL 703

QY 714 ARACTTIWVASALHAAVNFQYYPYAGYLPNRPTRASRRPMPEPGSHDYKKLGAGQKEADM 773

Db 704 AKTCTTIWVASALHAAVNFQYYPYAGYLPNRPTRASRRPMPEPGSHDYKKLGAGQKEADM 763

QY 774 VFIRTTISQFOTILGISLIEILSKHSSDEVYLGQDEPDRTWTSDAKALDAFKRFGSRLVQ 833

Db 764 VFIRTTISQFOTILGISLIEILSKHSSDEVYLGQDEPDRTWTSDAKALDAFKRFGSRLVQ 822

QY 834 IENRIKTMNDSPDLKRNKRGVEMPMYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887

Db 823 IEKRILDMNKDPALKNRNGPVKMPYMLLYPNTSDANGKALGLTAMGIPNSIVI 876

RESULT 2

T05941

lipoxigenase (EC 1.13.11.12) 1 - barley

C;Species: Hordeum vulgare (barley)

C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-May-2000

C;Accession: T05941

R;van Mechelen, J.R.; Smits, M.; Douma, A.C.; Rouster, J.; Cameron-Mills, V.; Heidekamp, Biochim. Biophys. Acta 1254, 221-225, 1995

A;Title: Primary structure of a lipoxigenase from barley grain as deduced from its cDNA

A;Reference number: Z15463; MUID:95127754; PMID:7827128

A;Accession: T05941

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-862 <VAN>

A;Cross-references: EMBL:L35931; NID:g532571; PIDN:AAA64893.1; PID:g532572

C;Genetics:

A;Gene: LoxA

C;Superfamily: lipoxigenase

C;Keywords: oxidoreductase

Query Match 62.2%; Score 2936.5; DB 2; Length 862;

Best Local Similarity 63.1%; Pred. No. 1.3e-203;

Matches 562; Conservative 110; Mismatches 187; Indels 31; Gaps 12;

QY 1 MFWHGVADRLTGKNEAWSEGKIRGTIVLVKKEVLDVGDGFNASLLDGVHRIILGWDDGVAF 60

Db 1 MLLGLLIDTLTGANKSA----RLKGTIVLMKKNVLDLNDFGATIIDGIGEFGLG--KGVTC 54

QY 61 QLVSATAADPSNGRGKVGKAAHLEAAVSLKSTADGETVYRVSVFWD-ESQIGIPGAVLV 119

Db 55 QLISSTAVDQDNGRGKVGAEAELEQWVTSLSPLTTGESKFGLTTFDWEVEKLGVPGAIVV 114

QY 120 RNLOHAEEFFLTKLTILEGVPK-GTVVFVANSWVYPKLYSQERFFANDTYLPSKMPAAL 178

Db 115 NNYHSSEFLKLTITLHDVPGRSGLTFVANSWIYPAANYRYSRVFFANDTYLPSQMPAAL 174

QY 179 VPYRQDELKILRGDNDPGPYQEHDRVRYDYNDLGDPKGEEHARPILGSGQEHYPYPR 238

Db 175 KPYRDELRNLRGDDQQQPFQEHDRIRYDYVNDLGE-----GRPILGNSDHPYPRR 227

QY 239 CRTGRHPTTKDPNSESRLFLNLNIYVPRDERFCHLKMDFLGYSLKTIIEAVLPTLGTFF 298

Db 228 GRTERKPNASDPSLESRLSILE-QIYVPRDEKFGHLKTSDFLGYSIKAITQGLPAVRTY 286

QY 299 VDDTPEFDSFEDILGLYELCPAENPLIAEIRKIPSEFLRSILPNGSHDHLKMLPLP 358

Db 287 VDTTPEFDSFQDIINLYEGIKLPKVALEELRQFFLQIKDLLPVGG-DSLJLPLVP 345

QY 359 NVTKSDVLKKAPEKFGWRTEDEEFARETLAGVNPVTKRLTEFFPAKSTLDPROYGDHTSK 418

Db 346 HIIQ-----ENKQAWRTDEEFAREVLAGVNPVTKRLTEFFPAKSTLDPROYGDHTSK 397

QY 419 ITEAHIRHNMGGLSVQNALRNKRLFLDHHDHMFYDEINELEGNFYASRTLLFLKDD 478

Db 398 ITAEHIEKNLEGLTVQQALESNRLYILDHHDREMFPLIDVNNLPGNFYATRTLFFLRGD 457

QY 479 GTLKPLAIELSLPHPDGQORGAVSKVYTPAHTG-VEGHVWQLAKAYACVNDSAWHQLISH 537

Db 458 GRITPLAIELSEPIIQGLLTAKSKVYTPVPSPSGVEGVWVWELAKAYAVVNDSGWHQLVSH 517

QY 538 WLNTHAVIEPFVIATNRQLSVVHPVHKLLSPHYRDTLNINALARQTLINAGGVFERTVFP 597

Db 518 WLNTHAVMEPFVISTNRHLSVTHPVHKLLSPHYRDTMTINALARQTLINAGGIFEMTVFP 577

QY 598 AKYALGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVIW 657

Db 578 GKFAIGMSAVVYKDWKTEQGLPDDLKRGMAVEDPSSPYKVRLLVSDYPYAADGLAIWH 637

QY 658 AIERWVKEYLDIYYPNDGELQRDVELQAWKVEVEEAHGDLDKORDWPRMDTVQQLARAC 717

Db 638 AIEQYVSEYLAIYYPNDGVLQGDTEVQAWWKETREVGHGDLKQAPWPKMQSVPELAKAC 697

QY 718 TTIWVASALHAAVNFQYYPYAGYLPNRPTRASRRPMPEPGSHDYKKLGAGQKEADMVFIR 777

Db 698 TTIWIGSALHAAVNFQYYPYAGYLPNRPTRASRRPMPEPGTEYAEEL---ERDPERAFIH 754

QY 778 TITSQFOTILGISLIEILSKHSSDEVYLGQDEPDRTWTSDAKALDAFKRFGSRLVQIENR 837

Db 755 TITSQIQTIIIGVSLLEVLKSHSSDELYLQGRDTPF-WTSDPKALEVFKRFSRDLVEIESK 813

QY 838 IKTMNDSPDLKRNKRGVEMPMYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887

Db 814 VVGMNHDPELKNRNGPAKFPYMLLYPNTSDHKG-AAAGLTAKGIPNSISI 862

RESULT 3

T05945

lipoxigenase (EC 1.13.11.12) 2 - barley

C;Species: Hordeum vulgare (barley)

C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-Jun-1999

C;Accession: T05945

R;van Mechelen, J.R.; Smits, M.; Graner, A.; Douma, A.C.; Schuurink, R.C.; Heidekamp, F submitted to the EMBL Data Library, September 1997

A;Description: Barley grain lipoxigenase isoenzymes: cDNA cloning, characterization and

A;Reference number: Z15465

A;Accession: T05945

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-864 <VAN>

A;Cross-references: EMBL:L37358; NID:g2429086; PIDN:AAB70865.1; PID:g2429087

A;Experimental source: cv. Triumph

C;Genetics:

A;Gene: LoxC

A;Map position: 7

C;Superfamily: lipoxigenase

C;Keywords: oxidoreductase

Query Match 60.6%; Score 2860; DB 2; Length 864;

Best Local Similarity 62.2%; Pred. No. 4.5e-198;

Matches 551; Conservative 117; Mismatches 188; Indels 30; Gaps 11;

QY	5	GVADRLTGKXKEAWSEGKIRGTURLVKKEVLVDVGDFNASLLDGVHRILGWDDGVAFQLVS	64
Db	6	GIVSDLTGGIRGA---HLKGSVVLMRKNALDFNDFGAHVMDGVTELLG--RGVTCQLIS	59
QY	65	ATAADPSNGGRGKVGKAAHLEAVV--SLKSTADGETVYRVVSFEWD-ESQIGIPGAVLVRN	121
Db	60	STNVDPHNNGGRGKVGAEANLEQWLLPTNLPFITTGENKFAVTFDWSVDKLGVPGAIIQVN	119
QY	122	LQHAEEFLKTLTLEGVPGKGTUVFVANSWVYPHKLYSQERIFFANDTYLPSKMPAALVPY	181
Db	120	NHASEFFLKTITLDNVPGRTIVFVANSWVYPOAKYRYNRVVFANDTYLPHQMPAALKPY	179
QY	182	RQDELKILRGDDNPGPYQEHDRVYRYDYNDLGDPPDKGEEHARPILGSGSQEHYPYPRCRT	241
Db	180	RDELRNLRGDDQCGPYLDHDRVYRYDYNDLGD-----SRDVLGGSKDLPYPRCRT	232
QY	242	GRHPTKKDPNSESRLFLNLNIYVPRDERFGLKMSDFLGYSLKTIIEAVLPTLGFVDD	301
Db	233	GRKPSDSKPDHESRLLLLVQNVYVLRDELFGHLKQSDLLGYTLKGWLDGIIILAIRTYVDL	292
QY	302	TPKEFDSFEDILGLYELGPEAPNNPLIAEIRKKIPSEFLRSILPNGSHDPLKMPLENNVI	361
Db	293	SPGEFDSFADILKLYEGGIKLPNIPALAEVVRKRFPLQLVKDLIPKGG-DFLLKLPKEII	351
QY	362	KSDVLKKAPEKFGWRTDEEFARETLAGVNPVPIKRLTEFFPAKSTLDPQYGDHTSKITE	421
Db	352	KVD--QKA-----WMTDEEFAREMLAGVNPMMIKRLTEFFPKSTLDPKYGDHTSTWTE	403
QY	422	AHIRNMGGISVQNALRNKRLFILDHHDHFMPLYLDEINELEGNFIYASRTLLFLKDDGTL	481
Db	404	EHVAKSLEGLTVQALAGNRLYIVDQHDNLMPEFLIDINNLDAFVYATRLLFLRGDGL	463
QY	482	KPLAIELSLPHDPDQQRGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSAWHQLISHWLNT	541
Db	464	APVAIELSSPLIQELTTAKSAVYTPQHAGVEGWIWQLAKAYASVNDYGWHLISHWLNT	523
QY	542	HAVIEPFVIATNRQLSVHPVHKLSSPHYRDTLNINALARQTILINAGGVFERTVFPKYA	601
Db	524	HAVMEPFVIATNRQLSVTHPVYKLLFPHYRDTMNINARAGLLINAGGVIENTVFPKHHA	583
QY	602	LGMSADVKSWNFEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPYAVDGLVINWAIER	661
Db	584	MPMSSMVYKHNFTQALPADLIKRGMAVEDASSPHKVRLLIKDYPYATDGLAVWDAIEQ	643
QY	662	WVKEYLDIYPNDGELQRDVELQAMWKEVREEAHGDLKDRDWPRMDTVQQLARACTII	721
Db	644	WVSDYLTIIYPNDGVLQGDVELQAMWKEVREVGHDLDKDAAWPKMQTVAELIKACATII	703
QY	722	WVASALHAAVNFQOPYAGYLPNRPTASRRPMPPEPGSHDYKKLGAQXKXADMVFIRITS	781
Db	704	WTGSALHAAVNFQOPYSGYHPNKPASRRPMPVPVQGSSEYAEI---ERDPEKAFIRITS	760
QY	782	QFOTILGISLIEILSKHSSDEVYLQORDEPDRWTSDAKALDAFKRFGSRLVQIENRIKM	841
Db	761	QFHALVGISLMEILSKHSSDEVYLGQHDTP-AWTSDAKALEAFKRFAGKLEGIEKQVVAM	819
QY	842	NDSPDLKNRKGFVEMPYMLLYPNTSDVTGEKAEGLTAMGPNISISI	887
Db	820	NSDPQLKNETGPAKFPYMLLYPNTSDHTGQ-AEGLTARGPNISISI	864

A;Residues: 1-865 <OHT>
A;Cross-references: EMBL:X64396; NID:g20266; PIDN:CAA45738.1; PID:g20267
A;Accession: S24576
A;Molecule type: protein
A;Residues: 19-24;27-39;355-369;506-520;549-561;622-626;672-677;743-748;806-817 <OHT1>
C;Superfamily: lipoxysenase
C;Keywords: oxidoreductase

Query Match 59.9%; Score 2829.5; DB 1; Length 865;
Best Local Similarity 62.1%; Pred. No. 7.2e-196;
Matches 553; Conservative 113; Mismatches 189; Indels 35;

[illegible]

Db 526 NTHAAIEPFIATNRQLSVLHPIHKLHHPFRDTMNALARQILINAGGVLEMTVFPK 585
QY 600 YALGMSADVYKSNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPAVDGLVIWAI 659
Db 586 YAMEMSAVYKSNVFPQALPADLVKRGVAVPDQSSPYGVRLLIKDYPAVDGLWISAI 645
QY 660 ERWVKEYLDIYYPNDGELQDVELQAWKKEVREAHGDLKDRDWWPRMDTVQQLARACTT 719
Db 646 KSWVTEYCNFYKSDLVKDELQAWKELREEGHDKKDEPWPWKQTRQELKDSCTI 705
QY 720 IIVASALHAAVNFQYYPAGYLPNRPTASRRPMPEPGSHDYKKLGAGQKEADMVFIRTI 779
Db 706 IIVIASALHAAVNFQYYPAGYLPNRPTLSRRPMPEPGTPEYEEL---KTNPDKAYLTI 762
QY 780 TSQFQTILGISLIEILSKHSSDEVYLGQRDEPDRWTSDAKALDAFKRFGSRLVQIENRIK 839
Db 763 TPQLQTLGLISLIEILSRHASDEIYLGQRDSSE-WTKDQEPAAAFERFGKKLSEIEDQII 821
QY 840 TMNDSPLKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887
Db 822 QMNGDKKWKNRSGPVNVPYTLFF-TSE-----QGLTGKGIPIINSVSI 862
RESULT 7
JQ2267
lipoxigenase (EC 1.13.11.12) Lox1 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear Cress)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JQ2267
R;Melan, M.A.; Dong, X.; Endara, M.E.; Davis, K.R.; Ausubel, F.M.; Peterman, T.K.
Plant Physiol. 101, 441-450, 1993
A;Title: An Arabidopsis thaliana lipoxigenase gene can be induced by pathogens, abscisic
A;Reference number: JQ2267; MUID:94105302; PMID:7506426
A;Accession: JQ2267
A;Molecule type: mRNA
A;Residues: 1-859 <MEL>
A;Cross-references: GB:L04637; NID:g289202; PIDN:AAA32827.1; PID:g289203
C;Comment: This enzyme catalyzes the hydroperoxidation of polyunsaturated fatty acids co
C;Superfamily: lipoxigenase
C;Keywords: fatty acid oxidation; oxidoreductase
Query Match 55.6%; Score 2626.5; DB 1; Length 859;
Best Local Similarity 58.0%; Pred. No. 3.2e-181;
Matches 512; Conservative 128; Mismatches 211; Indels 31; Gaps 13;
QY 8 DRLTGKNEAWSEGKIRGTVRLVKKEVLVDGDFNASLLDGVHRLGWDDGVAFQLVSATA 67
Db 7 DLTGGGNETTK-KVKGTVVLMKKNVLDNFDFNASFLDRLHFLG--NKITRLRVSSDV 63
QY 68 ADPSNGGRKGVKAAHLEAAVSLKSTADGETVYRVSEFWEDESQGIIPGAVLVRNLQHAEF 127
Db 64 TDSNGSKGLGKAAHLEDWITITSLTAGESAFKVTFDYETDFGYPGAFILRNSHFSEF 123
QY 128 FLKTLTLEGVPGKTVVAVNSWVYPHKLKYSQERIFFANDTYLPSKMPAALVPYRQDELK 187
Db 124 LLKSLTLEDVPGHGRVHYICNSWIYPKHYTTDRVFFSNKTYLPHTPATLLKYREEELV 183
QY 188 ILRGDDNPGYPQEHDRVYRYDYNLDLGDGDKGEEHARPILGSGQEHYPYPRRCRTGRHPTK 247
Db 184 SLRG-TGEGELKEWDRVYDYAYNDLGVPPK---NPRPVLGQTQYEPYPRRGTGRKPTK 239
QY 248 KDPNSESRL-FLNLNIIYVPRDERFGHLKMSDFLGYSLKTIIIAVLPTLGT FVDDTPKEF 306
Db 240 EDPQTESRLPITSSLDIYVPRDERFGHLKMSDFLAYALKAIQPALEAVFDTPKEF 299
QY 307 DSFEDILGLYELGPEAPNPNLIAEIRKIPSEFLRSILPNGSHDHLKMPPLPNVKSVDL 366
Db 300 DSFEDVLKIYEEGIDLPNOALIDSIVKNIPLEMLKEIFRTDGQKF-LKFPVPQVIKED-- 356
QY 367 KKAPEFKFGRWTDSEFARETLAGVNPVLIKRLTEFPAPKSTLDPQYGDHTSKITEAHIRH 426
Db 357 -----KTAMRTDEEFAREMLAGLNPVVIQLLKEFPKSKLDSYGNQNSTITKSHIEH 410

QY 427 NMGLSVQNALRNKRLFLDHDHDFMPYLDEINEGFIYASRTLLFLKDDGTLPKPLAI 486
Db 411 NLDGLTVEALEKERLFILDHDTLMPYLGVRVNTTK-TYASRTLLFLKDDGTLPKPLVI 469
QY 487 ELSLPHPDGQORGAVSKVYTPAHTGVEGHVWOLAKAYACVNDSAWHQLISHWLTHAVIE 546
Db 470 ELSLPHPNGDKFGAVSEVYTPGE-GVYDSLWOLAKAFVGVNDSCNHQLISHWQTHASIE 528
QY 547 PFVIATNRQLSVVHPVHKLSPHYRDTLNINALARQTLINAGGVFERITVFPAKYALGMSA 606
Db 529 PFVIATNRQLSVLHPVFKLLEPHFRDTMNINALARQILINGGGIFEITVFPSKYAMEMSS 588
QY 607 DVYKS-WNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPAVDGLVWAIERWVKE 665
Db 589 FIYKNHWTFFDQALPAELKKRGMAVEDPEAPHGLRLRIKDYPAVDGLEVWYAIESWVRD 648
QY 666 YLDIYYPNDGELQDVELQAWKKEVREAHGDLKDRDWWPRMDTVQQLARACTTIIWVAS 725
Db 649 YIFLFYKIEEDIQDTDELQAWKKEVREEGHGDKKSEPWPKMQTREELVESCTIIWVAS 708
QY 726 ALHAAVNFQYYPAGYLPNRPTASRRPMPEPGSHDYKKLGAGQKEADMVFIRITTSQFQT 785
Db 709 ALHAAVNFQYYPAGYLPNRPTISRQYMPKENTPEFEEL---EKNPDKVFELKTIITAQLQT 765
QY 786 ILGISLIEILSKHSSDEVYLGQRDEPDRWTSDAKALDAFKRFGSRLVQIENRIKTMNDSP 845
Db 766 LLGISLIEILSTHSSDEVYLGQRDSKE-WAAAEKALEAEAFKFGKVKKEIEKNIDERNDDE 824
QY 846 DLKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887
Db 825 TLKNRTGLVKMPYTLFFPSSEG-----GVTGRGIPNSVSI 859
RESULT 8
S44940
lipoxigenase (EC 1.13.11.12) - potato
C;Species: Solanum tuberosum (potato)
C;Date: 06-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 11-Jun-1999
C;Accession: S44940
R;Casey, R.
submitted to the EMBL Data Library, May 1994
A;Reference number: S44940
A;Accession: S44940
A;Molecule type: mRNA
A;Residues: 1-861 <CAS>
A;Cross-references: EMBL:X79107; NID:g486618; PIDN:CAAS5724.1; PID:g486619
C;Superfamily: lipoxigenase
C;Keywords: oxidoreductase
Query Match 55.0%; Score 2597; DB 2; Length 861;
Best Local Similarity 58.5%; Pred. No. 4.4e-179;
Matches 508; Conservative 112; Mismatches 222; Indels 26; Gaps 10;
QY 22 KIRGTVRLVKKEVLVDGDFNASLLDGVHRLGWDDGVAFQLVSATAADPSNGGRKGVKA 81
Db 18 KVKGTVMNMKNVLDFTDLAGSLTGKIFDVLG--QKVSFQLISSVQGDPTNGLQGHNSP 75
QY 82 AHLEAAVSLKS-TADGETVYRVSEFWEDESQGIIPGAVLVRNLQHAEEFLKTLTLEGVPGK 140
Db 76 AYLENSLFTLTPLTAGSETAFGVTFDWNEEFVGPVGAFLIKNMHINEFFLKSILTLEDVPH 135
QY 141 GTVVFVANSWVYPHKLKYSQERIFFANDTYLPSKMPAALVPYRQDELKILRGDDNPGPYQE 200
Db 136 GKVFVVCNSWVYPSLNYKSDRIFFANQYLPSETPELLRKRYRENEELLTRG-DGTGKREA 194
QY 201 HDRVYRYDYNDLGDGDKGEEHARPILGSGQEHYPYPRRCRTGRHPTKDPNSESRL-FLL 259
Db 195 WDRIYDYDIYNDLGNPDQKENVRTTLGSSAEYYPYPRRGTGRPTRTDPKSESRIPLIL 254
QY 260 NLNIYVPRDERFGHLKMSDFLGYSLKTIIIAVLPTLGT FVDDTPKEFDSFEDILGLYELG 319
Db 255 SLDIYVPRDERFGHLKMSDFLTALYSIVQILPELHALFDGTPNEFDSFEDVLRLEYEG 314

Db 790 TASDEIYLQRENPE-WTSDVEPRQSFQRFHDKLVNENKIVERNNDNRWKNRNGPVPKVP 848
QY 858 YMLLYPNTSDVTGEKAE-GLTAMGIPNSISI 887
Db 849 YMLLYPNAS---GDNSESLTGKIPNSVSI 876

RESULT 12
DASYL1
lipoxxygenase (EC 1.13.11.12) 2 - soybean
N;Alternate names: carotene oxidase 2; lipoxidase 2
C;Species: Glycine max (soybean)
C;Date: 31-Mar-1989 #sequence_revision 30-Jun-1991 #text_change 19-Jan-2001
C;Accession: A28161; A30831; A37160; S13536
R;Shibata, D.; Steczko, J.; Dixon, J.E.; Andrews, P.C.; Hermodson, M.; Axelrod, B.
J. Biol. Chem. 263, 6816-6821, 1988
A;Title: Primary structure of soybean lipoxxygenase L-2.
A;Reference number: A28161; MUID:88198254; PMID:2834391
A;Accession: A28161
A;Molecule type: mRNA
A;Residues: 1-865 <SHI>
A;Cross-references: GB:J03211; NID:g170013; PIDN:AAA33987.1; PID:g170014
A;Note: There are no disulfide bonds
R;Start, W.G.; Ma, Y.; Polacco, J.C.; Hildebrand, D.F.; Freyer, G.A.; Altschuler, M.
Plant Mol. Biol. 7, 11-23, 1986
A;Title: Two soybean seed lipoxxygenase nulls accumulate reduced levels of lipoxxygenase
A;Reference number: A30831
A;Accession: A30831
A;Molecule type: mRNA
A;Residues: 232-262, 'NL', 265-312, 'Y', 314-362, 'E', 364-399, 'P', 401-427, 'H', 429-485, 'G', 487-501, 'G', 501-502, 'G', 502-503, 'G', 503-504, 'G', 504-505, 'G', 505-506, 'G', 506-507, 'G', 507-508, 'G', 508-509, 'G', 509-510, 'G', 510-511, 'G', 511-512, 'G', 512-513, 'G', 513-514, 'G', 514-515, 'G', 515-516, 'G', 516-517, 'G', 517-518, 'G', 518-519, 'G', 519-520, 'G', 520-521, 'G', 521-522, 'G', 522-523, 'G', 523-524, 'G', 524-525, 'G', 525-526, 'G', 526-527, 'G', 527-528, 'G', 528-529, 'G', 529-530, 'G', 530-531, 'G', 531-532, 'G', 532-533, 'G', 533-534, 'G', 534-535, 'G', 535-536, 'G', 536-537, 'G', 537-538, 'G', 538-539, 'G', 539-540, 'G', 540-541, 'G', 541-542, 'G', 542-543, 'G', 543-544, 'G', 544-545, 'G', 545-546, 'G', 546-547, 'G', 547-548, 'G', 548-549, 'G', 549-550, 'G', 550-551, 'G', 551-552, 'G', 552-553, 'G', 553-554, 'G', 554-555, 'G', 555-556, 'G', 556-557, 'G', 557-558, 'G', 558-559, 'G', 559-560, 'G', 560-561, 'G', 561-562, 'G', 562-563, 'G', 563-564, 'G', 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QY 69 DPSNGGRGKVGKAAHLEAAVSLKSTADGETVYRVSVFEWDESQGIPIGAVLVRLNQHAEFF 128
Db 69 DAN--GKGKLGKATFLEGIITSLPTLGGAGQSAFKINFEWDDGSGILGAFYIKFMQTEFF 126
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QY 787 LGISLIEILSKHSSDEVYLGQRDEPDRWTSDAKALDAFKRFGSRLVQIENRIKTMNDSPD 846
Db 765 IDLSVIEILSRHASDEVYLGQRDEPDRWTSDAKALDAFKRFGSRLVQIENRIKTMNDSPD 823
QY 847 LKXKRGKPVMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887
Db 824 LKXKRGKPVMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 857

RESULT 14
S07075
lipoxigenase (EC 1.13.11.12) 2 [similarity] - garden pea
C;Species: Pisum sativum (garden pea)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: S07075
R;Ealing, P.M.; Casey, R.
Biochem. J. 264, 929-932, 1989
A;Title: The cDNA cloning of a pea (Pisum sativum) seed lipoxigenase. Sequence comparison
A;Reference number: S07075; MUID:90147555; PMID:2515855
A;Accession: S07075

A;Molecule type: mRNA
A;Residues: 1-864 <EAL>
A;Cross-references: EMBL:X17061; NID:g20801; PIDN:CAA34906.1; PID:g20802
C;Superfamily: lipoxigenase
C;Keywords: oxidoreductase

Query Match 52.1%; Score 2458.5; DB 1; Length 864;
Best Local Similarity 54.8%; Pred. No. 4.4e-169;
Matches 486; Conservative 128; Mismatches 216; Indels 57; Gaps 15;

QY 22 KIRGTVRLVKKEVLD-----VGDFN-----ASLLDGVHRIILGWDDGVAFQLV 63
Db 14 KIRGTVLMRKKNVLDFTNTIVSIGGNVHVIDSGINIGTLDGLTAFLG--RSVSLQLI 71
QY 64 SATAADPSNGGRGKVGKAAHLEAAVSLKSTADGETVYRVSVFEWDESQGIPIGAVLVRLNQL 123
Db 72 SATKSDAN--GKGKVGKDTTFLEGVLASLPTLGGESAFNIHFWDHEMGIPGAFYIKVM 129
QY 124 HAEFFLKTTLLEGVPGKGTVVVANSWVYVPHKLYSQERIFFANDTYLPSKMPAALVPYRQ 183
Db 130 QVEFLKSLTLEDVPHGTIRFVCSWYNAKLYKSPRIFFANKSYLPSETSPPLVKYRE 189
QY 184 DELKITLRGDDNPFGPYQEHDRVYRYDYNDLGDGPKGEEHARPILGSGQEHPPYPRRCRTGR 243
Db 190 EELQTLRG-DGTGERKLERIYDYDYNDLGNPDHGHARLPILGSGSTHPPYPRRCRTGR 248
QY 244 HPTKDPNSESRLFLNLNIYVPRDERFGLKMSDFLGYSLKTIIEAVLPTLGTTFVD--D 301
Db 249 YPTKDPNSEKPA---TETVYVPRDENFGLKSSDFLAYGIKSVSQCVPAFESAFDLNF 304
QY 302 TPKEFDSFEDILGLYELGPEAPNPLIAEIRKKIPSEFLRSILPNGSHDHPKMLPNVI 361
Db 305 TNEFDSFQDVRNLFEGGKILPLDVISTLSPLPVYKEIFRT-----DGEQVLKFTPPHVI 359
QY 362 KSDVLKKAPEFKGWRTEDEFARETLAGVNPVVIKRLTEPPAKSTLDPROYGDHTSKITE 421
Db 360 RVS-----KSAWMTDEEFAREMLAGVNPVCMIRGLQEFPPKSNLDPAEYGDHTSKISV 411
QY 422 AHTRHNMGGLSVQNALRNKRLFILDHHDHFMPLYLDEINELEGNFIIYASRTLLFLKDDGTL 481
Db 412 DVL--NLDGCTIDEALASGRFLIDYHDTFIPFLRRINETSAC-AYATRTILFLKENGTL 468
QY 482 KPLAIELSLPHDPGQQRGAVSKVYTPAHTGVEGHVWQLAKAYACVNDKSAWHQLISHWLNT 541
Db 469 KPVAIELSLPHDPGQQRGAVSKVILPADEGVESTIWLAKAYVNVNDSYHQLMSHWLNT 528
QY 542 HAVIEPFVIATNRQLSVVHPVHKLSPHYRDT-LNINALARQTLINAGGVFERTVFPKY 600
Db 529 HAVIEPFVIATNRQLSVVHPVHKLSPHYRDTLNINALARQTLINAGGVFERTVFPKY 588
QY 601 ALGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPAVDGLVWAIER 660
Db 589 AVEMSSAVYKYWVFTDQALPNDLIRKNMAVKDSSSPYGLRLIIEYDYPYAVDGLVWAIER 648
QY 661 RWVKEYLDIYYPNDGELQRDVELOAWKKEVREAAHGLDKDRDWPRMDTVQQLARACTTI 720
Db 649 TWVQDYVSLYYATDNDIKNDSELOHWWKEVVEKGGHGLDKDKPWWPKLQTFDELVEVCTII 708
QY 721 IWVASALHAAVNFQYVAGYLPNRPPTASRRPMPPEGSHDYKKGAGQKEADMVFIERTIT 780
Db 709 IWTASALHAAVNFQYVAGYLPNRPPTASRRPMPPEGSHDYKKGAGQKEADMVFIERTIT 765
QY 781 SQFQTLIGISLIEILSKHSSDEVYLGQRDEPDRWTSDAKALDAFKRFGSRLVQIENRIKT 840
Db 766 PKFQTLIDLSVIEILSRHASDEVYLGQRDEPDRWTSDAKALDAFKRFGSRLVQIENRIKT 824
QY 841 MNDSPDLKXKRGKPVMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887
Db 825 KXNDPSLYHVRGVPVQLPYTLHPSSK-----EGLTFRGIPNSISI 864

RESULT 15
S01142

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 03:49:23 ; Search time 20 Seconds
(without alignments)
2309.311 Million cell updates/sec

Title: US-10-059-909-16
Perfect score: 4723
Sequence: 1 MFVHGVDRLTGKKNKEAWSE.....VTGEKAEGLTAMGIPNSISI 887

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query %	Length	DB	ID	Description
1	2936.5	62.2	1	862	1	LOX1_HORVU	P29114 hordeum vul
2	2829.5	59.9	1	865	1	LOX2_ORYSA	P29250 oryza sativ
3	2627.5	55.6	1	860	1	LOXA_LYCES	P38415 lycopersico
4	2626.5	55.6	1	859	1	LOX1_ARATH	Q06327 arabidopsis
5	2597	55.0	1	861	1	LOX1_SOLTU	P37831 solanum tub
6	2510	53.1	1	859	1	LOXB_LYCES	P38416 lycopersico
7	2486	52.6	1	865	1	LOX2_SOYBN	P09439 glycine max
8	2473.5	52.4	1	857	1	LOX3_SOYBN	P09186 glycine max
9	2458.5	52.1	1	864	1	LOX2_PEA	P14856 pisum sativ
10	2437	51.6	1	861	1	LOX3_PEA	P09918 pisum sativ
11	2405.5	50.9	1	862	1	LOXA_PHAVU	P27480 phaseolus v
12	2375	50.3	1	853	1	LOX4_SOYBN	P38417 glycine max
13	2370.5	50.2	1	864	1	LOXX_SOYBN	P24095 glycine max
14	2355.5	49.9	1	839	1	LOX1_SOYBN	P08170 glycine max
15	2309	48.9	1	866	1	LOX1_LENCU	P38414 lens culina
16	2231	47.2	1	741	1	LOXB_PHAVU	P27481 phaseolus v
17	1667.5	35.3	1	896	1	LOXC_ARATH	P38418 arabidopsis
18	1650	34.9	1	896	1	LX23_HORVU	Q8gsm2 hordeum vul
19	1587.5	33.6	1	923	1	LOXC_ORYSA	P38419 oryza sativ
20	1559	33.0	1	936	1	LX21_HORVU	P93184 hordeum vul
21	1455	30.8	1	932	1	LX22_HORVU	Q8gsm3 hordeum vul
22	601	12.7	1	1066	1	AOSL_PLEHO	O16025 plexaura ho
23	538	11.4	1	711	1	LXE3_MOUSE	Q9wv07 mus musculu
24	513.5	10.9	1	676	1	LX1B_HUMAN	O15296 homo sapien
25	513	10.9	1	711	1	LXE3_HUMAN	Q9byj1 homo sapien
26	511.5	10.8	1	701	1	LOXR_MOUSE	O70582 mus musculu
27	507	10.7	1	677	1	LX1B_MOUSE	O35936 mus musculu
28	504	10.7	1	662	1	LOXE_MOUSE	P55249 mus musculu
29	503.5	10.7	1	662	1	LOXL_MOUSE	P39654 mus musculu
30	503.5	10.7	1	701	1	LOXR_HUMAN	O75342 homo sapien
31	486.5	10.3	1	662	1	LOX2_RAT	Q02759 rattus norv
32	485.5	10.3	1	673	1	LOX5_MOUSE	P48999 mus musculu
33	480	10.2	1	672	1	LOX5_MESAU	P51399 mesocricetu

RESULT 1
LOX1_HORVU
ID LOX1_HORVU STANDARD; PRT; 862 AA.
AC P29114; Q42845;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lipoxigenase 1 (EC 1.13.11.12).
GN LOX1.1 OR LOXA.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Triumph;
RX MEDLINE=95127754; PubMed=7827128;
RA van Mechelen J.R.; Smits M.; Douma A.C.; Rouster J.; Cameron-Mills V.;
RA Heidekamp F.; Valk B.E.;
RT "Primary structure of a lipoxigenase from barley grain as deduced from its cDNA sequence."
RT Biochim. Biophys. Acta 1254:221-225(1995).
RN [2]
RP SEQUENCE OF 274-294 AND 832-845.
RC STRAIN=cv. Triumph; TISSUE=Embryo;
RX MEDLINE=92207997; PubMed=1554746;
RA Doderer A.; Kokkelink I.; van der Veen S.; Valk B.E.; Schram A.W.;
RA Douma A.C.;
RT "Purification and characterization of two lipoxigenase isoenzymes from germinating barley."
RL Biochim. Biophys. Acta 1120:97-104(1992).
CC -!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND DEVELOPMENT, PEST RESISTANCE, AND SENESENCE OR RESPONSES TO WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING A CIS, CIS-1,4-PENTADIENE STRUCTURE.
CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-hydroperoxyoctadeca-9,11-dienoate.
CC -!- COFACTOR: Iron, one atom tightly bound per molecule.
CC -!- SUBUNIT: Monomer.
CC -!- DEVELOPMENTAL STAGE: IN BOTH QUIESCENT AND GERMINATING SEEDS.
CC -!- MISCELLANEOUS: WITH LINOLEATE AS SUBSTRATE, LIPOXYGENASE 1 SHOWS A SPECIFICITY FOR CARBON 9 AS THE SITE FOR HYDROPEROXIDATION (IN CONTRAST TO LIPOXYGENASE 2, WHICH SHOWS A PREFERENCE FOR CARBON 13).
CC -!- SIMILARITY: Belongs to the lipoxigenase family.
CC -!- SIMILARITY: Contains 1 PLAT domain.

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Db 76 AYLENFLLTLPLAAGETAAGVTDFWNEEFGVPGAFVIXNMHINEFFLKSLTLEDVPHNG 135

QY 142 TVFVANSWVYPKLYSQERIFFANDTYLPSKMPAALVPYRQDELKILRGDDNPPYQEH 201

Db 136 KVHFVCNSWVYPSFRYKSDRIFFANQYLPSETPELLRKYRENELVTLRG-DGTGKEAW 194

QY 202 DRVRYDYNDLGDGPKGEEHARPIILGGSQEHYPYRRRCRGRHPTKKDPNSESRL-FLIN 260

Db 195 DRIYDYDVNDLGNPDQKENVRTILGGSADYPYPRRGRTGPPTRTDPKSESRIPLILS 254

QY 261 LNIYVPRDRERFGLKMSDFLGYSLKTIIEAVLPTLGTTFVDDTPKEFDSFEDILGLYLGP 320

Db 255 LDIYVPRDRERFGLKMSDFLTALYSIVQFILPELHALFDGTPNEFDSFEDVLRLEYGGI 314

QY 321 EAPNPLIAEIRKKIPSEFLRSILPNSGSHDPLKMPLEPNVIXSDVLKKAPEFKFGWRTDE 380

Db 315 KLPOGPLFKALTDAIPLEMIRELLRTDG-EGILRFPTPLVIX-----DSKTAWRTDE 365

QY 381 EFARETLAGVNPVVIKRLTEFFPAKSTLDPQYGDHTSKITEAHIRHNMGGLSVQNALRNK 440

Db 366 EFAREMLAGVNPVVISRLEEFFPAKSLDPPELYGNQNSITTAEHIEGKLDGLTDEAINSN 425

QY 441 RLFILHDHFMPPYLDDEINELEGNFIYASRTLLFLKDDGTLKPLAIELSLPHDPDQQRGA 500

Db 426 KLFILNHDDVLIPLRINTTTTK-TYASRTLLFLQDNGSLKPLAIELSLPHDPDQFGV 484

QY 501 VSKVYTPAHTGVEGHVWQAKAYACVNDSSAHQLISHWLNTHAVIEPFVIATNRQLSVH 560

Db 485 TSKVYTPSDQGVGSIWQAKAYAVAVNDSSGVHQLISHWLNTHAVIEPFVIATNRQLSVLH 544

QY 561 PVKLLSPHYRDTLNINALARQTLINAGGVFERTVFPKAYALGMSADVYKSNFNEQALP 620

Db 545 PIHKLLYPHFRDTMNINALARQTLINAGGVLESTVFPKPFAMEMSAVVYKDWVFPDQALP 604

QY 621 ADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVIWAIERWVKEYLDIYPNDGELQRD 680

Db 605 ADLVKRGVAVEDSSSPHGVRLIIDDYPIYAVDGLVIAISAKSVWTDYCSFYGSNEEILKD 664

QY 681 VELQAWKVEVEEBAHGDLDKRDWPRMDTVQQLARACTTIWVASALHAAVNFQYYPYAG 740

Db 665 NELQAWKVEVREVGDKKNEPWAEMETPQELIDSCCTIIWIASALHAAVNFQYYPYAG 724

QY 741 YLPNPTASRRPMPEPGSHDYKKGAGQKEADVMVFIRITITSQFOTILGISLIEILSKHSS 800

Db 725 YLPNPTVSRKFMPEPGTPEYBEL---KKNPDKAFKLTITAQLQTLGVSLEILSRHTT 781

QY 801 DEVYLGQRDEPDRWTSDAKALDAFKRFGSRLVQIENRIKTMNDSPDLKNRKGPVEMPYML 860

Db 782 DEIYLGQRESPE-WTKOKEPLAAPERFGNKLTDIEKQIMQRNGNIIITNRTPGVNAPYTL 840

QY 861 LYPNTSDVTGEKAEGLTAMGIPNSISI 887

Db 841 LFPTSEG-----GLTGKIPNSVSI 860

RESULT 4

LOX1_ARATH

ID LOX1_ARATH STANDARD; PRT; 859 AA.

AC Q06327;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Lipoxigenase 1 (EC 1.13.11.12).

GN LOX1 OR ATIG55020 OR F14C21.3 OR F14C21.54.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OC NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia; TISSUE=Root;

RX MEDLINE=94105302; PubMed=7506426;

RA Melan M.A., Dong X., Endara M.E., Davis K.R., Ausubel F.M.,

RA Peterman T.K.;

RT "An Arabidopsis thaliana lipoxigenase gene can be induced by

RT pathogens, abscisic acid, and methyl jasmonate.";

RL Plant Physiol. 101:441-450(1993).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Landsberg erecta;

RX MEDLINE=94137782; PubMed=8305494;

RA Melan M.A., Nemhauser J.M., Peterman T.K.;

RT "Structure and sequence of the Arabidopsis thaliana lipoxigenase 1

RT gene.";

RL Biochim. Biophys. Acta 1210:377-380(1994).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;

RX MEDLINE=21016719; PubMed=11130712;

RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Militischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis

RT thaliana.";

RL Nature 408:816-820(2000).

CC -!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF

CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND

CC DEVELOPMENT, PEST RESISTANCE, AND SENESCENCE OR RESPONSES TO

CC WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING

CC A CIS, CIS-1,4-PENTADIENE STRUCTURE.

CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-

CC hydroperoxyoctadeca-9,11-dienoate.

CC -!- COFACTOR: Iron, one atom tightly bound per molecule.

CC -!- SUBUNIT: Monomer.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- INDUCTION: BY WOUNDING, ABSCISIC ACID (ABA) AND METHYL JASMONATE.

CC -!- SIMILARITY: Belongs to the lipoxigenase family.

CC -!- SIMILARITY: Contains 1 PLAT domain.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; L04637; AAA32827.1; -.

CC EMBL; U01843; AAA17036.1; -.

CC EMBL; AC069144; AAG51123.1; -.

CC PIR; JQ2267; JQ2267.

CC HSSP; P08170; 2SBL.

CC InterPro; IPR000907; Lipoxigenase.

CC InterPro; IPR001024; Lipoxigenase_LH2.

CC InterPro; IPR008976; PLAT LH2.

CC Pfam; PF00305; lipoxigenase; 1.

CC Pfam; PF01477; PLAT; 1.

CC PRINTS; PR00087; LIPOXYGENASE.

CC SMART; SMO0308; LH2; 1.

CC PROSITE; PS00711; LIPOXYGENASE_1; 1.

CC PROSITE; PS00081; LIPOXYGENASE_2; 1.

CC PROSITE; PS50095; PLAT; 1.

KW	Oxidoreductase; Dioxxygenase; Iron; Multigene family.
FT	DOMAIN 21 161 PLAT.
FT	METAL 519 519 IRON (BY SIMILARITY).
FT	METAL 524 524 IRON (BY SIMILARITY).
FT	METAL 711 711 IRON (BY SIMILARITY).
FT	METAL 859 859 IRON (BY SIMILARITY).
SQ	SEQUENCE 859 AA; 98045 MW; 49378EBACD5FF579 CRC64;
Query Match	
Best Local Similarity 55.6%; Score 2626.5; DB 1; Length 859;	
Matches 512; Conservative 128; Mismatches 211; Indels 31; Gaps 13;	
QY	8 DRLTGKNEAWSEKIRGTVRLVKKEVLDVGDNFASLLDGVHRIILGWDDGVAFQLVSATA 67
DB	7 DLTGGNETTK-KVGTIVLMKKNVLDNFNDNASFLDLRHEFLG--NKITRLVSSDV 63
QY	68 ADPSNGGRGKVGKAAHLEEAUVSLKSTADGETVYRVVSFEWDESGIPGAVLVRNLQHAEF 127
DB	64 TDSENGSKGLGKAHLEDWITITISLTAGESAFKVTDPYETDFGYPGAFILRNHFSEF 123
QY	128 FLKTLTLEGVPGKGTGVFVANSVYVPHKLYSQERIFFANDTYLPSKMPAALVPYRQDELK 187
DB	124 LLKSLTLEDPVGHGRVHYICNSWIYPAKHYYTDRVFFSNKYTLPHETPATLLKYREELV 183
QY	188 ILRGDDNPGPYQEHDRVYRYDNDLGDPPKGEHARPILGSGQEHYPYRRRCRTGRHPTK 247
DB	184 SLRG-TGEGELKEWDRVYDAYVNDLGVPPK--NRPVLGGTQETPYPPRRGRTRKPKTK 239
QY	248 KDPNSERL-FLNLNIYVPRDERFGHLKMSDFGLYSKTIIEAVLPTLTGTFVDDTPKEF 306
DB	240 EDPQTESRLPITSSLDIYVPRDERFGHLKMSDFLAYALKAIAQFIQPALEAVFDDTPKEF 299
QY	307 DSFEDILGLYELGPEAPNPLIAIRKKIPSEFLRSILPNSGSHDPLKMPLPNVKSDVL 366
DB	300 DSFEDVLKYEIGIDLNPQALIDSIVKNIPLEMLKEIFRTDGQKF-LKFPVPQVIKED-- 356
QY	367 KKAPEKFGWRTDEEFARETLAGVNPVVIKRLTEFPAKSTLDPQYGDHTSKITEAHIRH 426
DB	357 -----KTAWRTDEEFAREMLAGLNPVVIQLLKEFPKSKLDSESYGNQNSTTKSHIEH 410
QY	427 NMGLSVQNALNRKRLFILDHDFHMPYLDIENELEGNFIYASRTLLFLKDDGLKPLAI 486
DB	411 NLDGLTVEEALEKERLFIIDHDTLMPYLGVRNVTITTK-TYASRTLLFLKDDGLKPLVI 469
QY	487 ELSLPHDPGQQRGAVSKVYTPAHTGVEGHVWQLAKAYACVNSAWHQLISHWLNTHAVIE 546
DB	470 ELSLPHDPGDKFGAVSEVYTPGE-GVYDSLWQLAKAFVGVNDSGNHQLISHWMTASIE 528
QY	547 PFVIATNRQLSVVHPVHKLSPHYRDTLNALAROTLINAGGVFERTVFPKAYALGMSA 606
DB	529 PFVIATNRQLSVLHPVFKLLEPHFRDTMNALARQILINGGGIFEITVFPSPKYAMEMSS 588
QY	607 DVYKS-WNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVIWATERWKE 665
DB	589 FIYXNHWTFPDQALPAELKKRGMAVEDPEAPHGLRLRIKDYPIYAVDGLVFWAIESWVRD 648
QY	666 YLDIYVNDGELQRDVELQAWKKEVREEAHGDLKORDMWPRMDTVQQLARACTIILWVAS 725
DB	649 YIFLFYKIEEDIQTDTELQAWKKEVREEGHGDKKSEPWPKMQTREELVESCTIILWVAS 708
QY	726 ALHAAVNFQGYPYAGYLPNRPASRRPMPEPGSHDYKKLGAGQKEADMVFIRITISQFOT 785
DB	709 ALHAAVNFQGYPYVAGYLPNRPISRQYMPKENTPEFEEL--EKNPKDVKFLKTIQAOLQ 765
QY	786 ILGISLIEILSKHSSDEVYLGQDEPDWRWTSDAKALDAFKRFGSRLVQIENIKTMNDSP 845
DB	766 LLGISLIEILSTHSSDEVYLGQDSKE-WAAEKEALEAFKFGKEKVEIEKNIDERNDDE 824
QY	846 DLKPKGFPVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
DB	825 TLKNTGLVKMPYTLILFPSSSEG-----GVTGRGIPNSVSI 859

RESULT 5

LOX1_SOLUTU STANDARD; PRT; 861 AA.

AC P37831;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Lipoxxygenase 1 (EC 1.13.11.12).

GN LOX1.1 OR LOX1.

OS Solanum tuberosum (Potato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC lamids; Solanales; Solanaceae; Solanum.

OX NCBI_TaxID=4113;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Desiree; TISSUE=Tuber;

RX MEDLINE=95175602; PubMed=7870815;

RA Casey R.;

RT "Sequence of a cDNA clone encoding a potato (Solanum tuberosum) tuber lipoxxygenase.";

RL Plant Physiol. 107:265-266(1995).

CC -!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND DEVELOPMENT, PEST RESISTANCE, AND SENESCENCE OR RESPONSES TO WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING A CIS, CIS-1,4-PENTADIENE STRUCTURE.

CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-hydroperoxyoctadeca-9,11-dienoate.

CC -!- COFACTOR: Iron, one atom tightly bound per molecule.

CC -!- SUBUNIT: Monomer (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -!- SIMILARITY: Belongs to the lipoxxygenase family.

CC -!- SIMILARITY: Contains 1 PLAT domain.

CC -----

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CC -----

DR EMBL; X79107; CAA55724.1; -.

DR PIR; S44940; S44940.

DR HSSP; P09186; 1LNH.

DR InterPro; IPR000907; Lipoxxygenase.

DR InterPro; IPR001024; Lipoxxygenase_LH2.

DR InterPro; IPR008976; PLAT_LH2.

DR Pfam; PF00305; lipoxxygenase; 1.

DR Pfam; PF01477; PLAT; 1.

DR PRINTS; PR00087; LIPOXYGENASE.

DR SMART; SM00308; LH2; 1.

DR PROSITE; PS00711; LIPOXYGENASE 1; 1.

DR PROSITE; PS00081; LIPOXYGENASE_2; 1.

DR PROSITE; PS50095; PLAT; 1.

DR Oxidoreductase; Dioxxygenase; Iron; Multigene family.

KW DOMAIN 29 160 PLAT.

FT METAL 522 522 IRON (BY SIMILARITY).

FT METAL 527 527 IRON (BY SIMILARITY).

FT METAL 713 713 IRON (BY SIMILARITY).

FT METAL 861 861 IRON (BY SIMILARITY).

SQ SEQUENCE 861 AA; 96966 MW; 09732A6751DEE20D CRC64;

Query Match 55.0%; Score 2597; DB 1; Length 861;

Best Local Similarity 58.5%; Pred. No. 8.7e-180;

Matches 508; Conservative 112; Mismatches 222; Indels 26; Gaps 10;

QY 22 KIRGTVRLVKKEVLDVGDNFASLLDGVHRIILGWDDGVAFQLVSATAADPSNGRGKVGKA 81

DB 18 KVRGTVVMNMKNVLDFTDLAGSLTGKIFDVLG--QKVSFQLISSVQGDPTNGLQKHNSP 75

QY 82 AHLEEAUVSLKS-TADGETVYRVVSFEWDESGIPGAVLVRNLQHAEFFLTKTLTLEGVPGK 140

Db 76 AYDENSELTPLTAGSETAFGVTFDWNEEFGVPGAFIKNMGHINEFFLKSLTLEDVFNH 135
QY 141 GTVVVFVANSWVYPKLYSQERIFFEANDTYLPSKMPAALVYRQDELKILRGDNDPGPYQE 200
Db 136 GKVHFCNSWVYPSLNYKSDRIFFANQPYLPSETPELLRKYRENELLTRG-DGTGKREA 194
QY 201 HDRVRYDYNDLGDGPKGEEHARPILGGSQEHYPYPRRORTGRHPTKDPNSERL-FL 259
Db 195 WDRYDYNDLGNPDQGGKENVRTTLGGSAAEYYPYPRRORTGRPTRTDPKSESRIPL 254
QY 260 NLNIYVPRDERFGLKMSDFLGYSKLTIEAVLPTLGTFTVDDTPKEFDSFEDILGLYELG 319
Db 255 SLDIYVPRDERFGLKMSDFLTVALKSIVQFIPPELHALFDGTPNEFDSFEDVRLYE 314
QY 320 PEAPNPLIAEIRKIPSEFLSILPNSGSHDHPKMPNPVNIKSDVLKKAPEKFGWRTD 379
Db 315 IKLPQGLFKALTAAPLEMITRELLRTDG-EGILRFPFPLVIK-----DSKTAWRTD 365
QY 380 EEFARETLAGVNPVVIKRLTEPPAKSTLDRQYGDHTSKITEAHIRHNMGSLSVQNALRN 439
Db 366 EEFAREMLAGVNPVVIISRLQEPFKSKLDPEAYGNQNSTITAETHIEDKLDGLTVDEAMN 425
QY 440 KRLFLDHDHFMYPYLDEINELEGNFYASRTLLFLKDDGTLKPLAIELSLPHDPGQQRG 499
Db 426 NKLFIHLNHDVILPYLRRINTITK-AYASRTLLFLQDNGSLKPLAIELSFPHDPGQFG 484
QY 500 AVSKVYTPAHTGVEGHVWQLAKAYACVNDSAWHQLISHWLNTHAVIEPFVIATNRQLSV 559
Db 485 VTSKVYTPSDQGVESIIWQLAKAYVAVNDVGVLHQLISHWLNTHAVIEPFVIATNRQLSV 544
QY 560 HPVHKLLSPHYRDTLNINALARQTLINAGGVFERTVPAKVALGMSADVYKSWNFNEQAL 619
Db 545 HPIHKLLYPHFRDTMNNASARQLLVNAGGVLESTVFQSKFAMEMSAVVYKDWVFPDQAL 604
QY 620 PADLVKRGVAVPDQSSPYGVRLIKDYPIYAVDGLVINWAIERWVKEYLDIYYPNDGELQR 679
Db 605 PADLVKRGVAVEDSSPHGVRLIIEDYPYAVDGLLEIWSAISKSWVTDYCSFYGSDEILK 664
QY 680 DVELQAWKWEVREEAHGDLKDRDWPMDTVQQLARACTTIWVASALHAAVNFQYPIYA 739
Db 665 DNELOAWKWELEVGHDGKNEPWPWPEMETPQELIDSTTIWIASALHAAVNFQYPIYA 724
QY 740 GYLPNRTASRRPMPEPGSHDYKLGAGQKEADVMVFIRITITSQFOTILGISLIEILSKHS 799
Db 725 GYLPNRTVSRFEMPEPGTPEVEEL---KRNPDKAFKLTITAQLTLLGVSILVILSRHT 781
QY 800 SDEVYLGORDEPRWTSDAKALDAFKRFGSRLVQIENRIKTMNDSPDLKNRKGPVEMPYM 859
Db 782 TDEIVLGQRESPE-WTKDKEPLAADFRTGKLTLDIEKQIIQRNGDNILNTRSGPVNAPYT 840
QY 860 LLYPNTSDVTGEKAEGLTAMGIPNSISI 887
Db 841 LLFPTSEG-----GLTGKIGIPNSVSI 861
RESULT 6
LOXB LYCES
ID LOXB LYCES STANDARD; PRT; 859 AA.
AC P384I6;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lipoxigenase B (EC 1.13.11.12).
GN LOX1.2 OR LOXB.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Caruso; TISSUE=Pericarp;

RX MEDLINE=95062736; PubMed=7972514;
RA Ferrie B.J., Beaudoin N., Burkhardt W., Bowsher C.G., Rothstein S.J.;
RT "The cloning of two tomato lipoxigenase genes and their differential
RL expression during fruit ripening.";
RL Plant Physiol. 106:109-118(1994).
CC -|- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF
CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND
CC DEVELOPMENT, PEST RESISTANCE, AND SENESENCE OR RESPONSES TO
CC WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING
CC A CIS, CIS-1,4-PENTADIENE STRUCTURE.
CC -|- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
CC hydroperoxyoctadeca-9,11-dienoate.
CC -|- COFACTOR: Iron, one atom tightly bound per molecule.
CC -|- SUBUNIT: Monomer (By similarity).
CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
CC -|- TISSUE SPECIFICITY: Fruit specific.
CC -|- SIMILARITY: Belongs to the lipoxigenase family.
CC -|- SIMILARITY: Contains 1 PLAT domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; U09025; AAA53183.1; -.
DR PIR; T06339; T06339.
DR HSSP; P09186; 1LNH.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase_LH2.
DR InterPro; IPR008976; PLAT_LH2.
DR Pfam; PF00305; lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS50095; PLAT; 1.
KW Oxidoreductase; Dioxygenase; Iron; Multigene family.
FT DOMAIN 34 158
FT METAL 521 521 IRON (BY SIMILARITY).
FT METAL 526 526 IRON (BY SIMILARITY).
FT METAL 711 711 IRON (BY SIMILARITY).
FT METAL 859 859 IRON (BY SIMILARITY).
SQ SEQUENCE 859 AA; 97122 MW; DAD79B10AE627434 CRC64;
Query Match 53.1%; Score 2510; DB 1; Length 859;
Best Local Similarity 56.7%; Pred. No. 1.7e-173;
Matches 502; Conservative 111; Mismatches 240; Indels 32; Gaps 13;
QY 5 GVADRLTGKNKEAWSEGKIRGTVRLVKKEVLVDGDFNASLLDGVHRIILGWDDGVAFQLVS 64
Db 5 GIVDAILGKD----DRPKVGRVILMKKNVLDFINIGASWVDGISDLIG--QKVSIGLIS 58
QY 65 ATAADPSNGGRGKVGKAAHLEAAVWSLKSTADGETVYRVSVFEWDESQ-GIPGAVLVRLNQ 123
Db 59 GSV--NYDGLLEGKLSNPAYLESWLTDTITPITAGESFTSVTFDWRDEFVPGAFIKNLH 116
QY 124 HAEFLKTLTLEGVPGKGTVVVFVANSWVYPKLYSQERIFFEANDTYLPSKMPAALVYPRQ 183
Db 117 LNEFLKSLTLEDVPNYGKTHFCVNSWVYPAFRYKSDRIFFANQAYLPSETPOPLRKYRE 176
QY 184 DELKITLRGDDNPGPYQEHDRVYRYDYNDLGDGPKGEEHARPILGGSQEHYPYPRRORTGR 243
Db 177 NELVALRG-DGTGKLEEDRWVDYACYNLDGEPDKGEEYARPILGSSSEYYPYPRRORTGR 235
QY 244 HPTKDPNSESRLFL-LNLNIYVPRDERFGLKMSDFLGYSKLTIEAVLPTLGTFTVDDT 302
Db 236 EPTKADPNCESRNPLPMSLDIYVPRDERFGLHVKKSFLTSSLSKSLQTLPPAFKALCDNT 295
QY 303 PKFEFDSFEDILGLYELGPEAPNPLIAEIRKKIPSEFLRSLPNSGSHDHPKMPNPVNIK 362

Db 296 PNEFNSFADVLNLYEGGKILPEGPWLKAITDNISSEILKDIQTDGQG-LLKYPTPQVIQ 354
Qy 363 SDVLKKAPEKFGWRTDEEFARETLAGVNPVVIKRLTEFPAKSTLDPKQYGDHTSKITEA 422
Db 355 GD-----KTAWRTDEEFGREMLAGSNPVLISRLQEPFPPSKLDPTIYGNQNSTITTE 406
Qy 423 HIRHNMGLSVQNALRNKRLFILDDHDFMPYLDEINELEGNFIYASRTLLFLKDDGTLK 482
Db 407 HVQDKLNGLTVNEAIKSNRFLFILNHHDIVMPLLRKINMSANTKAYASRTLLFLQDDRTLK 466
Qy 483 PLAIELSLPHDPGQQRGAQVSKVYTPAHTGVEGHVWQLAKAYACVNDNSAWHQLISHWLNT 542
Db 467 PLAIELSLPHDPGQDQFTVSKVYTPADQGVESIQWQFAKAYAVNDMGIHQHQLISHWLNT 526
Qy 543 AVIEPFVIATNRQLSVVHPVHKLKLSPHYRDTLNINALARQTLINAGGVFERTVFPKAYAL 602
Db 527 AVIEPFVATNRHLSVLHPHKLHHPFRNTMNLALARETLTYDGG-FETSLFPKAYSM 585
Qy 603 GMSADVYKSNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVIWAIERW 662
Db 586 EMSAAAYKDWVPEQALPADLLKRGVAVEDLSSPHGIRLLILDYPIYAVDGLGLEIWAISKW 645
Qy 663 VKEYLDIYVNDGELQRDVELQAWKVEVREAHGDLKDRDWPRMDTVQQLARACTIILW 722
Db 646 VTEYCKFYKSDTEVEKDTLOAWKELREEGHGDKKDEAWPKLQTRQELRDCCTIILW 705
Qy 723 VASALHAAVNFQOYPYAGYLPNRPASRRPMPPEPGSHDYKLGAGQKEADMFVIRITISQ 782
Db 706 IASALHAAHFGLYSYAGYLPNRPILSCNLMPEPGSVYEEL---KTNPKDKVFLKTFVPQ 762
Qy 783 FQTILGISLIBILSKHSSDEVYLGQDEPDRTWTSADKALDAPKRFSGRLVQIENRIKTMN 842
Db 763 LQSLLEISIFEVSSRRHASDEVYLGQDSIE-WTKDKEPLVAFERFGKMLSDIENRIMMN 821
Qy 843 DSPDLKNRKGPVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
Db 822 SHKSWKNRSGPNVPYTLFFP-TSE-----EGLTGKGIENSVSI 859

RESULT 7
LOX2 SOYBN STANDARD; PRT; 865 AA.
ID LOX2 SOYBN STANDARD; PRT; 865 AA.
AC P09439;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Seed lipoxigenase-2 (EC 1.13.11.12) (L-2).
GN LOX1.2 OR LOX2.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88198254; PubMed=2834391;
RA Shibata D., Steczko J., Dixon J.E., Andrews P.C., Hermodson M.,
RA Axelrod B.;
RT "Primary structure of soybean lipoxigenase L-2";
RL J. Biol. Chem. 263:6816-6821(1988).
RN [2]
RP SEQUENCE OF 231-865 FROM N.A.
RA Start W.G., Ma Y., Polacco J.C., Hildebrand D.F., Freyer G.A.,
RA Altschuler M.;
RT "Two soybean seed lipoxigenase nulls accumulate reduced levels of
RT lipoxigenase transcripts";
RL Plant Mol. Biol. 7:11-23(1986).
CC -!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF
CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND
CC DEVELOPMENT, PEST RESISTANCE, AND SENESCENCE OR RESPONSES TO
CC WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING
CC A CIS, CIS-1,4-PENTADIENE STRUCTURE.

CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
CC hydroperoxyoctadeca-9,11-dienoate.
CC -!- COFACTOR: Iron, one atom tightly bound per molecule.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: SOYBEAN CONTAINS AT LEAST 4 DISTINCT ISOENZYMES,
CC L-1, L-2, L-3A AND L-3B IN DRY SEEDS, AND AT LEAST TWO DISTINCT
CC ISOZYMES IN THE HYPOCOTYL/RADICLE REGION OF THE SEEDLING STEM.
CC -!- SIMILARITY: Belongs to the lipoxigenase family.
CC -!- SIMILARITY: Contains 1 PLAT domain.
CC -!- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN AT POSITIONS 691
CC TO 865 DUE TO A FRAMESHIFT.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J03211; AAA33987.1; --.
CC PIR; A28161; DASYL1.
CC HSP; P08170; 2SBL.
CC InterPro; IPR000907; Lipoxigenase.
CC InterPro; IPR001024; Lipoxigenase_LH2.
CC InterPro; IPR008976; PLAT_LH2.
CC Pfam; PF00305; lipoxigenase; 1.
CC Pfam; PF01477; PLAT; 1.
CC PRINTS; PR00087; LIPOXYGENASE.
CC SMART; SM00308; LH2; 1.
CC PROSITE; PS00711; LIPOXYGENASE_1; 1.
CC PROSITE; PS00081; LIPOXYGENASE_2; 1.
CC PROSITE; PS50095; PLAT; 1.
CC Oxidoreductase; Dioxygenase; Iron; Multigene family.
KW DOMAIN 50 175 PLAT.
FT METAL 527 527 IRON (BY SIMILARITY).
FT METAL 532 532 IRON (BY SIMILARITY).
FT METAL 718 718 IRON (BY SIMILARITY).
FT METAL 865 865 IRON (BY SIMILARITY).
FT CONFLICT 263 264 KP -> NL (IN REF. 2).
FT CONFLICT 313 313 D -> Y (IN REF. 2).
FT CONFLICT 400 400 L -> P (IN REF. 2).
FT CONFLICT 428 428 L -> H (IN REF. 2).
FT CONFLICT 486 486 D -> G (IN REF. 2).
FT CONFLICT 502 502 V -> G (IN REF. 2).
FT CONFLICT 534 534 V -> L (IN REF. 2).
SQ SEQUENCE 865 AA; 97145 MW; 74CBD32E3E4A0C85 CRC64;

Query Match 52.6%; Score 2486; DB 1; Length 865;
Best Local Similarity 54.5%; Pred. No. 9.4e-172;
Matches 487; Conservative 137; Mismatches 196; Indels 74; Gaps 15;

Qy 22 KIRGTVRLVKVEYLD---VGDFN-----ASLLDGVHRIILGWDDGVAFQLV 63
Db 18 KIKGTVLMRKKNVLDNFNSVADLTGKNVGLIGTGLNVVGSTLDNLTAFLG--RSVALQLI 75

Qy 64 SATAADPSNGGRGKVGKAAHLEEAUVSLKSTADGETVYRVSVFEWDESQGI PGAVLVRNLQ 123
Db 76 SAT--KPLANGKGVKDTFLEGIIVSLPTLGAGESAFNIQFEWDESMGIPGAFYIKNYM 133

Qy 124 HAEFFLKTLTLEGVPGKGTVVVFVANSWVYPHKLYSQERIFFPANDTYLPSKMPAALVPYRQ 183
Db 134 QVEFYLKSLTLEDVNPQGTIRFCVNSWVYNTKLYKSVIRIFFANHTYVPSETPAALVGyre 193

Qy 184 DELKILRGDDNPGPYQEHDRVYRYDYNLDGDPDKGEEHARPIILGSGQEHYPYRRCRTGR 243
Db 194 EELKNLRG-DGKERKEHDRIYDYVDVNDLGNPDHGENFARPIILGSGSTHPYRRCRTGR 252

Qy 244 HPTKDPNSESRLFLNLNLYVPRDEREGHLKMSDFLGSYSLKTIIEAVLPTLTGTFVD--D 301
Db 253 YPTRKDNSEK-----PGEVYVPRDENFGLHKSSDFLAYGIKLSQYVLPAFESVFDLNF 307

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QY 302 TPKEFDSFEDILGLYELGPEAPNPNPLIABIRKKIPSEFLRSILP-----NGSHDHPL 353
Db 308 TPNEFDSFQDVRDLHEGG-----IKLPTVEISTIMPLPVVKELFRTDGEQVL 354
QY 354 KMPLPNVKSVDLVKKAPFKFGWRTDEEPARETLAGVNPVIRKRLTEFPKASTLDRPQYQ 413
Db 355 KFPFPHVIVQS-----KSAMWTDDEFAEMVAGVNPVIRGLQEFPPKSNLDPTIYG 406
QY 414 DHTSKITEAHRHNMGGSLVQNALRNKRLFLDHDHDFMPYLDNEINELEGNFIYASRTLL 473
Db 407 EQTSKITADAL--DLDDGYTDEALASRRLEMLDYHDVEMPYIRRNQTYAK-AYATRTIL 463
QY 474 FLKDDGTLKPLAIELSLPHPDGQORGAVSKVYTPAHTGVGHVWQLAKAYACVNDSAMHQ 533
Db 464 FLRENGTLKPVATELSLPHPDGDLGSAVSQVILPAKEGVES*IWLLAKAYVVVNDSCYHQ 523
QY 534 LISHWLNTHAVIEPFIATNRQLSVVHPVHKLLSPHYRDTLNINALAROTLINAGVFEER 593
Db 524 LMSHWLNTHAVIEPFIATNRHLSALHPYIKLLTPHYRDTMNINALARQSLINADGIEK 583
QY 594 TVFPKAYALGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKOYPYAVDGL 653
Db 584 SFLPSKHSVEMSSAVYKNWVFTDQALPADLIRKGVAIKPSAPHGRLRLIEDYPYAVDGL 643
QY 654 VIWVAIERWVKEYLDIYPNDGELORDVELQAWKVEVREAHGDLKDRDWPRMDTVQQL 713
Db 644 EIWAALKTWQEVSVLYARDDDVKPDSQLQWKEAVEKGHGDLDKDPWPKLQTIIEEL 703
QY 714 ARACITIIWASALHAAVNFQYQYAGYLPNRPNTASRRPMPBPESHGDKYKLGAGOKBADM 773
Db 704 VEICTIIITWASALHAAVNFQYQYPIGFIILNRPNTSSRRLLPEKGTPEYEEWVKSHQKA-- 761
QY 774 VFIRITTSQFQTLIGISLIEILSKHSSDEVYLGQRPDPRWTSDAKALDAFKRFGSRLVQ 833
Db 762 -YLRTITSQFQTLVDSLVEILSRHASDEVYLGQRDNP-HWTSDSKALQAFQKFGNKLKE 819
QY 834 IENRIKTWNSPDLKRNKGPVEMPYMLYPNTSDVTGEKAGLTAMGIPNSISI 887
Db 820 IEELKRNKNDQSLNRLGPVQLPYTLHPN-----SEGLTCRGIPNSISI 865
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RESULT 8

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LOX3 SOYBN STANDARD; PRT; 857 AA.
AC P09186; Q39838;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Seed lipoxigenase-3 (EC 1.13.11.12) (L-3).
GN LOX1.3 OR LOX3.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RA Yenofsky R.L., Fine M., Liu C.;
RT "Isolation and characterization of a soybean (Glycine max)
RT lipoxigenase-3 gene."
RL Mol. Gen. Genet. 211:215-222 (1988).
RN [2]
RP REVISIONS.
RA Yenofsky R.L.;
RL Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF ASN-713.
RC STRAIN=cv. Provar;
RX MEDLINE=95092758; PubMed=7999759;
RA Kramer J.A., Johnson K.R., Dunham W.R., Sands R.H., Funk M.O. Jr.;
RT "Position 713 is critical for catalysis but not iron binding in
RT soybean lipoxigenase 3."
RL Biochemistry 33:15017-15022 (1994).
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RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RC STRAIN=cv. Provar;
RX MEDLINE=97440646; PubMed=9294864;
RA Skrzypczak-Jankun E., Amzel L.M., Kroa B.A., Funk M.O. Jr.;
RT "Structure of soybean lipoxigenase L3 and a comparison with its
RT L1 isoenzyme."
RL Proteins 29:15-31 (1997).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RC STRAIN=cv. Provar;
RX MEDLINE=99119225; PubMed=9922163;
RA Pham C., Jankun J., Skrzypczak-Jankun E., Flowers R.A., Funk M.O. Jr.;
RT "Structural and thermochemical characterization of lipoxigenase-
RT catechol complexes."
RL Biochemistry 37:17952-17957 (1998).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RC STRAIN=cv. Provar;
RX MEDLINE=21547069; PubMed=11686682;
RA Skrzypczak-Jankun E., Bross R.A., Carroll R.T., Dunham W.R.,
RA Funk M.O. Jr.;
RT "Three-dimensional structure of a purple lipoxigenase."
RL J. Am. Chem. Soc. 123:10814-10820 (2001).
CC -1- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF
CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND
CC DEVELOPMENT, PEST RESISTANCE, AND SENESCENCE OR RESPONSES TO
CC WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING
CC A CIS, CIS-1,4-PENTADIENE STRUCTURE.
CC -1- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
CC hydroperoxyoctadeca-9,11-dienoate.
CC -1- COFACTOR: Iron, one atom tightly bound per molecule.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- MISCELLANEOUS: SOYBEAN CONTAINS AT LEAST 4 DISTINCT ISOENZYMES,
CC L-1, L-2, L-3A AND L-3B IN DRY SEEDS, AND AT LEAST TWO DISTINCT
CC ISOZYMES IN THE HYPOCOTYL/RADICLE REGION OF THE SEEDLING STEM.
CC -1- SIMILARITY: Belongs to the lipoxigenase family.
CC -1- SIMILARITY: Contains 1 PLAT domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X06928; CAA30016.1; --
CC EMBL; X13302; CAA31664.1; ALT_SEQ.
CC EMBL; U50081; AAB41272.1; --
CC PDB; 1LNH; 29-MAR-96.
CC PDB; 1NO3; 03-JUN-03.
CC PDB; 1IK3; 14-NOV-01.
CC InterPro; IPR000907; Lipoxigenase.
CC InterPro; IPR001024; Lipoxigenase_LH2.
CC InterPro; IPR008976; PLAT_LH2.
CC Pfam; PF00305; lipoxigenase; 1.
CC Pfam; PF01477; PLAT; 1.
CC PRINTS; PR00087; LIPOXYGENASE.
CC SMART; SM00308; LH2; 1.
CC PROSITE; PS00711; LIPOXYGENASE_1; 1.
CC PROSITE; PS00081; LIPOXYGENASE_2; 1.
CC PROSITE; PS50095; PLAT; 1.
CC Oxidoreductase; Dioxigenase; Iron; Multigene family; 3D-structure.
KW DOMAIN 38 163
FT METAL 518 518 IRON.
FT METAL 523 523 IRON.
FT METAL 709 709 IRON.
FT METAL 857 857 IRON.
FT VARIANT 25 25 H -> D (IN STRAIN PROVAV).
FT VARIANT 57 57 P -> S (IN STRAIN PROVAV).
FT VARIANT 112 112 L -> P (IN STRAIN PROVAV).
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FT VARIANT 201 201
FT VARIANT 382 382
FT VARIANT 428 428
FT VARIANT 630 630
FT MUTAGEN 713 713
FT MUTAGEN 713 713
FT STRAND 11 20
FT HELIX 21 24
FT TURN 26 28
FT HELIX 29 31
FT HELIX 50 54
FT TURN 55 57
FT STRAND 58 64
FT STRAND 76 81
FT STRAND 85 86
FT TURN 89 91
FT TURN 94 95
FT STRAND 96 104
FT TURN 107 109
FT STRAND 112 119
FT STRAND 125 133
FT STRAND 141 149
FT STRAND 151 151
FT HELIX 152 154
FT STRAND 159 162
FT TURN 169 171
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FT HELIX 217 219
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FT TURN 391 394
FT STRAND 398 398
FT TURN 403 404
FT HELIX 415 420
FT TURN 421 422
FT STRAND 424 428
FT TURN 431 433
FT HELIX 434 440
FT TURN 441 444
FT STRAND 450 456
FT TURN 458 459
FT STRAND 462 472
FT TURN 474 475
FT STRAND 481 486
FT HELIX 492 520
FT TURN 521 522

V -> I (IN STRAIN PROVAR).
E -> D (IN STRAIN PROVAR).
G -> D (IN STRAIN PROVAR).
A -> T (IN STRAIN PROVAR).
N->A,S: NO LOSS OF IRON-BINDING; LOSS OF CATALYTIC ACTIVITY.
N->H: NO LOSS OF IRON-BINDING; NO CHANGE IN CATALYTIC ACTIVITY.

FT HELIX 523 536
FT TURN 539 540
FT HELIX 542 547
FT HELIX 548 551
FT TURN 552 553
FT HELIX 554 564
FT TURN 565 565
FT TURN 568 569
FT HELIX 571 575
FT TURN 577 578
FT HELIX 579 581
FT HELIX 582 590
FT TURN 591 592
FT HELIX 595 598
FT HELIX 600 606
FT TURN 607 608
FT STRAND 610 612
FT TURN 614 615
FT TURN 617 618
FT STRAND 620 622
FT TURN 625 626
FT HELIX 628 649
FT TURN 650 651
FT HELIX 655 659

Query Match 52.4%; Score 2473.5; DB 1; Length 857;
Best Local Similarity 55.3%; Pred. No. 7.4e-171;
Matches 487; Conservative 133; Mismatches 212; Indels 49; Gaps 14;

QY 22 KIRGTVRVLKKEVLDVG-----DFNASLLDGVHRIIGWDDGVAFQLVSATAA 68
Db 11 KIKGTVVLMRKNVLSVTSVGGIIGQGLDLVGSTLDTLTAFLG--RPVSLQLISATKA 68
QY 69 DPSNGGRGKVGKAAHLEEAUVSLKSTADGETVYRVSEFWDSEQIGIPGAVLVRNLQHAEPF 128
Db 69 DAN--GKGLGKATFLEGIITSPTLGAGQSAFKINFENDGSGILGAFYIKNFMQTEFF 126
QY 129 LKTLTLEGVPGKGTVVVFVANSWYYPHKLYSQERIFFANDTYLPSKMPAALVPYRQDELKI 188
Db 127 LVSLTLEDIPNHGSIHFVCNSWIYNAKLFKSDRIFFANQYLPSETPAPLVKYREELHN 186
QY 189 LRGGDNPQYQEHDRVYRYDYNDLGDPPDKGEEHARPIILGGSQEHYPYPRRCRTGRHPTKK 248
Db 187 LRG-DGTGERKEWERVYDYVDVNDLGDPPDKGENHARPVLGNDTFPPYPRGRGTGRKPTRK 245
QY 249 DPNSESLFLNLNIYVPRDERFGLKMSDFLGYSLKTIEAVLPTLGTFFVD--DTPKEF 306
Db 246 DPNSESR----SNDVYLPRDEAFGLKSSDFLTGYGLKSVSQNVLPLLQSAFDLNFIFREF 301
QY 307 DSFEDILGLYELGPEAPNPNLIAIRKKIPSEFLRSILPNGSHDHPKMPLEPNVIXSDVL 366
Db 302 DSFDEVHGLYGGIKLPTD-IISKIS---PLPVLKEIFRTDG-EQALKFPPPKVIQVS-- 354
QY 367 KKAPEEFKFWRTDEEFARETLAGVNPVIIKRLTEFFPAKSTLDPQYGDHTSKITEAHIRH 426
Db 355 -----KSAWMTDEEFAREMLAGVNPNLIRCLKEFPFRSKLDSQVYGDHTSQITKEHLEP 408
QY 427 NMGLSVQNALRNKRLFILDHHDFMPYLDENELEGNFIYASRTLLFLKDDGTLKPLAI 486
Db 409 NLEGLTVDEAIONKRLFLLGHHDPIMPYLRNRINATSK-AYATRTILFLKNDGTLRPLAI 467
QY 487 ELSLPHPDGQQRGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSSAWHQLISHWLNTHAVIE 546
Db 468 ELSLPHPDGQDQSGAFSQVFLPADEGVESIIWLLAKAYVVVNDSCYHQLVSHWLNTHAVVE 527
QY 547 PFVIATNRQLSVVHPVHKLSPHYRDTLNLINALARQTLINAGGVFERTVFPKVALGMSA 606
Db 528 PFIATNRHLSVVHPYIKLLHPHYRDTMNINGLARLSLVNDGGVIEQTFWLWGRYSVEMSA 587
QY 607 DVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPAVDGLVWIAERWVKEY 666
Db 588 VVYKDWVFTDQALPADLIKRGWAIEDPSCPHGIRLVIEDYPYAVDGLGLEIWDIAIKTWVHEY 647

Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.

[3]
SEQUENCE OF 426-752 FROM N.A.
Start W.G., Ma Y., Polacco J.C., Hildebrand D.F., Freyer G.A.,
Altschuler M.;
"Two soybean seed lipoxigenase nulls accumulate reduced levels of
lipoxigenase transcripts.";
Plant Mol. Biol. 7:11-23(1986).
[4]
MUTAGENESIS OF SOME HISTIDINE RESIDUES, AND REVISIONS TO 479-482.
MEDLINE=92232702; PubMed=1567851;
Steczko J., Doncho G.P., Clemens J.C., Dixon J.E., Axelrod B.;
"Conserved histidine residues in soybean lipoxigenase: functional
consequences of their replacement.";
Biochemistry 31:4053-4057(1992).
[5]
MUTAGENESIS OF SOME HISTIDINE RESIDUES.
MEDLINE=92360013; PubMed=1497657;
Steczko J., Axelrod B.;
"Identification of the iron-binding histidine residues in soybean
lipoxigenase L-1.";
Biochem. Biophys. Res. Commun. 186:686-689(1992).
[6]
ACTIVE SITE, AND IRON LIGANDS.
MEDLINE=93298753; PubMed=8518276;
Minor W., Steczko J., Bolin J.T., Otwinowski Z., Axelrod B.;
"Crystallographic determination of the active site iron and its
ligands in soybean lipoxigenase L-1.";
Biochemistry 32:6320-6323(1993).
[7]
X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
MEDLINE=93276267; PubMed=8502991;
Boyington J.C., Gaffney B.J., Anzel L.M.;
"The three-dimensional structure of an arachidonic acid
15-lipoxigenase.";
Science 260:1482-1486(1993).
[8]
X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS).
MEDLINE=96346062; PubMed=8718858;
Minor W., Steczko J., Stec B., Otwinowski Z., Bolin J.T., Walter R.,
Axelrod B.;
"Crystal structure of soybean lipoxigenase L-1 at 1.4-A resolution.";
Biochemistry 35:10687-10701(1996).
[9]
X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS).
MEDLINE=21305677; PubMed=11412104;
Tomchick D.R., Phan P., Cymborowski M., Minor W., Holman T.R.;
"Structural and functional characterization of second-coordination
sphere mutants of soybean lipoxigenase-1.";
Biochemistry 40:7509-7517(2001).
-!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF
DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND
DEVELOPMENT, PEST RESISTANCE, AND SENSITIVE OR RESPONSES TO
WOUNDING. WITH LINOLEATE AS SUBSTRATE, L-1 SHOWS A PREFERENCE FOR
CARBON 13 AS THE SITE FOR HYDROPEROXIDATION (IN CONTRAST TO L-2
AND L-3, WHICH UTILIZE EITHER CARBON 9 OR 13).
-!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
hydroperoxyoctadeca-9,11-dienoate.
-!- COFACTOR: Iron, one atom tightly bound per molecule.
-!- SUBUNIT: Monomer.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- INDUCTION: THE HYDROPEROXIDE PRODUCT SERVES TO ACTIVATE THE
RESTING ENZYME. THE ACTIVATION IS ACCOMPANIED BY THE OXIDATION
OF FE(2+)/ENTADIENE STRUCTURE. L-1 PREFERS ANIONIC SUBSTRATE.
-!- MISCELLANEOUS: SOYBEAN CONTAINS AT LEAST 4 DISTINCT ISOENZYMES,
L-1, L-2, L-3A AND L-3B IN DRY SEEDS, AND AT LEAST TWO DISTINCT
ISOZYMES IN THE HYPOCOTYL/RADICLE REGION OF THE SEEDLING STEM.
-!- SIMILARITY: Belongs to the lipoxigenase family.
-!- SIMILARITY: Contains 1 PLAT domain.
-!- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN AT POSITIONS 663
TO 697 DUE TO A FRAMESHIFT.

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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

EMBL; J02795; AAA33986.1; -
EMBL; X67304; CAA47717.1; ALT_FRAME.
PIR; S25064; DASYL2.
PDB; 1F8N; 04-JUL-01.
PDB; 1FGM; 24-OCT-01.
PDB; 1FGO; 04-JUL-01.
PDB; 1FGQ; 04-JUL-01.
PDB; 1FGR; 18-JUL-01.
PDB; 1FGT; 04-JUL-01.
PDB; 1YGE; 23-JUL-97.
PDB; 2SBL; 27-FEB-95.
InterPro; IPR000907; Lipoxigenase.
InterPro; IPR001024; Lipoxigenase_LH2.
InterPro; IPR008976; PLAT_LH2.
Pfam; PF00305; lipoxigenase; 1.
Pfam; PF01477; PLAT; 1.
PRINTS; PR00087; LIPOXYGENASE.
SMART; SM00308; LH2; 1.
PROSITE; PS00711; LIPOXYGENASE_1; 1.
PROSITE; PS00081; LIPOXYGENASE_2; 1.
PROSITE; PS50095; PLAT; 1.
Oxidoreductase; Dioxigenase; Iron; Multigene family; 3D-structure.
FT DOMAIN 16 145 PLAT.
FT METAL 499 499 IRON.
FT METAL 504 504 IRON.
FT METAL 690 690 IRON.
FT METAL 839 839 IRON.
FT MUTAGEN 494 494 H->Q: 37% OF WILD-TYPE ACTIVITY.
FT MUTAGEN 494 494 H->S: 8% OF WILD-TYPE ACTIVITY.
FT MUTAGEN 499 499 H->Q: INACTIVE.
FT MUTAGEN 504 504 H->Q,S: INACTIVE.
FT MUTAGEN 517 517 H->Q: 33% OF WILD-TYPE ACTIVITY.
FT MUTAGEN 522 522 H->Q: 1% OF WILD-TYPE ACTIVITY.
FT MUTAGEN 531 531 H->Q: 20% OF WILD-TYPE ACTIVITY.
FT MUTAGEN 690 690 H->Q: INACTIVE.
FT CONFLICT 426 427 AK -> RN (IN REF. 3).
FT CONFLICT 558 560 LPS -> AL (IN REF. 3).
FT CONFLICT 572 574 KNW -> EL (IN REF. 3).
FT CONFLICT 641 641 N -> P (IN REF. 3).
FT CONFLICT 741 748 KLPTLSL -> SCRLSLAV (IN REF. 3).
FT STRAND 7 16
FT HELIX 17 19
FT TURN 20 20
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FT TURN 37 38
FT STRAND 40 50
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FT STRAND 62 63
FT STRAND 66 68
FT TURN 76 77
FT STRAND 79 86
FT HELIX 89 91
FT STRAND 94 101
FT STRAND 107 114
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FT HELIX 159 170
FT TURN 179 180
FT STRAND 186 187

FT	STRAND	189	189
FT	TURN	195	197
FT	HELIX	199	201
FT	STRAND	206	206
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FT	TURN	229	230
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FT	TURN	311	312
FT	HELIX	313	316
FT	STRAND	318	319
FT	STRAND	324	326
FT	HELIX	331	333
FT	HELIX	339	341
FT	HELIX	343	352
FT	TURN	356	357
FT	STRAND	360	361
FT	HELIX	373	376
Query Match 49.9%; Score 2355.5; DB 1; Length 839;			
Best Local Similarity 53.4%; Pred. No. 2.5e-162;			
Matches 465; Conservative 140; Mismatches 223; Indels 43; Gaps 14;			
QY	22	KIRGTVRLVKKEVLDVGDNFNASLLDGVHRIILGWDDGVAFLQVLSATAADPSNGRGKVGKA	81
DB	7	KIKGTVLMKNELEVP-DGSAVDNLNAFLG--RSVSLQLISATKADAH--GKGKVGKD	61
QY	82	AHLEAVVSLKSTADGETVYRVSPFEWDESQGIPIGAVLVRLNQLCHAEFFLKTLLTLEGVPGKG	141
DB	62	TFLEGINTSLPTLGAGESAFNIHFEPWDSMGIPGAFYIKNYMQVEFFLKSLLTLEAISNQG	121
QY	142	TVFVANSWYVPHKLYSQERIFFANDTYLPSKMPAALVPYRQDELKILRGDDNPGPYQEH	201
DB	122	TIRFVCNSWYNTKLYKSVRIFFANHTYVPSETPAPLVSVREELKSLRG-NGIGERKEY	180
QY	202	DRVYRYDYNDLGDGPKGEEHARPILGSGQEHPPRRCRIGRHTKDPNSESER--LFL	259
DB	181	DRYDYDVNDLGNPKSEKLARPVLGSSSTFPYPRRGRTGRGPTVTDNTEKQGEVF--	238
QY	260	NLNIYVPRDERFGLKMSDFLGYSLKTIIEAVLPTLGTFFD--DTPKEFDSFEDILGLYE	317
DB	239	----YVPRDENLGLKSKDALEIGTKSLSQIVQPAFESAFDLKSTPIEFHSPQDVHDLYE	294
QY	318	LGPEAPNPLIAEIRKKIPSEFLRSILPNSGSHDHPKMPLPNVIKSDVLKKAPEKPGWR	377
DB	295	GGIKLPRDVISTILPLPVIKELYRT-----DGHILKFPQPHVVQVS-----QSAWM	341
QY	378	TDEEFARETLAGVNPVLIKRLTEFFPAKSTLDPROYGDHTSKITEAHIRHNMGGLSVQNAL	437
DB	342	TDEEFAREMAGVNPVIRGLEEFPPKSNLDPAYIGDQSSKITADSL--DLDDGYTMDAL	399
QY	438	RNKRLFILDHHDHMPYLDEINELEGNFIIYASRTLLFLKDDGTLKPLAIELSLPHDPGQQ	497
DB	400	GSRRLFLMDYHDIFMPYVRQINQLNSAKTYATRTILFLREDGTLKPVAIELSPLHSGADL	459
QY	498	RGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSAWHQLISHWLNTHAVIEPFIATNRQLS	557
DB	460	SAAVSQVVLPAKEGVESTIWLAKAYVIVNDSCYHQLMSHWLNTHAAMEPFIATHRHLS	519
QY	558	VHPVHKLSPHYRDTLNLINARQTLINAGGVFERTVTPAKYALGMSADVYKSWNFNEQ	617

DB	520	VLHPIYKLLTPHYRNNMNLARQSLINANGIIETTFLPKSYSEMSSAVYKMWVFTDQ	579
QY	618	ALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVIWMAIERWVKEYLDIYYPNDGEL	677
DB	580	ALPADLIKRGVAIKDPSTPHGVRLIEDYPYAADGLEIWAIAIKTWQEVPLYAYRDDDV	639
QY	678	QRDVELQAWKEVREEAHGDLKDRDWPRMDTVQQLARACTIILWVASALHAAVNFQYVP	737
DB	640	KNDSELOHWKKEAVEKGHGDLKDKPWPFKLQTLLEDLVEVCLIIIIWIASALHAAVNFQYVP	699
QY	738	YAGYLPNRPRTASRRPMPEPGSHDYKGLGAGQKEADMVFIRITTSQFOTILGISLIELSK	797
DB	700	YGGLIMNRPRTASRRLLPEKGTPEYEMINNHEKA---YLRTITSKLPTLSLSVIELST	756
QY	798	HSSDEVILGQDEPDRWTSDAKALDAFKRFGSRLVQIENRIKTMNDSPDLK-NRKGPVEM	856
DB	757	HASDEVILGQDNP-HWTSDSKALQAFQKFGNKLKEIEKLVRRNNDPSLOGNRLGPVQL	815
QY	857	PYMLLYPNTSDVTGEKAEGLTAMGIPNSISI	887
DB	816	PYTLLYPSSE-----EGLTFRGIPNSISI	839

RESULT 15

LOX1_LENCU.

ID LOX1_LENCU STANDARD; PRT; 866 AA.

AC P384I4;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Lipoxigenase (EC 1.13.11.12).

GN LOX1.1

OS Lens culinaris (Lentil).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Lens.

OX NCBI_TaxID=3864;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Seedling shoot;

RX MEDLINE=94162308; PubMed=8117753;

RA Hilbers M.P., Rossi A., Finazzi-Agro A., Veldink G.A.,

RA Vliegenthart J.F.G.;

RT "The primary structure of a lipoxigenase from the shoots of etiolated

RT lentil seedlings derived from its cDNA."

RL Biochim. Biophys. Acta 1211:239-242(1994).

CC -1- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF

CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND

CC DEVELOPMENT, PEST RESISTANCE, AND SENESCENCE OR RESPONSES TO

CC WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING

CC A CIS, CIS-1,4-PENTADIENE STRUCTURE.

CC -1- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-

CC hydroperoxyoctadeca-9,11-dienoate.

CC -1- COFACTOR: Iron, one atom tightly bound per molecule.

CC -1- SUBUNIT: Monomer (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- SIMILARITY: Belongs to the lipoxigenase family.

CC -1- SIMILARITY: Contains 1 PLAT domain.

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CC EMBL; X71344; CAA50483.1; -.

DR HSP; P08170; 2SBL.

DR InterPro; IPR000907; Lipoxigenase.

DR InterPro; IPR001024; Lipoxigenase_LH2.

DR InterPro; IPR008976; PLAT_LH2.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 06:32:08 ; Search time 78 Seconds
(without alignments)
3588.008 Million cell updates/sec

Title: US-10-059-909-16
Perfect score: 4723
Sequence: 1 MFVHGVDRLTGKNKEAWSE.....VTGEKAEGLTAMGIPNSISI 887

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3703	78.4	877	10 Q8S6D6	Q8S6D6 oryza sativ
2	3369.5	71.3	876	10 Q42846	Q42846 hordeum vul
3	3052	64.6	864	10 Q8W0V2	Q8W0V2 zea mays (m
4	3049	64.6	864	10 Q9AXG8	Q9AXG8 zea mays (m
5	3023	64.0	866	10 Q8S6D9	Q8S6D9 oryza sativ
6	3018.5	63.9	863	10 Q8S6E8	Q8S6E8 oryza sativ
7	2960	62.7	870	10 Q7Y1F4	Q7Y1F4 oryza sativ
8	2958	62.6	873	10 Q9LKL4	Q9LKL4 zea mays (m
9	2860	60.6	864	10 Q42847	Q42847 hordeum vul
10	2768	58.6	862	10 Q9LEA9	Q9LEA9 prunus dulc
11	2754.5	58.3	873	10 Q93YI8	Q93YI8 corylus ave
12	2739	58.0	884	10 Q7X9G5	Q7X9G5 fragaria an
13	2730	57.8	862	10 Q8W4X6	Q8W4X6 prunus dulc
14	2724.5	57.7	862	10 Q43800	Q43800 nicotiana t
15	2714.5	57.5	865	10 Q93WZ2	Q93WZ2 gossypium h
16	2701.5	57.2	862	10 Q9FTI7	Q9FTI7 lycopersico

17	2695.5	57.1	862	10 Q43191	Q43191 solanum tub
18	2630.5	55.7	857	10 Q41238	Q41238 solanum tub
19	2626.5	55.6	860	10 Q43190	Q43190 solanum tub
20	2624.5	55.6	857	10 Q8GV02	Q8GV02 brassica na
21	2605	55.2	861	10 Q24379	Q24379 solanum tub
22	2604	55.1	861	10 Q9SC16	Q9SC16 solanum tub
23	2603	55.1	844	10 Q9SAP1	Q9SAP1 solanum tub
24	2603	55.1	861	10 Q43189	Q43189 solanum tub
25	2601	55.1	864	10 Q49150	Q49150 solanum tub
26	2599	55.0	861	10 Q22507	Q22507 solanum tub
27	2598.5	55.0	854	10 Q9FNX7	Q9FNX7 arabidopsis
28	2596.5	55.0	881	10 Q9M463	Q9M463 cucumis sat
29	2592	54.9	861	10 Q22508	Q22508 solanum tub
30	2578.5	54.6	882	10 Q9LUW0	Q9LUW0 arabidopsis
31	2552	54.0	858	10 Q9ZU05	Q9ZU05 persea amer
32	2511	53.2	859	10 Q42873	Q42873 lycopersico
33	2498.5	52.9	876	10 Q41430	Q41430 solanum tub
34	2478.5	52.5	866	10 Q39870	Q39870 glycine max
35	2433	51.5	877	10 Q42705	Q42705 cucumis sat
36	2426.5	51.4	878	10 Q42704	Q42704 cucumis sat
37	2423.5	51.3	878	10 Q42710	Q42710 cucumis sat
38	2420	51.2	865	10 Q24320	Q24320 phaseolus v
39	2394	50.7	853	10 Q43446	Q43446 glycine max
40	2393.5	50.7	856	10 Q42780	Q42780 glycine max
41	2393.5	50.7	868	10 Q24470	Q24470 pisum sativ
42	2389	50.6	859	10 Q43440	Q43440 glycine max
43	2385.5	50.5	858	10 Q04919	Q04919 vicia faba
44	2353.5	49.8	856	10 Q9M684	Q9M684 phaseolus v
45	2353	49.8	839	10 Q43438	Q43438 glycine max

ALIGNMENTS

RESULT 1
Q8S6D6 PRELIMINARY; PRT; 877 AA.
AC Q8S6D6;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Putative lipoxigenase.
GN OSJNB0024B16.26.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
RA Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
RA Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G.,
RA VanAken S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbush J.,
RA Salzberg S.L., White O., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSJNB0024B16 genomic sequence."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AC093017; AAL83623.1; -.
DR Gramene; Q8S6D6; -.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016165; F:lipoxigenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR01024; Lipoxigenase_LH2.
DR InterPro; IPR08976; PLAT_LH2.
DR Pfam; PF00305; lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS50095; PLAT; 1.

SQ SEQUENCE 877 AA; 98697 MW; 984EBB61CDD9B7C CRC64;

Query Match 78.4%; Score 3703; DB 10; Length 877;
Best Local Similarity 78.9%; Pred. No. 6.5e-276;
Matches 697; Conservative 71; Mismatches 105; Indels 10; Gaps 3;

QY 5 GVADRLTGKKEAWSEGKIRGTAVLVKKEVLDVGDVFNASLLDGVHRIILGWDDGVAFQLVS 64
DB 5 GFFDRLTGRNKEAWKEGRIRGTAVLVKKEVLDVGDVFNASLLDGVHRIILGWDDGVAFQLVS 64

QY 65 ATAADPSNGRGKVGKAAHLEEAVALSKSTADGETVYRVSEFDESQGIPIGAVLVNLOH 124
DB 65 ATARDPSNGRGKVGKAAHLEEAVALSKSTADGETVYRVSEFDESQGIPIGAVLVNLOH 124

QY 125 AEFFLKTLLTLEGVPGKGTAVLVKKEVLDVGDVFNASLLDGVHRIILGWDDGVAFQLVS 184
DB 125 AEFFLKTLLTLEGVPGKGTAVLVKKEVLDVGDVFNASLLDGVHRIILGWDDGVAFQLVS 184

QY 185 ELKILRGDDNPGPYQEHDRVYRYDYNLDGDPDKGEEHARPIILGSGQEHPPRRCTGRH 244
DB 185 ELNILRGDDNPGPYQEHDRVYRYDYNLDGDPDKGEEHARPIILGSGQEHPPRRCTGRH 244

QY 245 PTKKOPNSRSRLFLNLNIYVPRDERFGLKMSDFLGSYLKTIIEAVLPTLGTVDVTPK 304
DB 245 PTKKOPNSRSRLFLNLNIYVPRDERFGLKMSDFLGSYLKTIIEAVLPTLGTVDVTPK 304

QY 305 EFDSFQDIMEYEGGLKVANASALAEIKRVPFELIKSLLPVAG-DQVLKLPVHVKED 363
DB 305 EFDSFQDIMEYEGGLKVANASALAEIKRVPFELIKSLLPVAG-DQVLKLPVHVKED 363

QY 365 VLKKAPEKFGWRTDEEFARETLAGVNPVVIKRLTEFPKSTLDPKQYGDHSTKITEAHI 424
DB 365 VLKKAPEKFGWRTDEEFARETLAGVNPVVIKRLTEFPKSTLDPKQYGDHSTKITEAHI 424

QY 425 RHNMGGLSVONALRNKRLFILDDHDFMPYLDIENEGNFYASRTLLFLKDDGTLKPL 484
DB 425 RHNMGGLSVONALRNKRLFILDDHDFMPYLDIENEGNFYASRTLLFLKDDGTLKPL 484

QY 485 AIELSLPHDPGQORGAVSKVYTPAHTGVEGHVWOLAKAYACVNDASAWHOLISHWLNTHAV 544
DB 485 AIELSLPHDPGQORGAVSKVYTPAHTGVEGHVWOLAKAYACVNDASAWHOLISHWLNTHAV 544

QY 545 IEPFVIATNRQLSVVHPVHKLSPHYRDTLNINALARQTLINAGGVFERTVFPKAYALGM 604
DB 545 IEPFVIATNRQLSVVHPVHKLSPHYRDTLNINALARQTLINAGGVFERTVFPKAYALGM 604

QY 605 SADVYKWNFNEQALPADLVKRGVAVPDQSSPYGVRLIKDYPYAVDGLVIWAIERWVK 664
DB 605 SADVYKWNFNEQALPADLVKRGVAVPDQSSPYGVRLIKDYPYAVDGLVIWAIERWVK 664

QY 665 EYLDIYPNDGELQDVELQAWKEVREBAHGDLDKORDWPRMDTVQOLARACTIILWA 724
DB 665 EYLDIYPNDGELQDVELQAWKEVREBAHGDLDKORDWPRMDTVQOLARACTIILWA 724

QY 725 SALHAAVNFQYQYAGFLPNRPTASRRPMPEPGSHDYKLGAGQKEADMVFIRITTSQFQ 784
DB 725 SALHAAVNFQYQYAGFLPNRPTASRRPMPEPGSHDYKLGAGQKEADMVFIRITTSQFQ 784

QY 785 TILGISLIEILSKHSSDEVYLGQDEPDRWTSADAKALDAFKRGSRLVQIENRIKTMNDS 844
DB 785 TILGISLIEILSKHSSDEVYLGQDEPDRWTSADAKALDAFKRGSRLVQIENRIKTMNDS 844

QY 845 PDLKNRKGPVEMPMYLLYPNTSDVTGEKAEGLTAMGIPNSISI 887
DB 845 PDLKNRKGPVEMPMYLLYPNTSDVTGEKAEGLTAMGIPNSISI 887

RESULT 2
Q42846 PRELIMINARY; PRT: 876 AA.
AC Q42846;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Lipoxigenase (EC 1.13.11.12).
GN LOXB.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Triumph;
RX MEDLINE=99308521; PubMed=10380814;
RA van Mechelen J.R., Schuurink R.C., Smits M., Graner A., Douma A.C.,
RA Sedee N.J., Schmitt N.F., Valk B.E.;
RT "Molecular characterization of two lipoxigenases from barley."
RL Plant Mol. Biol. 39:1283-1298(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Triumph;
RA Van Mechelen J.R.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; L37359; AAB60715.1; -.
DR PIR; T05943; T05943.
DR KSP; P08170; 2SBL.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016165; F:lipoxigenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR01024; Lipoxigenase_LH2.
DR InterPro; IPR008976; PLAT_LH2.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS00095; PLAT; 1.
KW Oxidoreductase.
SQ SEQUENCE 876 AA; 98978 MW; 5EF5B57FF641B56B CRC64;

Query Match 71.3%; Score 3369.5; DB 10; Length 876;
Best Local Similarity 72.5%; Pred. No. 3.1e-250;
Matches 648; Conservative 87; Mismatches 134; Indels 25; Gaps 9;

QY 1 MFHGVADRLTGKKEAWSEGKIRGTAVLVKKEVLDVGDVFNASLLDGVHRIILGWDDGVAF 60
DB 1 MLLHGLVDELDTGKKEAWKEGRIRGTAVLVKSDVLDLGDHNASLLDGVHRIILGWDDGVAF 60

QY 61 QLVSATAADPSNGRGKVGKAAHLEEAVALSKSTADGETVYRVSEFDESQGIPIGAVLV 120
DB 61 RLVSATAADPSNGRGKVGKAAHLEEAVALSKSTADGETVYRVSEFDESQGIPIGAVLV 120

QY 121 NLQHAFFLKTLLTLEGVPGKGTAVLVKKEVLDVGDVFNASLLDGVHRIILGWDDGVAF 180
DB 121 NLYRSEYLLKTLLTLEGVPGKGTAVLVKKEVLDVGDVFNASLLDGVHRIILGWDDGVAF 180

QY 181 YRQDELKILRGDDNPGPYQEHDRVYRYDYNLDGDPDKGEEHARPIILGSGQEHPPRRCR 240
DB 181 YRQDELKILRGDDNPGPYQEHDRVYRYDYNLDGDPDKGEEHARPIILGSGQEHPPRRCR 240

QY 241 TGRHPTKIDPNSERSL---FLNLNIYVPRDERFGLKMSDFLGSYLKTIIEAVLPTLG 296
DB 241 TGRHPTKIDPNSERSL---FLNLNIYVPRDERFGLKMSDFLGSYLKTIIEAVLPTLG 296

QY 297 TFVDDTPKEFDSFQDIYNLVYDGLKVPDNLQHLKELKKN-SLOPIKSLAVAGDDDS--KLA 351
DB 297 TFVDDTPKEFDSFQDIYNLVYDGLKVPDNLQHLKELKKN-SLOPIKSLAVAGDDDS--KLA 351

QY 357 LPNVIKSDVLKKAPEKFGWRTDEEFARETLAGVNPVVIKRLTEFPKSTLDPKQYGDHT 416
DB 357 LPNVIKSDVLKKAPEKFGWRTDEEFARETLAGVNPVVIKRLTEFPKSTLDPKQYGDHT 416


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Db 465 LAIELSLPHIEGNLTSAKSKVHTPASSGIESVWVQAKAYAVAVNDGSMHQLISHWLNTHA 524
QY 544 VIEPFVIATNRQLSVVHPVHKLSPHYRDTLNALARQTLINAGGVFERTVFPKAYALG 603
Db 525 VMEPFVIATNRQLSVTHPVYKLLQPHYRDTMTINALARQTLINAGGVFERTVFPKGHALA 584
QY 604 MSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLIKDYPIYAVDGLVWAIERWV 663
Db 585 MSSAVYKWNFTQGLPDDLKRGIAIKDPSSPKVKLLIKDYPIYATDGLAIWQAIEQWV 644
QY 664 KEYLDIYPNDGELQRDVELQAWWKEVREZAHGDLKDRDWPRMDTVQQLARACTTIWV 723
Db 645 TEYCAIYPNDGVQLQDVELQAWWKEVREVGHDLDADWPKMQSLPELTACTTIWI 704
QY 724 ASALHAAVNFGQYPIYAGYALPNRPTASRRPMPPEPGSHDYKKLGAGQKEADMFIRITISQF 783
Db 705 ASALHAAVNFGQYPIYAGYALPNRPTISRRPMPPEPGSKYEYTEL--DENPEKFFIRITISQF 761
QY 784 QTILGISLIEILSKHSSDEVYLGQDEPRDWTSDAKALDAFKRFGSLVQIENRIKTMND 843
Db 762 QTILGSLIEILSKHSADEIYLGQDTPPE-WTSDPKALEAFKFRSRLVLEIESKVLNMNK 820
QY 844 SPDLKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887
Db 821 DPLLKNRVGPANFPYTLMPFNTSDNKG-AAEGITARGIPNSISI 863
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RESULT 7
QY1F4
ID QY1F4 PRELIMINARY; PRT; 870 AA.
AC QY1F4;
DT 01-OCT-2003 (TremBLrel. 25, Created)
DT 01-OCT-2003 (TremBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Lipoxigenase L-2; lipoxigenase.
GN OSJNBA0057G07.15.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA Overton II L.L., Teitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA Padrosh D.W., Tallon L.J., Koo H., Zismann V., Heiao J., Blunt S.,
RA Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSJNBA0057G07 genomic sequence.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC117988; AAP44707.1; -.
SQ SEQUENCE 870 AA; 97183 MW; 63344755867DA6E0 CRC64;
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Query Match 62.7%; Score 2960; DB 10; Length 870;
Best Local Similarity 63.9%; Pred. No. 1.1e-218;
Matches 569; Conservative 112; Mismatches 178; Indels 32; Gaps 14;

QY 5 GVADRLTGKKEAWSEGKIRGTVELVKKEVLVDVGFNASELLDGVHRIILGWDDGVAFQLVS 64
Db 4 GIIIGLGTG-NKNA----RLKGSVLMRKNALDINDFGATVIDGISEFLG--RGVTCQLVS 56

QY 65 ATAADPSNGRGKVGKAAHLEAAVSLKSTADGETVTVYVSFEWD-ESQIGPGLVLRNLQ 123
Db 57 SSLVDPNNGNRGRVGTASLEQWLTSLPSTTGESKFGVTFEWEKMGIPGAIIVKNNH 116
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QY 124 HAEFFLKTILTEGVPGKGTVVVANSWVPHKLYSOERIFFEANDTYLPSKMPAALVPYRQ 183
Db 117 AAEFFLKTITLDNVPGHGVVANSWIYPASKYRNVRFESNDTSLPSKMPAALKPYRD 176
QY 184 DELKILRGDDNPGPYQEHDRVRYDYNDLGDPKGEHARPILGGSQEHYPYPRCRTGR 243
Db 177 DELNLRGDDQOGPYQEHDRVRYDYNDLGEPSG--NPRVLGSPDRPYPRGRGTGR 234
QY 244 HPTKXDPNSESRLFLNLNTIYVPRDERFGLHKMSDFLGYSLKTIIEAVLPTLGTFFDDTP 303
Db 235 KPTKTPTAESRLSLE-NIYVPRDERFGLHKMADFGLYSIKALVDGIVPAIRTVDLTP 293
QY 304 KEFDSFEDILGLYELGPEAPNPLIAEIRKKIPSEFLRSILPNGSHDHPKMLPNNVIKS 363
Db 294 GEFSFKDILKLYEGGLKLPISIPALEELRKRFPQLVKDLIPAGG-DYLLKLPNPHVIRE 352
QY 364 DVLKKAPEFKFGRWRTDEEFAREETLAGVNPVVIKRLTEFFPAKSTLDPRQYGDHSTKITEAH 423
Db 353 D--KKA-----WMTDDEFAREILAGVNPVVIARLTFFPRSRRLDPARYGDQTSITAAH 404
QY 424 IRHNMGGLSVQNALRNKRLFIIDHHDHFMPIYLDINELEGNFYIASRTLLFLKDDGTLPK 483
Db 405 VERGLEGLTVQQAIDGNLLVVDHHDHFMPIYLLDINSDDNFYIATRTLLFLRGDGTLP 464
QY 484 LAIELSLPH-PDGOQORGAVSKVYTPAHTG-----VEGHVWQLAKAYACVNDSAWHQLIS 536
Db 465 LAIELSLPHLQDDGLITARSTVYTPAARGGTGAGAVEWVWQLAKAYVNVNDYCHQLIS 524
QY 537 HWLNTHAVIEPFVIATNRQLSVVHPVHKLSPHYRDTLNALARQTLINAGGVFERTV 596
Db 525 HWLNTHAVMEPFVIATNRQLSVVHPVHKLSPHYRDTLNALARQTLINAGGVFERTV 584
QY 597 PAKYALGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLIKDYPIYAVDGLVIW 656
Db 585 PRKHALLAMSSAFYKOWSFADQALPDDLKVRGVAVPDQSPYKVRLLIEDIYPIYANDGLAVW 644
QY 657 WAIERWVKEYLDIYPNDGELQRDVELQAWWKEVREZAHGDLKDRDWPRMDTVQQLARA 716
Db 645 HAEQWATEYLAIYYPNDGVQLQDAELQAWWKEVREVGHDIKDATWWPEMKTVAELVKA 704
QY 717 CTTIIWVASALHAAVNFGQYPIYAGYALPNRPTASRRPMPPEPGSHDYKKLGAGQKEADMFVI 776
Db 705 CATIIWGSALHAAVNFGQYPIYAGYALPNRPSVSRPMPPEPGTKEYDELA---RDPEKVFV 761
QY 777 RTITSQFQTLIGISLIEILSKHSSDEVYLGQDEPRDWTSDAKALDAFKRFGSLVQIEN 836
Db 762 RTITKQQAIVGISLIEILSKHSSDEVYLGQDTPPE-WTSDAKALEAFKFRFGARLTEIES 820
QY 837 RIKTMNDSPDLKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887
Db 821 RVVAMNKPDRKRNVRGPTNFPYTLTYPNTSDLKGD-AAGLSARGIPNSISI 870
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RESULT 8
Q9LKL4
ID Q9LKL4 PRELIMINARY; PRT; 873 AA.
AC Q9LKL4;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Lipoxigenase (EC 1.13.11.12).
GN LOX.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seedling;
RA Han O., Choi E., Kim Y., Kim E.;
RT "Methyl Jasmonate Induces Biphasic Accumulation of Lipoxigenase mRNA
in Maize Seedlings.";
```

RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF271894; AAF76207.1; -.
DR HSSP; P08170; 2SBL.

DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016165; F:lipoxygenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR000907; Lipoxygenase.
DR InterPro; IPR001024; Lipoxygenase_LH2.
DR InterPro; IPR008976; PLAT_LH2.

DR Pfam; PF00305; lipoxygenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PRO0087; LIPOXYGENASE.

DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS50095; PLAT; 1.

KW Oxidoreductase.

SQ SEQUENCE 873 AA; 98163 MW; 1E70C3C1898CA979 CRC64;

Query Match 62.6%; Score 2958; DB 10; Length 873;
Best Local Similarity 63.6%; Pred. No. 1.5e-218;
Matches 561; Conservative 115; Mismatches 180; Indels 26; Gaps 11;

QY 10 LTGKNKEAWSEGKIRGTVRLVKKEV--LDVGDFNASLLDGVHRIILGWDGVAFLVLSATA 67
DB 14 LTGSNKNA----HLKGNVVLVRKTVLGLDVTSLGSLLDGIGEFGL--RGVTCQLISSTV 67

QY 68 ADPSNGGRGKVGKAAHLEAAVSLKSTADGETVTVRSFEWD-ESQIGPGLVLRNLQHA 126
DB 68 VDPNNGNRGKLGAEASLEQWLLNPPPLSSSENQPRVTFDWEVEKQIGIPGAIIVKNNHASE 127

QY 127 FFLKTLTLEGVPGKGTVVVFVANSWVYPHKLYSQRIFFANDTYLPSKMPAALVPRQDEL 186
DB 128 FFLKTTITLNDVPGHGTIVFVANSWIYQSKYRNRVFFSNDTYLPSQMPAALKPYRDDEL 187

QY 187 KILRGDDNPGPYQEHDRVYRYDYNDLGDGPKGEEHARPILGSGQEHYPRRCRTGRHPT 246
DB 188 RNLRGDDQGGPYQEHDRVYRYDYNDLGLPDSG--NPRPVLGTKELPYRRCRTGRKPT 245

QY 247 KKDPSNLSRLFLNLNIYVPRDERFGLKMSDFLGYSLKTIIEAVLPTLGTFFVDDTPKEF 306
DB 246 KSDPNSRLTLVDGVDVYVPRDERFGHIKSDFGYAIKALVNAVIPAIRTYVDLSPGEF 305

QY 307 DSFEDILGLYELGPEAPNPLIAEIRKKIPSEFLRSILPNSGSHDPLKMPPLPNVKSVDL 366
DB 306 DSFKDIMKLYEGGIQLPKIPALEDLRKQFPLEVKDVLVPGG-DYLLKLPMPQIIEK-- 362

QY 367 KKAPEFKGWRTEEFARBTLAGVNPVIRKLTFFPAKSTLDPKQYGDHTSKITEAHIRH 426
DB 363 -----KTGWTDEEFGREILAGVNPMLVKRLTEFPFPRSSLDPSKYGDHTSTIREADLEN 416

QY 427 NMGGLSVQNALRNKRLFIIDHHDHFMYPYLDINELEGNFIYASRTLLFLKDDGTLKPLAI 486
DB 417 KLEGLTVQALHGNRLVILDHHDNFMFPFLVRVNSLEGNFIYATRTVLELRGDGTLVPVAI 476

QY 487 ELSLPHPDGQQRGAVSKVYTP-AHTGVEGHVWQLAKAYACVNDSAWHQLISHWLNTHAVI 545
DB 477 ELSLPELRDGLTTAKSTVYTPKSTTGAEAWVWHLAKAYANVDYCHQLISHWLNTHAVM 536

QY 546 EPFVIATNRQLSVVHPVKLLSPHYRDTLNLNALARQTLINAGGVFERTVFPKAYALGMS 605
DB 537 EPFVIATNRQLSVTHPVHKLPLPHYRDTWNINSNARQMLVNAAGGIFETVFPQYAFEMS 596

QY 606 ADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVWIAERWKE 665
DB 597 SVIYKDNWTFEQALPDDLKRGMAVADPSSPYKVRLLVEDYPIYASDGLAIWHAIEQWTE 656

QY 666 YLDIYYPNDGELQORDVELQAWKKEVREEAHGDLKDRDWPRMDTVQOLARACTIIVWAS 725
DB 657 YLAVIYPNDGVLRADVELQAWKKEAREVGHADLKDAPWPKMQTVLAEVLKACTIIVIAS 716

QY 726 ALHAAVNFQYPYAGVLPNRPASRRPMPEPGSHDYKKLGAQKEADMVFIRTTITSQFOT 785

Db 717 ALHAAVNFQYPYAGVLPNRPVSVRKMPAPGSDYAEAL---ERKPEKVFVRTITTSQFQA 773
QY 786 ILGISLIEILSKHSSDEVYLGORDEPDRWTSDAKALDAFKRFGSRLVQIENRIKTMNDSP 845
Db 774 LVGISLLEILSSHSSDEVYLGQDTEKE-WTSDAKAQAFKRFGARLIEIKRVVTMNAADP 832
QY 846 DLKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887
Db 833 RLKNRNGPAEFPTLLYPNTSDTKGD-AAGITAKGIPNSISI 873

RESULT 9
Q42847

ID Q42847 PRELIMINARY; PRT; 864 AA.

AC Q42847;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Lipoxygenase 2 (EC 1.13.11.12).

GN LOXC.

OS Hordeum vulgare (Barley).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;

OC Triticeae; Hordeum.

OX NCBI_TaxID=4513;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99308521; PubMed=10380814;

RA van Mechelen J.R.; Schuurink R.C.; Smits M.; Graner A.; Douma A.C.;

RA Sedee N.J.; Schmitt N.F.; Valk B.E.;

RT "Molecular characterization of two lipoxygenases from barley.";

RL Plant Mol. Biol. 39:1283-1298(1999).

RN [2]

RP SEQUENCE FROM N.A.

RA Van Mechelen J.R.;

RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; L37358; AAB70865.1; -.

DR PIR; T05945; T05945.

DR HSSP; P08170; 2SBL.

DR GO; GO:0005506; F:iron ion binding; IEA.

DR GO; GO:0016165; F:lipoxygenase activity; IEA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR000907; Lipoxygenase.

DR InterPro; IPR001024; Lipoxygenase_LH2.

DR InterPro; IPR008976; PLAT_LH2.

DR Pfam; PF00305; lipoxygenase; 1.

DR Pfam; PF01477; PLAT; 1.

DR PRINTS; PRO0087; LIPOXYGENASE..

DR SMART; SM00308; LH2; 1.

DR PROSITE; PS00711; LIPOXYGENASE_1; 1.

DR PROSITE; PS50095; PLAT; 1.

KW Oxidoreductase.

SQ SEQUENCE 864 AA; 96748 MW; A15DA282FB7F9973 CRC64;

Query Match 60.6%; Score 2860; DB 10; Length 864;
Best Local Similarity 62.2%; Pred. No. 5.3e-211;
Matches 551; Conservative 117; Mismatches 188; Indels 30; Gaps 11;

QY 5 GVADRLLTGKNKEAWSEGKIRGTVRLVKKEVLDVGDFNASLLDGVHRIILGWDGVAFLVLS 64
DB 6 GIVSDLTGGIRGA----HLKGSVVLNRKNALDFNDFGAHVMGVTTELLG--RGVTCQLIS 59

QY 65 ATAADPSNGGRGKVGKAAHLEAAV--SLKSTADGETVTVRSFEWD-ESQIGPGLVLRN 121
DB 60 STNVDHNNNGGRGKVGAEANLEQWLLPTNLPFTTGENKFAVTFDWSVDKLGVPGAIIVKN 119

QY 122 LQHAFFLKTLLTEGVPGKGTVVVFVANSWVYPHKLYSQRIFFANDTYLPSKMPAALVPI 181
DB 120 NHASEFFLKTITLNDVPGRGTVIVFVANSWVYQAKYRNRVFFANDTYLPHQMPAALKPY 179

QY 182 RQDELKILRGDDNPGPYQEHDRVYRYDYNDLGDGPKGEEHARPILGSGQEHYPRRCRT 241

Db 180 RDELRLNRGDDQGPYLDHDRVYRDVYNDLGD-----SRDLVGGSKDLPYPRRCRT 232

QY 242 GRHPTKDPNSESRLFLNLNIYVPRDERFGHLKMSDFLGYSIKTIIIEAVLPTLTGTFVDD 301

Db 233 GRKPSDSKPDHESRLLLLVQNVYVLRDELFGHLKQSDLLGLYTLKGWLDGIIILAIRFYVDL 292

QY 302 TPKEFDSFEDILGLYELGPEAPNPLIAEIRKIPSEFLRSILPNSGSHDHPKMLPNVI 361

Db 293 SPGEFDSFADILKLYEGGIKLPNIPALEEVRKRFPLQVLKDLIPKGG-DFLLLKLPKEII 351

QY 362 KSDVLKKAPEKFGWRTDEEFARETLAGVNPVIRKLTTEFFAKSTLDPKQYGDHSHKITE 421

Db 352 KVD--QKA-----WMTDEEFAREMLAGVNPMMIKRLTEFFPKSTLDPKQYGDHSHKITE 403

QY 422 AHIRHNMGGLSVQNALRNKRLFLDHHDFMPYLDIENELEGNFIYASRTLLFLKDDGTL 481

Db 404 EHVAKSLEGLTVQALAGNRLYIVDQHDNLMPLFLIDINNLDASFVYATRTLLFLRGDGT 463

QY 482 KPLAIELSLPHDPDQQRGAVSKVYTPAHTGVEGHVWQAKAYACVNDSSAWHQLISHWLNT 541

Db 464 APVAIELSSPLTQELTTAKSAVYTPQHAGVEGWQAKAYASVNDYGHQHLISHWLNT 523

QY 542 HAVIEPFVIATNRQLSVVHPVHKLSPHYRDTLNINALARQTLINAGGVFERTVFPKAYA 601

Db 524 HAVMEPFVIATNRQLSVTHPVYKLLHPHYRDTMNINARAGLLINAGGVIENTVFPKHKA 583

QY 602 LGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLIKDYPYAVDGLVIWAIER 661

Db 584 MPMSMVYKHWNFTEQALPADLIRKGMVAVEDASSPHKVRLLIKDYPYATDGLAVWDAIEQ 643

QY 662 WVKEYLDIYVNDGELQRDVELQAWKVEVEEAHGDLDKDRDWPRMDTVQQLARACTII 721

Db 644 WVS DYLTIIYVNDGVLGQDVELQAWKVEVEVGHGDLKDAAWPKMTVAELIKACATII 703

QY 722 WVASALHAAVNFQGPYAGYLPNRPASRRPMPPEPGSHDYKLGAGQKEADMVFIRITTS 781

Db 704 WTGSALHAAVNFQGPYSGYHPNKPASRRPMPVQGSSEYAEI---ERDPEKAFIRITTS 760

QY 782 QFQTILGISLIEILSKHSSDEVYLGQRDWTSDAKALDAFKRFGSRLVQIENRIKTM 841

Db 761 QFHALVGISLIEILSKHSSDEVYLGQHDTP-AWTSDAKALEAFKRFGAKLEGIEKQVVAM 819

QY 842 NDSPDLKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887

Db 820 NSDPQLKNRCTGPAKFPYMLLYPNTSDHTGQ-AEGLTARGIPNSISI 864

RESULT 10

Q9LEA9 PRELIMINARY; PRT; 862 AA.

AC Q9LEA9;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Lipoxxygenase (EC 1.13.11.12).

GN LOX.

OS Prunus dulcis (Almond) (Prunus amygdalus).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.

OX NCBI TaxID=3755;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Scorza verde;

RX MEDLINE=21153257; PubMed=11231304;

RA Mita G., Gallo A., Greco V., Zaslura C., Casey R., Zacheo G.,

RA Santino A.;

RT "Molecular cloning and biochemical characterization of a lipoxxygenase

RT in almond (Prunus dulcis) seed.";

RL Eur. J. Biochem. 268:1500-1507(2001).

DR EMBL; AJ404331; CAB94852.1; --

DR HSSP; P08170; 2SBL.

DR GO; GO:0005506; F:iron ion binding; IEA.

DR GO; GO:0016165; F:lipoxxygenase activity; IEA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR000907; Lipoxxygenase.

DR InterPro; IPR001024; Lipoxxygenase_LH2.

DR InterPro; IPR008976; PLAT_LH2.

DR Pfam; PF00305; lipoxxygenase; 1.

DR Pfam; PF01477; PLAT; 1.

DR PRINTS; PR00087; LIPOXYGENASE.

DR SMART; SM00308; LH2; 1.

DR PROSITE; PS00711; LIPOXYGENASE_1; 1.

DR PROSITE; PS00081; LIPOXYGENASE_2; 1.

DR PROSITE; PS50095; PLAT; 1.

KW Oxidoreductase.

SQ SEQUENCE 862 AA; 98019 MW; EE078F795F435626 CRC64;

Query Match 58.6%; Score 2768; DB 10; Length 862;

Best Local Similarity 59.9%; Pred. No. 6.5e-204;

Matches 531; Conservative 125; Mismatches 202; Indels 28; Gaps 11;

QY 4 HGVADRLTGKKNKEAWSEGKIRGTVRIVKKEVLVDGDFNASLIDGVHRIILGWDDGVAFQLV 63

Db 3 HNLFDKITGQEQNGKNSRKIKGTIVLMKKNVLDNFENASVLDVRVHELLG--QGVSLQLI 60

QY 64 SATAADPSNGRGKVGKAAHLEEAUVSLKSTADGETVYRVSPFEWDESGQIGAVLVRNLQ 123

Db 61 SADHGDSNGFGKGLGEPAYLEDITITPLTIGDSAYKVTDFWEEIEIGVPGAILIKNH 120

QY 124 HAEFFLKTTLLEGVPGKGTIVFVANSWVYPHKLYSQERIFFANDTYLPSKMPAALVPYRQ 183

Db 121 HSEFFLKTITLEDVPRGRVHFCVNSWVYPAEKYTKDRVFFVYKTFLPSETPLPLRKVRE 180

QY 184 DELKILRGDDNPGPYQEHDRVRYDYNDLGDPKGEEHARPILGSGQEHYPYPRRCRTGR 243

Db 181 EELVHLRG-DKGELQEWDRVDYAYNDLGNPKPKYAPPTLGGSEYYPYPRRCRTGR 239

QY 244 HPTKKDPNSESRL-FLNLNIYVPRDERFGHLKMSDFLGYSIKTIIIEAVLPTLTGTFVDDT 302

Db 240 PPTKTDNSSESRIPLMSLNIYVPRDERFGHLKLSDFLAYALKSIVQFIRPELEALFDKT 299

QY 303 PKEFDSFEDILGLYELGPEAPNPLIAEIRKIPSEFLRSIL-PNGSHDHPKMLPNVI 361

Db 300 PNEFDSLEDLVLYKGGIPLPEG-LLKDIGDNIPAEMLKEIFRTDGA--QLLRFPMPQVI 356

QY 362 KSDVLKKAPEKFGWRTDEEFARETLAGVNPVIRKLTTEFFAKSTLDPKQYGDHSHKITE 421

Db 357 EED-----KSAWRTDEEFAREMLAGVNPVIRKLTTEFFAKSTLDPKQYGDHSHKITE 408

QY 422 AHIRHNMGGLSVQNALRNKRLFLDHHDFMPYLDIENELEGNFIYASRTLLFLKDDGTL 481

Db 409 QDIGNKLDGLTVHEALKQNKLFILDHHDALMPYLRRINS-TSNKIYASRTVFLKSDGTL 467

QY 482 KPLAIELSLPHDPDQQRGAVSKVYTPAHTGVEGHVWQAKAYACVNDSSAWHQLISHWLNT 541

Db 468 KPLVIELSLPHDPDQGFGRISKVYTPAEEGVEGSIWQAKAYAVAVNDSSGYHQLISHWLNT 527

QY 542 HAVIEPFVIATNRQLSVVHPVHKLSPHYRDTLNINALARQTLINAGGVFERTVFPKAYA 601

Db 528 HAVCEPVVIATNRQLSVVHPPIYKLLHPHYRDTMNINAFARQILINAGGILETTVFPARYA 587

QY 602 LGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLIKDYPYAVDGLVIWAIER 661

Db 588 MEMSSVYKDWVFTQALPADLIRNREGVAVKDNANSPHGLRLIDDDYPYAVDGLIWFPAIKT 647

QY 662 WVKEYLDIYVNDGELQRDVELQAWKVEVEEAHGDLDKDRDWPRMDTVQQLARACTII 721

Db 648 WVEDYCSFYKTDIIQKQIELQSWKWKELVEEGHGDKKDEPWPKVQTRKOLVETCTII 707

QY 722 WVASALHAAVNFQGPYAGYLPNRPASRRPMPPEPGSHDYKLGAGQKEADMVFIRITTS 781

Db 708 WTASALHAAVNFQGPYAGYLPNRPITISRKFMPEKGTPEYKEL---ESSPDTVFLKTTA 764

QY 782 QFQTILGISLIEILSKHSSDEVYLGQRDWTSDAKALDAFKRFGSRLVQIENRIKTM 841

Db	765	QLQTVLGIALLIEILSRHSTDEVYLGQDRTPE-WTADTEPLKAFKFGSKLAEIEDRITRM	823
Qy	842	NDSPDLKNRKGPVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI	887
Db	824	NNDEKLNKRVGPVMPYTLFLPTSEG-----GLTGRGIPNSVSI	862
RESULT 11			
Qy	93YI8	PRELIMINARY; PRT; 873 AA.	
AC	Q93YI8;		
DT	01-DEC-2001	(TrEMBLrel. 19, Created)	
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	
DE	Lipoxxygenase	(EC 1.13.11.12).	
GN	LOX.		
OS	Corylus avellana	(European hazel).	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;		
OC	eurosid I; Fagales; Betulaceae; Corylus.		
OX	NCBI_TaxID=13451;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=cv. Mortarella;		
RA	Santino A., Gallo A., Fasano P., Zasiura C., Casey R., Mita G.;		
RT	"Isolation and characterisation of a hazelnut (Corylus avellana)		
RT	lipoxxygenase gene."		
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AJ417975; CAD10740.1; -		
DR	GO; GO:0005506; F:iron ion binding; IEA.		
DR	GO; GO:0016165; F:lipoxxygenase activity; IEA.		
DR	GO; GO:0016491; F:oxidoreductase activity; IEA.		
DR	GO; GO:0006118; P:electron transport; IEA.		
DR	InterPro; IPR000907; Lipoxxygenase.		
DR	InterPro; IPR001024; Lipoxxygenase_LH2.		
DR	InterPro; IPR008976; PLAT_LH2.		
DR	Pfam; PF00305; lipoxxygenase; 1.		
DR	Pfam; PF01477; PLAT; 1.		
DR	PRINTS; PRO0087; LIPOXYGENASE.		
DR	SMART; SM00308; LH2; 1.		
DR	PROSITE; PS00711; LIPOXYGENASE_1; 1.		
DR	PROSITE; PS00081; LIPOXYGENASE_2; 1.		
DR	PROSITE; PS50095; PLAT; 1.		
KW	Oxidoreductase.		
SQ	SEQUENCE 873 AA; 99012 MW; 3ED67B939767B43C CRC64;		
Query Match			
Best Local Similarity 58.3%; Score 2754.5; DB 10; Length 873;			
Matches 530; Conservative 119; Mismatches 192; Indels 27; Gaps 11;			
Qy	22	KIRGTVRLVKKKEVLDVGFNASLLDGVHRIWGWDGVAFLVSAATAADPS-NGGRGKVGK	80
Db	31	KIEGSVLMKKNVLDNFNFNASVLDRVHELLG--QKVSLLQISAVNADPSANGLOGLGN	88
Qy	81	AAHLEAVVSLKSTADGETVYRVVSFEWDESQGIPIGAVLVRNLQHAFFFLKTLTLEGVPGK	140
Db	89	LAYLEHWISTITPLIAGESAFKVTDFDWEEDIAIPGAFILRNHHSEFYLSLTLEDVPGQ	148
Qy	141	GTVVVFVANSWVPHKLYSQERIFPANDTYLPSKMPAALVPYRQDELKILRGDDNPGPYQE	200
Db	149	GRIHFVNCNSWVYPADQYKQDRVFFSNKTFPLNETGPLLKYREEELVNLRG-DGTGELQE	207
Qy	201	HDRVRYDYNDLGDPPDKGEEHARPIILGGSQEHPPRRCRTGRHPTKKDPNSESRLFL-259	
Db	208	WDRVYDYAYNDLGNPDKGPVVRPVLGGSSEYPPRRGRTGRPPSETDNSESRLMLLK	267
Qy	260	NLNIYVPRDERFGLKMSDFLGYSLKTIIEAVLPTLGTFFVDVDDTPKEFDSFEDILGLYELG	319
Db	268	SLNIYVPRDERFGLKMSDFLAYALKAVAQFLKPELESFDSFSEFDSIQDVLKLYEGG	327
Qy	320	PEAPNNPLIAEIRKKIPSEHFLRSILPNGSHDHPKMLPLPNVIKSDVLKKAPEFKFGWRTD	379

Db	328	VKLDPG-LLQNIREDIPAEMLKEIFPT-EGEGLLKYMPQVIKED-----KSAWRTD	377
Qy	380	EEFAPETLAGVNPVVIKRLTEPPAKSTLDPROYGHTSKITEAHIRHNMGGSLVQNALRN	439
Db	378	EEFGREMLAGVNPVNIIRLQEPFPASKLDPKVYGDQASTITKEHIENNIDGLSDEAINK	437
Qy	440	KRLFIIDHHDHFMPLYLDEINELEGNFIYASRTLLFLKDDGTCLKPLAIELSLPHDPGQORG	499
Db	438	KKLFILDHDAIMPYLRRINSTSTK-TYASRTILFLKNDGTCLKPLVIELSLPHDPGQFG	496
Qy	500	AVSKVYTPAHTGVEGHVWQLAKAYACVNDSSAWHQLISHWLNTHAVIEPFFVIATNRQLSVV	559
Db	497	AISKVFTPAEEGVESIMWQLAKAYAVAVNDSGYHQLISHWLNTHAAIEPFFVIATNRQLSVL	556
Qy	560	HPVHKLLSPHYRDTLNINALARQTLINAGGVFERTVFPKAYALGMSADVYKSNFNEQAL	619
Db	557	HPIHKLHHPHFRDTMNIINAFARQILINAGGVLEATVFPKAYSMEMSSVVYKNWVPEQAL	616
Qy	620	PADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVIMWAIERWVKEYLDIYYPNDGELQR	679
Db	617	PADLTKRGMVAVKOSNSPHGDELLIEDYPIYAVDGLVIMWAIERWVKEYLDIYYPNDGELQR	676
Qy	680	DVELQAWWKEVREEAHGDLKDRDWWPRMDTVQQLARACTTIIWVASALHAAVNFQYPIYA	739
Db	677	DSELQSWWKEVREEAHGDLKDRDWWPRMDTVQQLARACTTIIWVASALHAAVNFQYPIYA	736
Qy	740	GYPNRPASRRPMPEGSHDYKKGAGQKEADMMVFIRTITSQFOTILGISLIELSKHS	799
Db	737	GYPNRPASRRPMPEGSHDYKKGAGQKEADMMVFIRTITSQFOTILGISLIELSKHS	793
Qy	800	SDEVYLGQRDEPDRWTSKALDAKDFKRGSRVQVQENRIKTMNDSPDLKNRKGPVEMPYM	859
Db	794	SDEVYLGQRDTPETWLDABALEAFERFGQKLAGIEDRIKMNNDKKWKNRVGPVKVPYT	852
Qy	860	LLYPNTSDVTGEKAEGLTAMGIPNSISI	887
Db	853	LLYPTSEG-----GITGKIPNSVSI	873
RESULT 12			
Qy	Q7X9G5	PRELIMINARY; PRT; 884 AA.	
AC	Q7X9G5;		
DT	01-OCT-2003	(TrEMBLrel. 25, Created)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last sequence update)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	
DE	Lipoxxygenase	(EC 1.13.11.12).	
GN	LOX.		
OS	Fragaria ananassa	(Strawberry).	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;		
OC	eurosid I; Rosales; Rosaceae; Rosoideae; Fragaria.		
OX	NCBI_TaxID=3747;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Fruit;		
RA	Leone A., Verdesca I., Mita G., Gerardi C., Zacheo G.;		
RT	"Isolation and characterization of a lipoxxygenase expressed in		
RT	strawberry fruit."		
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AJ578035; CAE17327.1; -		
KW	Oxidoreductase.		
SQ	SEQUENCE 884 AA; 100477 MW; F375D6C7A52E5B38 CRC64;		
Query Match			
Best Local Similarity 58.0%; Score 2739; DB 10; Length 884;			
Matches 526; Conservative 117; Mismatches 204; Indels 22; Gaps 9;			
Qy	22	KIRGTVRLVKKKEVLDVGFNASLLDGVHRIWGWDGVAFLVSAATAADPSNGG--RGKV	78
Db	35	KIRGTVRLVKKKEVLDVGFNASLLDGVHRIWGWDGVAFLVSAATAADPSNGG--RGKV	92
Qy	79	GKAAHLEAVVSLKSTADGETVYRVVSFEWDESQGIPIGAVLVRNLQHAFFFLKTLTLEGVP	138

Db 93 GKAYLEKWTATSLTAGTAFSASIDWDESMGVGALMITNHHHSQFLXTITLDDVL 152
QY 139 GKGTTFVANSWVYPKLYSQERIFFANDTYLPSKMPAALVPYRQDELKILRGDDNPGPY 198
Db 153 GHRVHFVANSWVYPKLYSQERIFFANDTYLPSKMPAALVPYRQDELKILRGDDNPGPY 211
QY 199 QEHDRVYDYNDLGDGPKGEEHARPILGSGQEHPPRRCRTRGRTGRKPTKTDHNSERLFL 258
Db 212 KEWDRVYDYNDLGDGPKGEEHARPILGSGQEHPPRRCRTRGRTGRKPTKTDHNSERLFL 271
QY 259 LNLNIYVPRDERFGLHKLMSDFLGYSKLTIIIEAVLPTLGTFTVDDTPKEFFSFEDILGLYEL 318
Db 272 LSLDIYVPRDERFGLHKLMSDFLGYSKLTIIIEAVLPTLGTFTVDDTPKEFFSFEDILGLYEL 331
QY 319 GEPAPNNPLIAEIRKKIPSEFLRSILPNSGSHDHPKPLPNVKSVDLKKAPFKFGWRT 378
Db 332 GIKLPNGPTLKLDRVWPWELKELL-RSDGERFLKFPMPDVIVKD-----KSAWRT 382
QY 379 DEEFARETLAGNPNVPIIKRLTEPPAKSTLDPKQGDHTSKITEAHIRHNMGGLSVQNALR 438
Db 383 DEEFARETLAGNPNVPIIKRLTEPPAKSTLDPKQGDHTSKITEAHIRHNMGGLSVQNALR 442
QY 439 NKRLFILDHDMFMPYLDEINELEGNFIYASRTLLFLKDDGTLKPLALIELSLPHPDGQQR 498
Db 443 SNRFFILDHDMFMPYLDEINELEGNFIYASRTLLFLKDDGTLKPLALIELSLPHPDGQQR 501
QY 499 GAVSKVYTPAHTGVEGHVQWAKAYACVNDSSAWHQLISHWLNTHAVIEPFIATNRQLSV 558
Db 502 GAVSKVYTPAHTGVEGHVQWAKAYACVNDSSAWHQLISHWLNTHAVIEPFIATNRQLSV 561
QY 559 VHPVHKLSPHYRDTLNALARQTLINAGGVFERTVFPKAYALGMSADVYKSWNFNEQA 618
Db 562 LHPVHKLSPHYRDTLNALARQTLINAGGVFERTVFPKAYALGMSADVYKSWNFNEQA 621
QY 619 LPADLVKRGVAVPDQSSPYGVRLIIKDYPAVADGLVWIAIERWVKEYLDIYYPNDGELQ 678
Db 622 LPADLVKRGVAVPDQSSPYGVRLIIKDYPAVADGLVWIAIERWVKEYLDIYYPNDGELQ 681
QY 679 RDVELQAWKVEEAAHGLKDRDWWPRMDTVQQLARACTTIIWVASALHAAVNFGQWY 738
Db 682 SDTELQKWEELRNEGHGDKAEPWPEMHTRAELIQSCTIIWVASALHAAVNFGQWY 741
QY 739 AGYLPNRPTASRRPMPGSHDYKLGAGQKEADWVFIRTTISQFOTILGISLIEILSKH 798
Db 742 AGYLPNRPTISRRFMPERTAEYAEI---ETNPDVAFKLTITSQLOTLLGVSLIEVLSRH 798
QY 799 SSDEVYLGQDEPDRTWTSDAKALDAFKRFGSLVQIENRIKTMNDSPDLKNRKGPVEMPY 858
Db 799 ATDEIYLGQDTPTE-WTSDGEALAAFGFGEKLEIEKRIETRTDRERLKNRVGPIKMPY 857
QY 859 MLLYPNTSDVTGEKAEGLTAMGIPNSISI 887
Db 858 TLLYPSTSDYSRE--GGLTKGIPNSISI 884

RESULT 13
Q8W4X6 PRELIMINARY; PRT; 862 AA.
ID Q8W4X6
AC Q8W4X6;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Lipoxigenase (EC 1.13.11.12).
GN LOX.
OS Prunus dulcis (Almond) (Prunus amygdalus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_Taxid=3755;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Scorza verde;

RA Mita G., Gallo A., Fasano P., Zasiura C., Casey R., Santino A.;
RT "Molecular cloning of an almond lipoxigenase gene expressed during the
RT early stages of seed development."
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ418043; CAD10779.2; -.
DR GO: GO:0005506; F:iron ion binding; IEA.
DR GO: GO:0016165; F:lipoxigenase activity; IEA.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR000907; Lipoxigenase.
DR InterPro: IPR001024; Lipoxigenase_LH2.
DR InterPro: IPR008976; PLAT_LH2.
DR Pfam: PF00305; lipoxigenase; 1.
DR Pfam: PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS00095; PLAT; 1.
KW Oxidoreductase.
SQ SEQUENCE 862 AA; 97751 MW; 3FAC9D205DCBC131 CRC64;

Query Match 57.8%; Score 2730; DB 10; Length 862;
Best Local Similarity 59.0%; Pred. No. S.Se-201;
Matches 523; Conservative 130; Mismatches 205; Indels 28; Gaps 11;
QY 4 HGVADRLTGKKEAWSEGKIRGTVRLVKKEVLVDGDFNASLLDGVHRLGWDGDAFQLV 63
Db 3 HNLFDKITGQEQNGKGRKIKGTIVLMKKNVLDNFNASVLDVRVHELLG--QGVSLQLI 60
QY 64 SATAADPSNGGRGKVGKAAHLEAAVSLKSTADGETVYRVSPFEWDESGQIPGAVLVRLN 123
Db 61 SADHGDSSENGFKGLGEPAYLEDWITITPLTVGDSAYNVTFDWEIEIGVPGAILKNNH 120
QY 124 HAEFFLKTTLTEGVPGKGTVVVANSWVYPKLYSQERIFFANDTYLPSKMPAALVPYRQ 183
Db 121 HSEFFLKTTLTEGVPGKGTVVVANSWVYPKLYSQERIFFANDTYLPSKMPAALVPYRQ 180
QY 184 DELKILRGDDNPGPYQEHDRVYDYNDLGDGPKGEEHARPILGSGQEHPPRRCRTRGR 243
Db 181 BELVHLRG-DGKGLQEWDRVYDYAYNDLGNPDGSKYARPTLGGSSGYPPPRGRTRGR 239
QY 244 HPTKDPNSESRL-FLNLNIYVPRDERFGLHKLMSDFLGYSKLTIIIEAVLPTLGTFTVDDT 302
Db 240 PATKDPNSESRIPLINSLNVYVPRDERFGLHKLMSDFLGYSKLTIIIEAVLPTLGTFTVDDT 299
QY 303 PKFDSFEDILGLYELGPEAPNNPLIAEIRKKIPSEFLRSIL-PNGSHDHPKMPPLNVI 361
Db 300 PNEFDSFEDVLKLYIGGIPLEG-LLKIDGDNIPAEMLKEIFRTDGA--QLLRFPMPQVI 356
QY 362 KSDVLKKAPEFKFGWRTDEEFARETLAGNPNVPIIKRLTEPPAKSTLDPKQGDHTSKITE 421
Db 357 EED-----KSAWRTDEEFARETLAGNPNVPIIKRLTEPPAKSTLDPKQGDHTSKITE 408
QY 422 AHIRHNMGGLSVQNALRNLKRLFILDHDMFMPYLDEINELEGNFIYASRTLLFLKDDGTL 481
Db 409 QDIGNKLDGLTVHEALKQNKLFILDHDMFMPYLDEINELEGNFIYASRTLLFLKDDGTL 467
QY 482 KPLAIELSLPHPDGQQRGAVSKVYTPAHTGVEGHVQWAKAYACVNDSSAWHQLISHWLN 541
Db 468 KPLVIELSLPHPDGQQRGAVSKVYTPAHTGVEGHVQWAKAYACVNDSSAWHQLISHWLN 527
QY 542 HAVIEPFIATNRQLSVVHVPVHKLSPHYRDTLNALARQTLINAGGVFERTVFPKAY 601
Db 528 HAVIEPFIATNRQLSVVHVPVHKLSPHYRDTLNALARQTLINAGGVFERTVFPKAY 587
QY 602 LGMSADVYKSWNFNEQAALPADLVKRGVAVPDQSSPYGVRLIIKDYPAVADGLVWIAIER 661
Db 588 MELSSVYKDWVTFTEQALPADLVKRGVAVPDQSSPYGVRLIIKDYPAVADGLVWIAIER 647
QY 662 WYKEYLDIYYPNDGELQDVELQAWKVEEAAHGLKDRDWWPRMDTVQQLARACTTII 721
Db 648 WVEDYCSFYKTTDDIIQEDTELQSWWKELVEEGHGDKKDEPWWPKMQTRDLVEITCTII 707

QY 722 WVASALHAAVNFQYYPYAGYLPNRPASRRPMPGSHDYKKGAGQKQKADWVFIRITTS 781
Db 708 WTASALHAAVNFQYYPYAGYLPNRPASRRPMPGSHDYKKGAGQKQKADWVFIRITTS 764
QY 782 QFQTILGISLIEILSKHSSDEVYLGQDEPDRWTSDAKALDAFKRFGSRLVQIENRIKTM 841
Db 765 QLQTVLGIALIEILSRHSTDEVYLGQDTPPE-WTADTEPLKAFDKFGRKLAKIEDRITSM 823
QY 842 NDSPDLKNRKGPVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
Db 824 NNDEKLKNRVGPVKMPYTLFPSTSG-----GLTGRGIPNSVSI 862

RESULT 14
Q43800
ID Q43800 PRELIMINARY; PRT; 862 AA.
AC Q43800;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Lipoxigenase (EC 1.13.11.12).
GN LOX1.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Wisconsin 38;
RA Veronesi C., Fournier J., Rickauer M., Marolda M.,
RA Esquerre-Tugaye M.T.;
RT "Nucleotide sequence of an elicitor-induced tobacco lipoxigenase cDNA
RT (PGR95-009).";
RL Plant Physiol. 108:1342-1342 (1995).
DR EMBL; X84040; CAA58859.1; --
DR PIR; S57964; S57964.
DR HSSP; P08170; 2SBL.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016165; F:lipoxigenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase_LH2.
DR InterPro; IPR008976; PLAT_LH2.
DR Pfam; PF00305; lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS50095; PLAT; 1.
KW Oxidoreductase.
SQ SEQUENCE 862 AA; 97552 MW; D2E7B8D323D5CE34 CRC64;

Query Match 57.7%; Score 2724.5; DB 10; Length 862;
Best Local Similarity 59.9%; Pred. No. 1.4e-200;
Matches 533; Conservative 111; Mismatches 215; Indels 31; Gaps 11;
QY 1 MFVHGVDRLTGKKEAWSEG-KIRGTVRLVKKEVLGVGDFNASLLDGVHRLGWDDGVA 59
Db 1 MFLKIVDAITGK-----DGKVKGTVLKKNVLDFTDINASVLDGVLEFLG--RRVS 53
QY 60 FQLVSATAADPSNGGRKVGKAARLEAAVSLKSTADGETVYRVSFWEDESQ-GIPGAVL 118
Db 54 LELISSVNADPANGLOGRKSKAAYLENLNLTNSTPIAAGESAFRTVFDWDEFGVPGAFI 113
QY 119 VRNLQHAEEFFLKTLLTEGVPGKGTWVFWANSVWYVPHKLYSQERIFFANDTYLPSKMPAAL 178
Db 114 IKNLHFSEFFLKSITLEDVFNHGKVFHVCNSVWYVANKYKSDRIFFANQAYLPSETDTL 173
QY 179 VPKRQDELKILRGDDNPGYQEHDRVRYDYNDLGDGPKGEEHARPILGSGQEHPPRR 238

Db 174 RKYRENELVTLRG-DGTGKLEEDRVYDYAYNDLGDGPKGQDLSRPPVLGSGSEYPYPRR 232
QY 239 CRTGRHPTKDPNSESRL-FLNLNLYVPRDERFGHLKMSDFGLYSKLTIEAVLPTLGT 297
Db 233 GRTGRKPTKDPNSESRIPLMSLDIYVPRDERFGHLKMSDFGLYSKLTIEAVLPTLGT 292
QY 298 FVDDTPKERDSFEDILGLYELGPEAPNNPLIAEIRKIPSEFLRSILPNSGSHDHPKMP 357
Db 293 LFDSTHNEFDSFEDVLKLYEGIKLPQGPILLKAITDSIPLEILKELL-RSDGEGLEFKYPT 351
QY 358 PNVIKSDVLKKAPEFKGWRTRDEEFARETLAGVNPVILKLTFFPAKSTLDRQYGDH 417
Db 352 PQVIQED-----KTAWRTDEEFGREMLAGVNPVILKLTFFPAKSTLDRQYGDH 403
QY 418 KITEAHIRHNMGGLSVQNALRNKLFILDDHDFHMPYLDEINELEGNFIYASRTLLFLKD 477
Db 404 TITREQIEDKLDGLTIDEAIKTNELFILNHHDIIMPYLRINTSTDTKTYASRTLLFLQD 463
QY 478 DGTLLPLAIELSLPHPDGQQRGAVSKVYTPAHTGVEGHVWOLAKAYACVNDSAWHQLISH 537
Db 464 NGTLKPSAIELSLPHPDGQQRGAVSKVYTPADQGVESIWOLAKAYAAVNDSGVHQLISH 523
QY 538 WLNTHAVIEPFFVIATNRQLSVVHPVHKLSPHYRDTLNALARQTLINAGGVFERTVFP 597
Db 524 WLNTHAIEPFFVIATNRQLSALHPIYKLLHPHFRETWNALARQTLINAGGVFERTVFP 583
QY 598 AKYALGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIAVDGLVIW 657
Db 584 AKYSMEMSAVYKDWVPEQALPDLIKRGVAVEDSSPLGIRLLIQDYPIAVDGLVIW 643
QY 658 AIERWVKYLDIYYPNDGELQDVELQAWKKEVREAHGDLKDRDWPRMDTVQQLARAC 717
Db 644 AIKSWVTEYCNYYKSDDAVQKDTLQAWKKEVREAHGDLKDRDWPRMDTVQQLARAC 703
QY 718 TTIIVASALHAAVNFQYYPYAGYLPNRPASRRPMPGSHDYKKGAGQKQKADWVFIR 777
Db 704 TITIIVASALHAAVNFQYYPYAGYLPNRPASRRPMPGSHDYKKGAGQKQKADWVFIR 760
QY 778 TITSQFQTLGISLIEILSKHSSDEVYLGQDEPDRWTSDAKALDAFKRFGSRLVQIENR 837
Db 761 TITPQLQTLGISLIEILSRHSSDTLYLGQRESPE-WTKDQEPLESAFARFGKLSIEDQ 819
QY 838 IKTMNDSPDLKNRKGPVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
Db 820 IMQMNVDKWKNRSGPVKVPYTLFPSTSG-----GLTGRGIPNSVSI 862

RESULT 15
Q93WZ2
ID Q93WZ2 PRELIMINARY; PRT; 865 AA.
AC Q93WZ2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Bacterial-induced lipoxigenase (EC 1.13.11.12).
GN LOX1.
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Reba B50; TISSUE=Cotyledon;
RA Assigbetse K., Jalloul A., Delannoy E., Marmey P., Daniel J.-F.,
RA Geiger J.-P., Nicole M.;
RT "Gossypium hirsutum bacterial-induced lipoxigenase mRNA."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF361893; AAK50778.2; --
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016165; F:lipoxigenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000907; Lipoxxygenase.
DR InterPro; IPR001024; Lipoxxygenase_LH2.
DR InterPro; IPR008976; PLAT_LH2.
DR Pfam; PF00305; lipoxxygenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS00095; PLAT; 1.
KW Oxidoreductase.
SQ SEQUENCE 865 AA; 98685 MW; 695CAC4E4A3BCE37 CRC64;

Query Match		57.5%;	Score 2714.5;	DB 10;	Length 865;
Best Local Similarity		60.7%;	Pred. No. 8.6e-200;		
Matches 537;		Conservative 102;	Mismatches 219;	Indels 27;	Gaps 11;
Qy	4	HGVADRLTGKNKEAWSEGKIRGTVRLVKKEVLDVGDVFNASLLDGVHRIILGWDGVAFLV	63		
Db	7	HAVAGDDNG-NKKMKPE-KIKGIVVMQKNVLDNFDFHASFLDGFHELLG--KRVSFQLI	62		
Qy	64	SATAADPSNGGRGKVGKAAHLEHAUVSLKSTADGETVYRVVSFEWDESQGI	123	PGAVLVRNLQ	
Db	63	SSQHVADNGLQGLKGEAYLEDDNSTETSAVAGESKFDVNFDFEEIIGLPGAFLIKNNH	122		
Qy	124	HAFFFLTKTLTLEGVPGKGTVVVANSWVYPHKLYSQERIFPANDTYLP	183	PSKMPAALVPYRQ	
Db	123	HSEFVLTTLTLEHVPGHGRFHFVNCNSWVYPDKKYDNRVFFTNKTYLP	182	PHDMPKPLLOYRE	
Qy	184	DELKILRGDDNPGPYQEHDRVYRYDYNDLGD	243	PKGEHARPILGGSQEHYP	RRCRTGR
Db	183	QELMTLRG-NGQELQEDWDRVYDYAYNDLGN	241	PKGEYARPVLG	SVKYPYRRGRTR
Qy	244	HPTKDPNSESRL-FLNLNLIYVPRDERFGLKMSDFLGYS	302	LTIIIEAVLPTLGT	FVDDT
Db	242	PPAKSDPKTESRIPLLMSLNIYVPRDERFGLKMSDFLAYALKSIVQFIV	301	PELQDLTDKT	
Qy	303	PKEFDSFEDILGLYELGPEADNPNLIAEIRKKIPSEFLRSILPNGSHDHP	362	PLKPLPNVIK	
Db	302	HNEFDSLEDVCLKYGGVCLKPSGPLDNIINNI	360	PLEMLKEIF-RTDEAQLLKFP	VPQVQIQ
Qy	363	SDVLKKAPEFKGWRTEDEFARETLAGVNPV	422	IIKRLTEFP	PAKSTLDP
Db	361	-----DSKTAWRTDEEFAREMLAGVNPV	412	IIRLQEFSPASNLDP	KVYGNQNSAITKE
Qy	423	HIRHNMGGLSVQNALRNKRLFLDHHDHMPYLDEINELEG	482	FIYASRTLLELKDDG	TLK
Db	413	HIEHNEGLTVEEALRTNRLFLDHHDSLMPYLRRINTTTK-TYASRT	471	IIILLRNDG	TLK
Qy	483	PLATELSLPHPDGQQRGAVSKVYTPAHTGVEGHVWQ	542	LAKAYACVND	SAWQHLSHWLNT
Db	472	PLVIELSLPHPNGDQLGAVNKVYTPAEHGVESIWQ	531	LAKAYAVAND	SGAHQLISHWLNT
Qy	543	AVIEPFVIATNRQLSVVHPVHKLLSPHYRDTLNIN	602	ALARQTLINAGGV	FERTVFP
Db	532	AAMEPFVIATNRQLSVVHPYIKLLYPHFRDTMN	591	INAFARQILINGG	GVLELTVP
Qy	603	GMSADVYKSNFNEQALPADLVKRGVAVPDQSSPY	662	GVRLLIKDY	PYAVDGLV
Db	592	EMSSVYKSNWLLDQALPRDLKRGVAVDDKSSPH	651	GLRLLIKDY	PYAVDGLV
Qy	663	VKEYLDIYYPNDGELQRDVELQAWKKEVREEAH	722	GLDKDRDWP	RMDTVQ
Db	652	VRDYCSFYKTDENVQQDPELQAWKKEVREEAH	711	GLDKDRDWP	RMDTVQ
Qy	723	VASALHAAVNFQGYPYAGYLPNRP	782	TASRRPMP	PEGSHDYK
Db	712	VASALHAAVNFQGYPYAGYLPNRP	768	TISRRFMP	KEGTPPEY
Qy	783	FQTLIGISLIEILSKHSSDEVYLGQRDEPDR	842	WTSDAKALDA	KRFGSRLV
Db	769	LQTLIGISLIEILSRHSSDEVYLGQRASPE	827	-WTSDETP	LAADFEG

Qy 843 DSPDLKQRKGPVEMPYMLLYPNTSDVTGEKABGLTAMGIPNSISI 887
Db 828 NDEQLKQRVGPVMPYTLTYTSEG-----GLTGKIPNSVSI 865
Search completed: March 23, 2004, 07:00:58
Job time : 83 secs